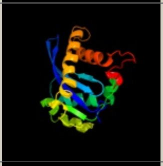
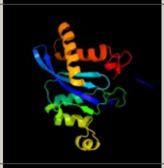
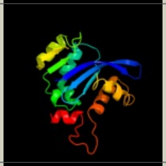
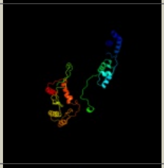
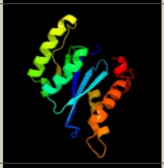
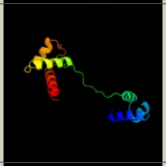
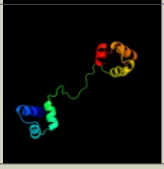
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0CF64
Date	Thu Jan 5 11:31:22 GMT 2012
Unique Job ID	ec1d332d9030e7e6

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	d1asua_	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	c3e7lD_	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 (ygit/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 hypoxic2 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 spoiiid 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	d1adra_	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	d1j5ya1	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 vrar; **PDBTitle:** nmr structure of the s. aureus vrar 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	d1rp3a2	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	d1nera_	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	d1or7a1	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	d1gdta1	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 sulfolobus tokodaii 7 complexed with its cognate ligand
104	c2pp5A	Alignment	not modelled	90.2	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator;

104	c2np5A_	Alignment	not modelled	90.2	17	**PDBTitle:** crystal structure of a transcriptional regulator (rha1_ro04179) from2 rhodococcus sp. rha1.
105	c3f1bA_	Alignment	not modelled	90.2	15	**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.
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	c1rnlA_	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 streptomyces2 coelicolor a3(2)
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 shewanella loihica 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 streptomyces coelicolor a3(2)
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 silicibacter2 pomeroyi
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 rhodococcus sp. rha1