


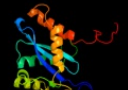
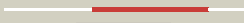


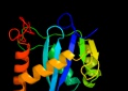


















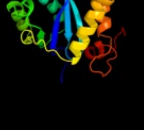



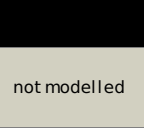


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0CF63
Date	Wed Jan 25 15:20:36 GMT 2012
Unique Job ID	8a2a082a0c43cf14

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f9kV_	 Alignment		99.9	18	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	18	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	d1bcoa2	 Alignment		99.8	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
6	c3nf9A_	 Alignment		99.8	17	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
7	d1exqa_	 Alignment		99.8	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic 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	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
10	d1cxqa_	 Alignment		99.7	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
11	c1bcoA_	 Alignment		99.7	13	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain

12	d1hyva_	Alignment		99.7	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
13	c1k6yB_	Alignment		99.6	18	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
14	c3hpgC_	Alignment		99.6	21	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
15	d1c6va_	Alignment		99.6	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
16	c3l2tB_	Alignment		99.6	15	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)
17	c3hosA_	Alignment		99.5	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
18	c3dlrA_	Alignment		99.3	14	PDB header: transferase Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain from pfv2 integrase
19	c6paxA_	Alignment		98.8	17	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		98.8	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
21	c1u78A_	Alignment	not modelled	98.6	10	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	98.4	18	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	98.0	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	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
25	c3f2kB_	Alignment	not modelled	97.2	20	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	c3hefB_	Alignment	not modelled	97.0	14	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small2 subunit
27	d2coba1	Alignment	not modelled	96.9	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
28	d1k78a1	Alignment	not modelled	96.8	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain

29	c1hlvA	Alignment	not modelled	96.7	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	d6paxa1	Alignment	not modelled	96.7	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
31	c2rn7A	Alignment	not modelled	96.6	12	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
32	c1umqA	Alignment	not modelled	96.4	24	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
33	d1umqa	Alignment	not modelled	96.4	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
34	d1ntca	Alignment	not modelled	96.3	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
35	c2elhA	Alignment		96.1	21	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
36	d1fipa	Alignment	not modelled	96.0	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
37	d1etxa	Alignment	not modelled	95.9	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
38	c3e7ID	Alignment	not modelled	95.8	8	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
39	d1ijwc	Alignment	not modelled	95.6	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
40	d1g2ha	Alignment	not modelled	95.5	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
41	d1hcra	Alignment	not modelled	95.5	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
42	d1etob	Alignment	not modelled	95.3	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
43	d1a04a1	Alignment	not modelled	94.7	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)
44	d2ao9a1	Alignment	not modelled	94.6	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
45	c2w48D	Alignment	not modelled	94.5	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
46	c3fmyA	Alignment	not modelled	94.5	6	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 (ygi/b3021)
47	c2cg4B	Alignment	not modelled	94.2	15	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
48	c2jvlA	Alignment	not modelled	94.0	12	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
49	c1zljE	Alignment	not modelled	93.9	11	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxia2 response regulator dosr c-terminal domain
50	d1fsea	Alignment	not modelled	93.9	10	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)
51	d1xsva	Alignment	not modelled	93.9	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
52	d1hlva1	Alignment	not modelled	93.7	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
53	c2q0oA	Alignment	not modelled	93.6	8	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing

54	c3sztB	Alignment	not modelled	93.4	8	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
55	d1s7oa	Alignment	not modelled	93.4	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
56	c1r71B	Alignment	not modelled	93.4	13	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
57	d1yioa1	Alignment	not modelled	93.3	18	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)
58	d2cg4a1	Alignment	not modelled	93.2	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
59	d1sq8a	Alignment	not modelled	93.1	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
60	c3t76A	Alignment	not modelled	93.1	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
61	d1l3la1	Alignment	not modelled	92.8	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)
62	d1bw6a	Alignment	not modelled	92.7	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
63	c2krfB	Alignment	not modelled	92.7	11	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
64	c3hugA	Alignment	not modelled	92.6	13	PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
65	c2l0kA	Alignment	not modelled	92.6	10	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
66	d1r71a	Alignment	not modelled	92.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
67	d1r69a	Alignment	not modelled	92.4	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
68	d1biaa1	Alignment	not modelled	92.3	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
69	c1h0mD	Alignment	not modelled	92.3	22	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
70	d1vz0a1	Alignment	not modelled	92.1	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
71	c1x3uA	Alignment	not modelled	92.1	11	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
72	c2x48B	Alignment	not modelled	92.0	28	PDB header: viral protein Chain: B: PDB Molecule: cag38821; PDBTitle: orf 55 from sulfolobus islandicus rudivirus 1
73	d1p4wa	Alignment	not modelled	91.8	19	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)
74	c3b7hA	Alignment	not modelled	91.8	3	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
75	c2xcjB	Alignment	not modelled	91.6	12	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
76	d1y9qa1	Alignment	not modelled	91.6	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
77	d1ladra	Alignment	not modelled	91.6	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
78	c3mzyA	Alignment	not modelled	91.6	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
79	c2ia0A	Alignment	not modelled	91.6	18	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)

80	c2iu5A	Alignment	not modelled	91.5	16	PDB header: transcription Chain: A: PDB Molecule: hth-type dhaklm operon transcriptional activator dhas; PDBTitle: dihydroxyacetone kinase operon activator dhas
81	c3cecA	Alignment	not modelled	91.5	18	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
82	c3qp5C	Alignment	not modelled	91.4	11	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
83	c3o60A	Alignment	not modelled	91.4	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin0861 protein; PDBTitle: the crystal structure of lin0861 from listeria innocua to 2.8a
84	dlj5ya1	Alignment	not modelled	91.4	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
85	c2vbzA	Alignment	not modelled	91.4	24	PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
86	d2ezla	Alignment	not modelled	91.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
87	c1z4hA	Alignment	not modelled	91.3	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
88	c2rnjA	Alignment	not modelled	91.3	13	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
89	c2w7nA	Alignment	not modelled	91.3	10	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
90	c2ao9H	Alignment	not modelled	91.2	19	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: phage protein; PDBTitle: structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
91	dlrp3a2	Alignment	not modelled	91.2	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
92	c3op9A	Alignment	not modelled	91.2	9	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
93	c2jpcA	Alignment	not modelled	91.0	17	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
94	c3gn5B	Alignment	not modelled	90.8	6	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
95	dlnera	Alignment	not modelled	90.8	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
96	c2p6tH	Alignment	not modelled	90.7	15	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
97	c3c3wB	Alignment	not modelled	90.6	8	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
98	c3ivpD	Alignment	not modelled	90.5	22	PDB header: dna binding protein Chain: D: PDB Molecule: putative transposon-related dna-binding protein; PDBTitle: the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
99	dlor7a1	Alignment	not modelled	90.3	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
100	d2icta1	Alignment	not modelled	90.3	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
101	dlgdtA1	Alignment	not modelled	90.2	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
102	c3onqB	Alignment	not modelled	90.2	10	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
103	c2e7xA	Alignment	not modelled	90.2	12	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
104	c2nn5A	Alignment	not modelled	90.2	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator;

104	c2npbA	Alignment	not modelled	90.2	17	PDBTitle: crystal structure of a transcriptional regulator (rha1_ro04179) from <i>rhodococcus</i> sp. rha1. PDB header: transcription regulator
105	c3f1bA	Alignment	not modelled	90.2	15	Chain: A: PDB Molecule: tetr-like transcriptional regulator; PDBTitle: the crystal structure of a tetr-like transcriptional regulator from <i>rhodococcus</i> sp. rha1.
106	c2fjrB	Alignment	not modelled	90.1	11	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
107	d1utxa	Alignment	not modelled	90.0	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
108	d1uxca	Alignment	not modelled	90.0	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
109	c1rn1A	Alignment	not modelled	90.0	19	PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl; PDBTitle: the nitrate/nitrite response regulator protein narl from narl
110	c1b0nA	Alignment	not modelled	90.0	20	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
111	c2d6yA	Alignment	not modelled	89.9	19	PDB header: gene regulation Chain: A: PDB Molecule: putative tetr family regulatory protein; PDBTitle: crystal structure of transcriptional factor sco4008 from <i>streptomyces2 coelicolor a3(2)</i>
112	c3gziA	Alignment	not modelled	89.9	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 <i>shewanella loihica</i> pv-4 at 2.05 a resolution
113	d2fq4a1	Alignment	not modelled	89.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
114	c2hxiA	Alignment	not modelled	89.8	25	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structural genomics, the crystal structure of a putative2 transcriptional regulator from <i>streptomyces coelicolor a3(2)</i>
115	c3eusB	Alignment	not modelled	89.7	14	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from <i>silicibacter2 pomeroyi</i>
116	d2np5a1	Alignment	not modelled	89.7	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
117	c1bdhA	Alignment	not modelled	89.7	16	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
118	d1lmb3	Alignment	not modelled	89.6	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
119	c2e1cA	Alignment	not modelled	89.6	15	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
120	c2oqgA	Alignment	not modelled	89.6	21	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from <i>rhodococcus</i> sp. rha1