























# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0CF90
Date	Thu Jan 5 11:31:49 GMT 2012
Unique Job ID	77f5e3cf13db2e1b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3f9kv_</a>	 Alignment		100.0	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
2	<a href="#">d1exqa_</a>	 Alignment		100.0	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
3	<a href="#">d1hyva_</a>	 Alignment		99.9	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
4	<a href="#">d1c6va_</a>	 Alignment		99.9	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
5	<a href="#">c1ex4A_</a>	 Alignment		99.9	16	<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
6	<a href="#">c3nf9A_</a>	 Alignment		99.9	16	<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
7	<a href="#">c3kksB_</a>	 Alignment		99.9	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
8	<a href="#">d1c0ma2</a>	 Alignment		99.9	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
9	<a href="#">c3hpgC_</a>	 Alignment		99.9	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
10	<a href="#">c1c0mA_</a>	 Alignment		99.9	21	<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
11	<a href="#">d1asua_</a>	 Alignment		99.9	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain

12	<a href="#">c1k6yB_</a>	Alignment		99.9	15	<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
13	<a href="#">c3l2tB_</a>	Alignment		99.8	19	<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)
14	<a href="#">d1bcoa2</a>	Alignment		99.8	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> mu transposase, core domain
15	<a href="#">d1cxqa_</a>	Alignment		99.8	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
16	<a href="#">c3dlrA_</a>	Alignment		99.7	16	<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
17	<a href="#">c1bcoA_</a>	Alignment		99.7	16	<b>PDB header:</b> transposase <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriophage mu transposase; <b>PDBTitle:</b> bacteriophage mu transposase core domain
18	<a href="#">c3hosA_</a>	Alignment		99.3	10	<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
19	<a href="#">c1u78A_</a>	Alignment		99.2	16	<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
20	<a href="#">d2jn6a1</a>	Alignment		99.1	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
21	<a href="#">c6paxA_</a>	Alignment		98.9	23	<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
22	<a href="#">d1pdnc_</a>	Alignment		98.8	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
23	<a href="#">c2rn7A_</a>	Alignment	not modelled	98.5	19	<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
24	<a href="#">c2k27A_</a>	Alignment	not modelled	98.0	23	<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
25	<a href="#">c2elhA_</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cgl1849-pa; <b>PDBTitle:</b> solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cgl1849-pa
26	<a href="#">d1k78a1</a>	Alignment	not modelled	97.9	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

27	<a href="#">d6paxa1</a>	Alignment	not modelled	97.7	18	<b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
28	<a href="#">d1bw6a_</a>	Alignment	not modelled	97.7	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
29	<a href="#">d1hlva1</a>	Alignment	not modelled	97.6	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
30	<a href="#">c1hlvA_</a>	Alignment	not modelled	97.6	22	<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
31	<a href="#">c3hefB_</a>	Alignment	not modelled	97.4	16	<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
32	<a href="#">d2coba1</a>	Alignment	not modelled	97.2	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain
33	<a href="#">c2zhha_</a>	Alignment	not modelled	96.9	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensitive transcriptional activator soxr; <b>PDBTitle:</b> crystal structure of soxr
34	<a href="#">d1q06a_</a>	Alignment	not modelled	96.8	13	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
35	<a href="#">c2vz4A_</a>	Alignment	not modelled	96.8	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator tipa; <b>PDBTitle:</b> the n-terminal domain of merr-like protein tipal bound to2 promoter dna
36	<a href="#">d1tc3c_</a>	Alignment	not modelled	96.6	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
37	<a href="#">d1r8da_</a>	Alignment	not modelled	96.5	13	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
38	<a href="#">c3gp4B_</a>	Alignment	not modelled	96.5	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
39	<a href="#">c1bdhA_</a>	Alignment	not modelled	96.3	26	<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
40	<a href="#">c2jmlA_</a>	Alignment	not modelled	96.2	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna binding domain/transcriptional regulator; <b>PDBTitle:</b> solution structure of the n-terminal domain of cara repressor
41	<a href="#">d1qpza1</a>	Alignment	not modelled	96.2	27	<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
42	<a href="#">c3gpvA_</a>	Alignment	not modelled	96.2	10	<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
43	<a href="#">c3hh0C_</a>	Alignment	not modelled	96.2	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal strcure of a transcriptional regulator, merr family2 from bacillus cereus
44	<a href="#">d1efaa1</a>	Alignment	not modelled	96.0	16	<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="#">d2bjca1</a>	Alignment	not modelled	96.0	16	<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
46	<a href="#">d2hsga1</a>	Alignment	not modelled	96.0	18	<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
47	<a href="#">d2ao9a1</a>	Alignment	not modelled	95.9	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Nanomeric phage protein-like
48	<a href="#">c3kxD_</a>	Alignment	not modelled	95.9	28	<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
49	<a href="#">c3sztB_</a>	Alignment	not modelled	95.8	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> quorum-sensing control repressor; <b>PDBTitle:</b> quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
50	<a href="#">c1zvva_</a>	Alignment	not modelled	95.8	17	<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
51	<a href="#">d1llib_</a>	Alignment	not modelled	95.8	23	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
52	<a href="#">c3qaoA_</a>	Alignment	not modelled	95.7	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> merr-like transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
53	<a href="#">d1xsva_</a>	Alignment	not modelled	95.7	18	<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

54	<a href="#">d1fsea_</a>	Alignment	not modelled	95.6	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
55	<a href="#">d1rioa_</a>	Alignment	not modelled	95.6	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
56	<a href="#">d1ijwc_</a>	Alignment	not modelled	95.5	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
57	<a href="#">d1or7a1</a>	Alignment	not modelled	95.5	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
58	<a href="#">d1rp3a2</a>	Alignment	not modelled	95.4	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> Sigma4 domain
59	<a href="#">c3hugA_</a>	Alignment	not modelled	95.4	27	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigI
60	<a href="#">c1zljE_</a>	Alignment	not modelled	95.4	14	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dormancy survival regulator; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosR c-terminal domain
61	<a href="#">d1hcra_</a>	Alignment	not modelled	95.3	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain
62	<a href="#">d1luxda_</a>	Alignment	not modelled	95.2	16	<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="#">c2q0oA_</a>	Alignment	not modelled	95.2	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional activator protein trar; <b>PDBTitle:</b> crystal structure of an anti-activation complex in bacterial quorum2 sensing
64	<a href="#">c2kpiA_</a>	Alignment	not modelled	95.2	27	<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
65	<a href="#">d1ntca_</a>	Alignment	not modelled	95.1	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
66	<a href="#">c3lsgD_</a>	Alignment	not modelled	95.1	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> two-component response regulator yesN; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of the two-2 component response regulator yesN from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
67	<a href="#">d2ofya1</a>	Alignment	not modelled	95.1	26	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
68	<a href="#">c2o8xA_</a>	Alignment	not modelled	95.1	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the "-35 element" promoter recognition domain of f2 mycobacterium tuberculosis sigC
69	<a href="#">d1a04a1</a>	Alignment	not modelled	95.1	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
70	<a href="#">c2krfB_</a>	Alignment	not modelled	95.1	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein coma; <b>PDBTitle:</b> nmr solution structure of the dna binding domain of competence protein2 a
71	<a href="#">c1h0mD_</a>	Alignment	not modelled	95.0	24	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional activator protein trar; <b>PDBTitle:</b> three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
72	<a href="#">d1r8ea1</a>	Alignment	not modelled	95.0	7	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
73	<a href="#">d1s7oa_</a>	Alignment	not modelled	95.0	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
74	<a href="#">c3mzyA_</a>	Alignment	not modelled	94.9	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-h factor; <b>PDBTitle:</b> the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
75	<a href="#">c3h5tA_</a>	Alignment	not modelled	94.9	22	<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
76	<a href="#">c3oouA_</a>	Alignment	not modelled	94.9	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2118 protein; <b>PDBTitle:</b> the structure of a protein with unkown function from listeria innocua
77	<a href="#">d1vz0a1</a>	Alignment	not modelled	94.8	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
78	<a href="#">c2ao9H_</a>	Alignment	not modelled	94.8	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> phage protein; <b>PDBTitle:</b> structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579

79	<a href="#">d1lmb3_</a>	Alignment	not modelled	94.8	23	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
80	<a href="#">d1l3la1</a>	Alignment	not modelled	94.8	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
81	<a href="#">c1x3uA_</a>	Alignment	not modelled	94.7	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein fixj; <b>PDBTitle:</b> solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
82	<a href="#">c1y9qA_</a>	Alignment	not modelled	94.6	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, hth_3 family; <b>PDBTitle:</b> crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
83	<a href="#">c3bdnB_</a>	Alignment	not modelled	94.6	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> lambda repressor; <b>PDBTitle:</b> crystal structure of the lambda repressor
84	<a href="#">c2jpcA_</a>	Alignment	not modelled	94.6	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
85	<a href="#">c1r71B_</a>	Alignment	not modelled	94.4	22	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor protein korb; <b>PDBTitle:</b> crystal structure of the dna binding domain of korb in2 complex with the operator dna
86	<a href="#">d1fipa_</a>	Alignment	not modelled	94.4	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
87	<a href="#">c2w48D_</a>	Alignment	not modelled	94.4	17	<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
88	<a href="#">c3e71D_</a>	Alignment	not modelled	94.3	10	<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
89	<a href="#">c2gm4B_</a>	Alignment	not modelled	94.3	14	<b>PDB header:</b> recombination, dna <b>Chain:</b> B: <b>PDB Molecule:</b> transposon gamma-delta resolvase; <b>PDBTitle:</b> an activated, tetrameric gamma-delta resolvase: hin chimera bound to2 cleaved dna
90	<a href="#">c2x4hA_</a>	Alignment	not modelled	94.3	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sso2273; <b>PDBTitle:</b> crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
91	<a href="#">d1p4wa_</a>	Alignment	not modelled	94.3	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
92	<a href="#">c3omtA_</a>	Alignment	not modelled	94.3	24	<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.
93	<a href="#">d1umqa_</a>	Alignment	not modelled	94.3	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
94	<a href="#">c1umqA_</a>	Alignment	not modelled	94.3	16	<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
95	<a href="#">d2b5aa1</a>	Alignment	not modelled	94.1	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
96	<a href="#">d1yioa1</a>	Alignment	not modelled	94.1	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
97	<a href="#">d1r71a_</a>	Alignment	not modelled	94.1	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
98	<a href="#">c2rnjA_</a>	Alignment	not modelled	94.1	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> nmr structure of the s. aureus vvar dna binding domain
99	<a href="#">d1nera_</a>	Alignment	not modelled	94.0	26	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
100	<a href="#">c3cloC_</a>	Alignment	not modelled	94.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
101	<a href="#">c2r0qF_</a>	Alignment	not modelled	94.0	23	<b>PDB header:</b> recombination/dna <b>Chain:</b> F: <b>PDB Molecule:</b> putative transposon tn552 dna-invertase bin3; <b>PDBTitle:</b> crystal structure of a serine recombinase- dna regulatory2 complex
102	<a href="#">c3gbgA_</a>	Alignment	not modelled	94.0	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tcp pilus virulence regulatory protein; <b>PDBTitle:</b> crystal structure of tox from vibrio cholerae o395
103	<a href="#">d1lcda_</a>	Alignment	not modelled	94.0	20	<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
104	<a href="#">c3bs3A_</a>	Alignment	not modelled	93.9	20	<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
105	<a href="#">c3frwF_</a>	Alignment	not modelled	93.8	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> putative trp repressor protein; <b>PDBTitle:</b> crystal structure of putative trpr protein from ruminococcus obeum
106	<a href="#">c3qp5C_</a>	Alignment	not modelled	93.8	22	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> cvir transcriptional regulator; <b>PDBTitle:</b> crystal structure of cvir bound to antagonist chlorolactone (cl)
107	<a href="#">d1etxa_</a>	Alignment	not modelled	93.6	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
108	<a href="#">c3oioA_</a>	Alignment	not modelled	93.6	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (arac-type dna-binding domain- <b>PDBTitle:</b> crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
109	<a href="#">c3ivpD_</a>	Alignment	not modelled	93.6	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> putative transposon-related dna-binding protein; <b>PDBTitle:</b> the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
110	<a href="#">c1bl0A_</a>	Alignment	not modelled	93.5	10	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (multiple antibiotic resistance protein); <b>PDBTitle:</b> multiple antibiotic resistance protein (mara)/dna complex
111	<a href="#">d1y9qa1</a>	Alignment	not modelled	93.4	19	<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
112	<a href="#">c2lcvA_</a>	Alignment	not modelled	93.3	20	<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
113	<a href="#">c1rn1A_</a>	Alignment	not modelled	93.3	17	<b>PDB header:</b> signal transduction protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate/nitrite response regulator protein narl; <b>PDBTitle:</b> the nitrate/nitrite response regulator protein narl from narl
114	<a href="#">c3mk1B_</a>	Alignment	not modelled	93.3	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator gadx; <b>PDBTitle:</b> crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
115	<a href="#">c2ev5B_</a>	Alignment	not modelled	93.2	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator mntr; <b>PDBTitle:</b> bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
116	<a href="#">c3c3wB_</a>	Alignment	not modelled	93.1	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> two component transcriptional regulatory protein devr; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
117	<a href="#">c3f6wE_</a>	Alignment	not modelled	93.0	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> xre-family like protein; <b>PDBTitle:</b> xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
118	<a href="#">c3korD_</a>	Alignment	not modelled	93.0	27	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> possible trp repressor; <b>PDBTitle:</b> crystal structure of a putative trp repressor from staphylococcus2 aureus
119	<a href="#">d1luxca_</a>	Alignment	not modelled	93.0	19	<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
120	<a href="#">d1g2ha_</a>	Alignment	not modelled	92.8	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like