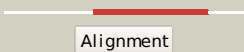

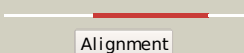

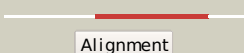

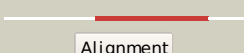



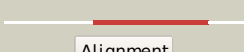

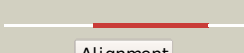

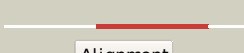









# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0CF81
Date	Thu Jan 5 11:31:39 GMT 2012
Unique Job ID	91c9a175ccce5fe4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1bcoa2</a>	 Alignment		99.7	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> mu transposase, core domain
2	<a href="#">c3f9kv</a>	 Alignment		99.7	17	<b>PDB header:</b> viral protein, recombination <b>Chain:</b> V: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> two domain fragment of hiv-2 integrase in complex with ledgf ibd
3	<a href="#">d1c0ma2</a>	 Alignment		99.6	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
4	<a href="#">c1c0mA</a>	 Alignment		99.6	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (integrase); <b>PDBTitle:</b> crystal structure of rsv two-domain integrase
5	<a href="#">d1asua</a>	 Alignment		99.6	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
6	<a href="#">c1bcoA</a>	 Alignment		99.5	15	<b>PDB header:</b> transposase <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriophage mu transposase; <b>PDBTitle:</b> bacteriophage mu transposase core domain
7	<a href="#">d1exqa</a>	 Alignment		99.5	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
8	<a href="#">c3nf9A</a>	 Alignment		99.5	20	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
9	<a href="#">c3hosA</a>	 Alignment		99.4	14	<b>PDB header:</b> transferase, dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element mariner, complete cds; <b>PDBTitle:</b> crystal structure of the mariner mos1 paired end complex with mg
10	<a href="#">c1ex4A</a>	 Alignment		99.4	23	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> hiv-1 integrase catalytic core and c-terminal domain
11	<a href="#">c3kksB</a>	 Alignment		99.4	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of catalytic core domain of biv integrase in crystal2 form ii

12	<a href="#">dlcxqa_</a>	Alignment		99.3	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
13	<a href="#">c1k6yB_</a>	Alignment		99.3	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of a two-domain fragment of hiv-1 integrase
14	<a href="#">dlc6va_</a>	Alignment		99.2	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
15	<a href="#">dlhyva_</a>	Alignment		99.2	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
16	<a href="#">c3hpgC_</a>	Alignment		99.2	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> visna virus integrase (residues 1-219) in complex with ledgf2 ibd: examples of open integrase dimer-dimer interfaces
17	<a href="#">c3l2tB_</a>	Alignment		99.0	16	<b>PDB header:</b> recombination/dna <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir)
18	<a href="#">c3dlrA_</a>	Alignment		98.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of the catalytic core domain from pfv2 integrase
19	<a href="#">c6paxA_</a>	Alignment		98.4	14	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein pax-6; <b>PDBTitle:</b> crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
20	<a href="#">c1u78A_</a>	Alignment		98.4	15	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element tc3 transposase; <b>PDBTitle:</b> structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
21	<a href="#">dlpdnc_</a>	Alignment	not modelled	98.2	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
22	<a href="#">c2k27A_</a>	Alignment	not modelled	97.7	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> paired box protein pax-8; <b>PDBTitle:</b> solution structure of human pax8 paired box domain
23	<a href="#">c2f7tA_</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mos1 transposase; <b>PDBTitle:</b> crystal structure of the catalytic domain of mos1 mariner2 transposase
24	<a href="#">c3f2kB_</a>	Alignment	not modelled	97.2	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histone-lysine n-methyltransferase setmar; <b>PDBTitle:</b> structure of the transposase domain of human histone-lysine2 n-methyltransferase setmar
25	<a href="#">c1hlvA_</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> major centromere autoantigen b; <b>PDBTitle:</b> crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
26	<a href="#">d2jn6a1</a>	Alignment	not modelled	96.5	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
27	<a href="#">c2elhA_</a>	Alignment	not modelled	96.3	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cgl11849-pa; <b>PDBTitle:</b> solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cgl11849-pa
28	<a href="#">c3hefB_</a>	Alignment	not modelled	95.8	9	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gene 1 protein; <b>PDBTitle:</b> crystal structure of the bacteriophage sf6 terminase small2 subunit

29	<a href="#">c1umqA</a>	Alignment	not modelled	95.7	11	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> photosynthetic apparatus regulatory protein; <b>PDBTitle:</b> 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	<a href="#">d1umqa</a>	Alignment	not modelled	95.7	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
31	<a href="#">d1k78a1</a>	Alignment	not modelled	95.3	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
32	<a href="#">d1ntca</a>	Alignment	not modelled	94.9	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
33	<a href="#">d6paxa1</a>	Alignment	not modelled	94.7	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
34	<a href="#">d1etxa</a>	Alignment	not modelled	94.5	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
35	<a href="#">d1fipa</a>	Alignment	not modelled	94.4	3	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
36	<a href="#">c3e7ID</a>	Alignment	not modelled	93.8	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4's dna binding2 domain
37	<a href="#">d1hlva1</a>	Alignment	not modelled	93.8	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
38	<a href="#">d1g2ha</a>	Alignment	not modelled	93.7	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
39	<a href="#">d1etob</a>	Alignment	not modelled	93.3	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
40	<a href="#">d2coba1</a>	Alignment	not modelled	93.1	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain
41	<a href="#">c3kxD</a>	Alignment	not modelled	92.2	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
42	<a href="#">c3h5tA</a>	Alignment	not modelled	92.1	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
43	<a href="#">c2rn7A</a>	Alignment	not modelled	91.9	6	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> is629 orfA; <b>PDBTitle:</b> nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
44	<a href="#">d2bjca1</a>	Alignment	not modelled	91.9	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
45	<a href="#">d1utxa</a>	Alignment	not modelled	91.0	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
46	<a href="#">c3bs3A</a>	Alignment	not modelled	90.7	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of a putative dna-binding protein from bacteroides2 fragilis
47	<a href="#">c1z4hA</a>	Alignment	not modelled	90.5	9	<b>PDB header:</b> protein binding, dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tor inhibition protein; <b>PDBTitle:</b> the response regulator tori belongs to a new family of2 atypical excisionase
48	<a href="#">c1bdhA</a>	Alignment	not modelled	90.3	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (purine repressor); <b>PDBTitle:</b> purine repressor mutant-hypoxanthine-palindromic operator2 complex
49	<a href="#">d2icta1</a>	Alignment	not modelled	90.2	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
50	<a href="#">d1adra</a>	Alignment	not modelled	90.1	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
51	<a href="#">d2ao9a1</a>	Alignment	not modelled	89.9	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Nanomeric phage protein-like
52	<a href="#">d1rzsa</a>	Alignment	not modelled	89.7	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
53	<a href="#">d1biaa1</a>	Alignment	not modelled	89.7	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
54	<a href="#">c3cecA</a>	Alignment	not modelled	89.7	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative antidote protein of plasmid maintenance system; <b>PDBTitle:</b> crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution

55	<a href="#">d1bw6a_</a>	Alignment	not modelled	89.5	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
56	<a href="#">d1jt6a1</a>	Alignment	not modelled	89.3	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
57	<a href="#">c3o60A_</a>	Alignment	not modelled	89.2	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin0861 protein; <b>PDBTitle:</b> the crystal structure of lin0861 from listeria innocua to 2.8a
58	<a href="#">c3omtA_</a>	Alignment	not modelled	89.2	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
59	<a href="#">c1zvva_</a>	Alignment	not modelled	89.0	13	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-resistance amylase regulator; <b>PDBTitle:</b> crystal structure of a ccpa-crh-dna complex
60	<a href="#">d1y9qa1</a>	Alignment	not modelled	88.8	8	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Probable transcriptional regulator VC1968, N-terminal domain
61	<a href="#">c3flbA_</a>	Alignment	not modelled	88.8	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tetr-like transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a tetr-like transcriptional regulator from2 rhodococcus sp. rha1.
62	<a href="#">d2hsqa1</a>	Alignment	not modelled	88.6	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
63	<a href="#">d1t56a1</a>	Alignment	not modelled	88.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
64	<a href="#">d1mkma1</a>	Alignment	not modelled	88.5	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator lclR, N-terminal domain
65	<a href="#">d1vi0a1</a>	Alignment	not modelled	88.5	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
66	<a href="#">d2fq4a1</a>	Alignment	not modelled	88.5	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
67	<a href="#">c2lcvA_</a>	Alignment	not modelled	88.5	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor cytr; <b>PDBTitle:</b> structure of the cytidine repressor dna-binding domain; an alternate2 calculation
68	<a href="#">d1lcda_</a>	Alignment	not modelled	88.4	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
69	<a href="#">c1vi0B_</a>	Alignment	not modelled	88.4	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of a transcriptional regulator
70	<a href="#">d1jhfa1</a>	Alignment	not modelled	88.3	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LexA repressor, N-terminal DNA-binding domain
71	<a href="#">d1efaa1</a>	Alignment	not modelled	88.3	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
72	<a href="#">d1j5ya1</a>	Alignment	not modelled	88.3	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
73	<a href="#">c2xcjB_</a>	Alignment	not modelled	88.2	16	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> c protein; <b>PDBTitle:</b> crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
74	<a href="#">c2l8nA_</a>	Alignment	not modelled	88.1	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor cytr; <b>PDBTitle:</b> nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
75	<a href="#">c3gpva_</a>	Alignment	not modelled	88.1	5	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
76	<a href="#">c2cg4B_</a>	Alignment	not modelled	88.1	6	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
77	<a href="#">d2fbqa1</a>	Alignment	not modelled	88.1	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
78	<a href="#">c2guhA_</a>	Alignment	not modelled	88.0	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1
79	<a href="#">c3kkcB_</a>	Alignment	not modelled	88.0	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> tetr family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of tetr transcriptional regulator from2 streptococcus agalactiae 2603v
80	<a href="#">c2p6tH_</a>	Alignment	not modelled	87.9	6	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> transcriptional regulator, lrp/asnc family; <b>PDBTitle:</b> crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
						<b>Fold:</b> Putative DNA-binding domain

81	<a href="#">d1r8da_</a>	Alignment	not modelled	87.9	5	<b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
82	<a href="#">c3clcC_</a>	Alignment	not modelled	87.9	9	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> crystal structure of the restriction-modification controller protein2 c.esp13961 tetramer in complex with its natural 35 base-pair operator
83	<a href="#">c2ppxA_</a>	Alignment	not modelled	87.9	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1735; <b>PDBTitle:</b> crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
84	<a href="#">d2ppxa1</a>	Alignment	not modelled	87.9	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
85	<a href="#">c3i4pA_</a>	Alignment	not modelled	87.8	6	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, asnc family; <b>PDBTitle:</b> crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
86	<a href="#">c3ppbB_</a>	Alignment	not modelled	87.7	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr family transcription regulator; <b>PDBTitle:</b> crystal structure of a putative tetr family transcription regulator2 (shew_3104) from shewanella sp. pv-4 at 2.10 a resolution
87	<a href="#">c2kpiA_</a>	Alignment	not modelled	87.7	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sos-response transcriptional repressor, lexa; <b>PDBTitle:</b> solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
88	<a href="#">c3b7hA_</a>	Alignment	not modelled	87.6	12	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> prophage lp1 protein 11; <b>PDBTitle:</b> crystal structure of the prophage lp1 protein 11
89	<a href="#">c2ia0A_</a>	Alignment	not modelled	87.5	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator pf0864; <b>PDBTitle:</b> transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
90	<a href="#">d3c07a1</a>	Alignment	not modelled	87.4	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
91	<a href="#">c3b81A_</a>	Alignment	not modelled	87.4	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, acrr family; <b>PDBTitle:</b> crystal structure of predicted dna-binding transcriptional regulator2 of tetr/acrr family (np_350189.1) from clostridium acetobutylicum at3 2.10 a resolution
92	<a href="#">c2nx4A_</a>	Alignment	not modelled	87.4	0	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family protein; <b>PDBTitle:</b> the crystal structure of a the putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1.
93	<a href="#">c2dg7A_</a>	Alignment	not modelled	87.4	4	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
94	<a href="#">c2l0kA_</a>	Alignment	not modelled	87.4	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> stage iii sporulation protein d; <b>PDBTitle:</b> nmr solution structure of a transcription factor spoiiiid in complex2 with dna
95	<a href="#">c2e7xA_</a>	Alignment	not modelled	87.3	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> 150aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
96	<a href="#">c2w48D_</a>	Alignment	not modelled	87.3	14	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> sorbitol operon regulator; <b>PDBTitle:</b> crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
97	<a href="#">d2g3ba1</a>	Alignment	not modelled	87.2	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
98	<a href="#">d1pb6a1</a>	Alignment	not modelled	87.2	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
99	<a href="#">c3op9A_</a>	Alignment	not modelled	87.2	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> pli0006 protein; <b>PDBTitle:</b> crystal structure of transcriptional regulator from listeria innocua
100	<a href="#">d1xsva_</a>	Alignment	not modelled	87.1	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
101	<a href="#">c2of7A_</a>	Alignment	not modelled	87.1	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> structural genomics, the crystal structure of a tetr-family2 transcriptional regulator from streptomyces coelicolor a3
102	<a href="#">c2ebyA_</a>	Alignment	not modelled	87.1	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ybaq; <b>PDBTitle:</b> crystal structure of a hypothetical protein from e. coli
103	<a href="#">d1lmb3_</a>	Alignment	not modelled	87.1	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
104	<a href="#">c2vbzA_</a>	Alignment	not modelled	87.0	9	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan



105	<a href="#">d2np5a1</a>	Alignment	not modelled	87.0	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
106	<a href="#">c2eh3A_</a>	Alignment	not modelled	87.0	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of aq_1058, a transcriptional regulator (terr/acrr2 family) from aquifex aeolicus vf5
107	<a href="#">d1ui5a1</a>	Alignment	not modelled	87.0	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
108	<a href="#">c3bcgA_</a>	Alignment	not modelled	86.9	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator acrr; <b>PDBTitle:</b> conformational changes of the acrr regulator reveal a2 mechanism of induction
109	<a href="#">c2oerA_</a>	Alignment	not modelled	86.8	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> probable transcriptional regulator from pseudomonas2 aeruginosa
110	<a href="#">d2vkva1</a>	Alignment	not modelled	86.8	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
111	<a href="#">c3eusB_</a>	Alignment	not modelled	86.8	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding protein; <b>PDBTitle:</b> the crystal structure of the dna binding protein from silicibacter2 pomeroyi
112	<a href="#">c3on4D_</a>	Alignment	not modelled	86.7	14	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of tetr transcriptional regulator from legionella2 pneumophila
113	<a href="#">d2b5aa1</a>	Alignment	not modelled	86.7	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
114	<a href="#">c3cjdB_</a>	Alignment	not modelled	86.6	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of putative tetr transcriptional regulator2 (yp_510936.1) from jannaschia sp. ccs1 at 1.79 a resolution
115	<a href="#">c3lwiA_</a>	Alignment	not modelled	86.6	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative tetr-family transcriptional regulator2 (yp_752756.1) from syntrophomonas wolfei str. goettingen at 2.07 a3 resolution
116	<a href="#">d2cg4a1</a>	Alignment	not modelled	86.6	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
117	<a href="#">c1jumB_</a>	Alignment	not modelled	86.6	5	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical transcriptional regulator in qaca <b>PDBTitle:</b> crystal structure of the multidrug binding transcriptional2 repressor qacr bound to the natural drug berberine
118	<a href="#">c2f07A_</a>	Alignment	not modelled	86.6	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> yvdt; <b>PDBTitle:</b> crystal structure of yvdt from bacillus subtilis
119	<a href="#">c2cfxD_</a>	Alignment	not modelled	86.6	13	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator lrpc; <b>PDBTitle:</b> structure of b.subtilis lrpc
120	<a href="#">c3dcfB_</a>	Alignment	not modelled	86.6	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator of the tetr/acrr <b>PDBTitle:</b> crystal structure of transcriptional regulator of the2 tetr/acrr family (yp_290855.1) from thermobifida fusca yx-3 er1 at 2.50 a resolution