Phyre^2

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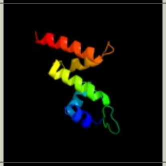
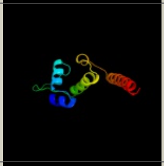
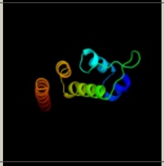
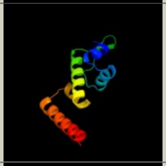
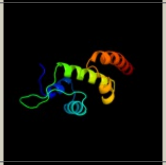
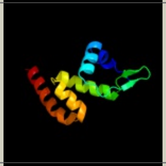
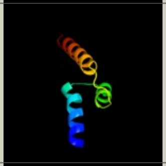
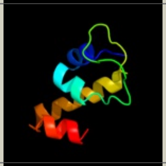
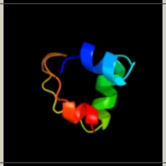
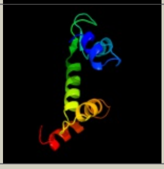
Description	P63264
Date	Thu Jan 5 12:08:02 GMT 2012
Unique Job ID	a1cde512907d542b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3d6zA_	Alignment		99.8	16	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**multidrug-efflux transporter 1 regulator; **PDBTitle:** crystal structure of r275e mutant of bmrr bound to dna and rhodamine
2	d1r8da_	Alignment		99.8	14	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
3	c2zhhA_	Alignment		99.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensitive transcriptional activator soxr; **PDBTitle:** crystal structure of soxr
4	c2vz4A_	Alignment		99.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional activator tipa; **PDBTitle:** the n-terminal domain of merr-like protein tipal bound to2 promoter dna
5	c3gp4B_	Alignment		99.7	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
6	c3hh0C_	Alignment		99.7	13	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal strucure of a transcriptional regulator, merr family2 from bacillus cereus
7	d1q06a_	Alignment		99.7	12	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
8	d1r8ea1	Alignment		99.7	19	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
9	c3qaoA_	Alignment		99.7	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**merr-like transcriptional regulator; **PDBTitle:** the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
10	c3gpvA_	Alignment		99.7	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
11	c2jmlA_	Alignment		99.5	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator; **PDBTitle:** solution structure of the n-terminal domain of cara repressor

12	c2dg6A_	Alignment		99.4	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of the putative transcriptional regulator sco55502 from streptomyces coelicolor a3(2)
13	d1q08a_	Alignment		97.2	10	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
14	c2ev2B_	Alignment		94.6	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** structure of rv1264n, the regulatory domain of the mycobacterial2 adenylyl cylcase rv1264, at ph 8.5
15	c1fx7C_	Alignment		94.6	10	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis
16	c2kfsA_	Alignment		94.2	13	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical regulatory protein; **PDBTitle:** nmr structure of rv2175c
17	c1z4hA_	Alignment		94.0	7	**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
18	c1g3wA_	Alignment		93.2	9	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** cd-cys102ser dtxr
19	d1j9ia_	Alignment		93.0	15	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
20	c2it0A_	Alignment		91.5	10	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of a two-domain ider-dna complex crystal2 form ii
21	c3ezfA_	Alignment	not modelled	91.1	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**para; **PDBTitle:** partition protein
22	c2wusR_	Alignment	not modelled	90.9	23	**PDB header:**structural protein **Chain:** R: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** bacterial actin mreb assembles in complex with cell shape2 protein rodz
23	c3fymA_	Alignment	not modelled	90.5	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the 1a structure of ymfm, a putative dna-binding membrane2 protein from staphylococcus aureus
24	c2x4hA_	Alignment	not modelled	90.2	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
25	c2h09A_	Alignment	not modelled	90.2	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
26	c3by6C_	Alignment	not modelled	89.3	11	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**predicted transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator from oenococcus oeni
27	c3cuoB_	Alignment	not modelled	88.6	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator ygav; **PDBTitle:** crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
28	c3hruA_	Alignment	not modelled	88.5	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+

29	c3jthA_	Alignment	not modelled	86.2	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription activator hlyu; **PDBTitle:** crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
30	c2du9A_	Alignment	not modelled	85.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulators; **PDBTitle:** crystal structure of the transcriptional factor from c.glutamicum
31	c3f6vA_	Alignment	not modelled	85.0	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family **PDBTitle:** crystal structure of possible transcriptional regulator for2 arsenical resistance
32	d1ku9a_	Alignment	not modelled	84.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
33	c2oqgA_	Alignment	not modelled	84.3	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
34	c2ev5B_	Alignment	not modelled	83.9	3	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
35	d1pm6a_	Alignment	not modelled	82.8	14	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
36	c3b7hA_	Alignment	not modelled	82.7	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
37	d2d1ha1	Alignment	not modelled	82.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
38	d2ofya1	Alignment	not modelled	82.1	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
39	d1r1ua_	Alignment	not modelled	81.1	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
40	c3clcC_	Alignment	not modelled	81.1	9	**PDB header:**transcription regulator/dna **Chain:** C: **PDB Molecule:**regulatory protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
41	c2zkzC_	Alignment	not modelled	80.5	10	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional repressor pagr; **PDBTitle:** crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
42	d1stza1	Alignment	not modelled	79.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
43	d2hsga1	Alignment	not modelled	79.2	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
44	d1utxa_	Alignment	not modelled	78.8	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
45	d1mkma1	Alignment	not modelled	78.8	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
46	c3neuA_	Alignment	not modelled	77.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1836 protein; **PDBTitle:** the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
47	d1y7ya1	Alignment	not modelled	77.5	7	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
48	c2o3fC_	Alignment	not modelled	77.4	20	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative hth-type transcriptional regulator ybbh; **PDBTitle:** structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
49	d1qpza1	Alignment	not modelled	77.3	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
50	c2ppxA_	Alignment	not modelled	77.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1735; **PDBTitle:** crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
51	d2ppxa1	Alignment	not modelled	77.3	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
52	d2o3fa1	Alignment	not modelled	77.1	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**RpiR-like
53	c1b0nA_	Alignment	not modelled	76.5	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein (sinr protein); **PDBTitle:** sinr protein/sini protein complex
54	d2jn6a1	Alignment	not modelled	76.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like

						Family: Cgl2762-like
55	c3eqxB_	Alignment	not modelled	76.4	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**fic domain containing transcriptional regulator; **PDBTitle:** crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
56	d1r1ta_	Alignment	not modelled	75.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
57	d1j5ya1	Alignment	not modelled	75.8	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
58	c2kkoB_	Alignment	not modelled	75.0	24	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**possible transcriptional regulatory protein **PDBTitle:** solution nmr structure of the homodimeric winged helix-turn-2 helix dna-binding domain (fragment 1-100) mb0332 from3 mycobacterium bovis, a possible arsr-family transcriptional4 regulator. northeast structural genomics consortium target5 mbr242e.
59	d1efaa1	Alignment	not modelled	74.4	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
60	c1r22B_	Alignment	not modelled	73.8	14	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**transcriptional repressor smtb; **PDBTitle:** crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
61	d2b5aa1	Alignment	not modelled	73.7	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
62	c2ebyA_	Alignment	not modelled	73.3	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq; **PDBTitle:** crystal structure of a hypothetical protein from e. coli
63	d1jt6a1	Alignment	not modelled	73.2	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
64	d2p4wa1	Alignment	not modelled	72.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF1790-like
65	c3bs3A_	Alignment	not modelled	71.8	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
66	d1xd7a_	Alignment	not modelled	71.7	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator Rrf2
67	c1u78A_	Alignment	not modelled	70.6	8	**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
68	d1biaa1	Alignment	not modelled	70.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
69	c3kxaD_	Alignment	not modelled	70.2	22	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
70	c3iwfA_	Alignment	not modelled	70.0	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
71	c3fmyA_	Alignment	not modelled	69.9	14	**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)
72	d1fp2a1	Alignment	not modelled	69.9	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Plant O-methyltransferase, N-terminal domain
73	c3f6oB_	Alignment	not modelled	69.6	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable transcriptional regulator, arsr family **PDBTitle:** crystal structure of arsr family transcriptional regulator,2 rha00566
74	c2kpjA_	Alignment	not modelled	69.2	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sos-response transcriptional repressor, lexa; **PDBTitle:** solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
75	d1uxca_	Alignment	not modelled	69.1	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
76	c2hs5A_	Alignment	not modelled	68.6	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator gntr; **PDBTitle:** structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1
77	d2o7ta1	Alignment	not modelled	68.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
78	d1t56a1	Alignment	not modelled	68.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
						PDB header:transcription

79	c2y75F_	Alignment	not modelled	68.0	18	**Chain:** F: **PDB Molecule:**hth-type transcriptional regulator cymr; **PDBTitle:** the structure of cymr (yrzc) the global cysteine regulator2 of b. subtilis
80	c3c7jA_	Alignment	not modelled	68.0	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of transcriptional regulator (gntr family member)2 from pseudomonas syringae pv. tomato str. dc3000
81	d2fq4a1	Alignment	not modelled	67.9	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
82	c2bnoA_	Alignment	not modelled	67.9	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
83	c3k69A_	Alignment	not modelled	67.6	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcription regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
84	d1v7ba1	Alignment	not modelled	67.5	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
85	c3pqkD_	Alignment	not modelled	67.3	20	**PDB header:**transcription **Chain:** D: **PDB Molecule:**biofilm growth-associated repressor; **PDBTitle:** crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
86	c3izbV_	Alignment	not modelled	67.3	11	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**40s ribosomal protein rps25 (s25e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
87	d2fbqa1	Alignment	not modelled	66.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
88	c2jscB_	Alignment	not modelled	66.7	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator rv1994c/mt2050; **PDBTitle:** nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
89	d2g3ba1	Alignment	not modelled	66.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
90	c2di3A_	Alignment	not modelled	66.7	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bacterial regulatory proteins, gntr family; **PDBTitle:** crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum
91	c3t76A_	Alignment	not modelled	66.5	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
92	c2dg7A_	Alignment	not modelled	66.4	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
93	c2xzm8_	Alignment	not modelled	66.4	13	**PDB header:**ribosome **Chain:** 8: **PDB Molecule:**rps25e,; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
94	d1sq8a_	Alignment	not modelled	66.3	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
95	c3o60A_	Alignment	not modelled	66.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0861 protein; **PDBTitle:** the crystal structure of lin0861 from listeria innocua to 2.8a
96	c3f52A_	Alignment	not modelled	66.2	23	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
97	d1r69a_	Alignment	not modelled	66.1	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
98	d1uxda_	Alignment	not modelled	66.1	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
99	d1ui5a1	Alignment	not modelled	65.9	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
100	c3op9A_	Alignment	not modelled	65.7	0	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
101	c2fq4A_	Alignment	not modelled	65.7	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** the crystal structure of the transcriptional regulator (tetr family)2 from bacillus cereus
102	d3c07a1	Alignment	not modelled	65.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
103	d1adra_	Alignment	not modelled	65.4	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
104	c2oerA_	Alignment	not modelled	65.3	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** probable transcriptional regulator from pseudomonas2 aeruginosa

105	c3omtA_	Alignment	not modelled	65.3	5	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
106	d2g7sa1	Alignment	not modelled	65.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
107	c2nx4A_	Alignment	not modelled	65.0	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family protein; **PDBTitle:** the crystal structure of athe putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1.
108	d2vkva1	Alignment	not modelled	65.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
109	c3f1bA_	Alignment	not modelled	64.8	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.
110	d1sfxa_	Alignment	not modelled	64.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
111	d2i10a1	Alignment	not modelled	64.8	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
112	c1vi0B_	Alignment	not modelled	64.7	5	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator
113	c2l8nA_	Alignment	not modelled	64.5	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
114	d2gena1	Alignment	not modelled	64.5	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
115	d1u2wa1	Alignment	not modelled	64.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
116	c3lwfD_	Alignment	not modelled	64.0	16	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
117	d2bjca1	Alignment	not modelled	63.9	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
118	d1lcda_	Alignment	not modelled	63.9	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
119	c1y9qA_	Alignment	not modelled	63.8	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, hth_3 family; **PDBTitle:** crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
120	d1b0na2	Alignment	not modelled	63.7	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like