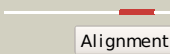
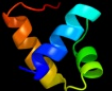
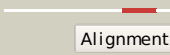

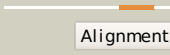

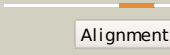

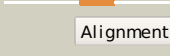

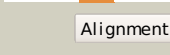





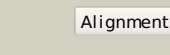

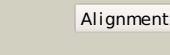
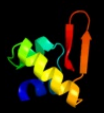
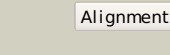












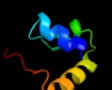





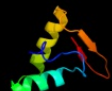










#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">dlz05a1</a>	 Alignment		92.3	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
2	<a href="#">dlz6ra1</a>	 Alignment		92.0	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ROK associated domain
3	<a href="#">clz6rC_</a>	 Alignment		88.6	11	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> mlc protein; <b>PDBTitle:</b> crystal structure of mlc from escherichia coli
4	<a href="#">clz05A_</a>	 Alignment		86.9	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, rok family; <b>PDBTitle:</b> crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
5	<a href="#">c2z99A_</a>	 Alignment		83.4	12	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of scpb from mycobacterium tuberculosis
6	<a href="#">d1t6sa2</a>	 Alignment		82.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ScpB/YpuH-like
7	<a href="#">d1sfxa_</a>	 Alignment		79.5	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
8	<a href="#">c3eyvA_</a>	 Alignment		75.3	15	<b>PDB header:</b> transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative iron uptake regulatory protein; <b>PDBTitle:</b> structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
9	<a href="#">c2fu4B_</a>	 Alignment		74.7	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
10	<a href="#">c2v9vA_</a>	 Alignment		71.0	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> crystal structure of moorella thermoacetica selb(377-511)
11	<a href="#">c3eqxB_</a>	 Alignment		70.4	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> fic domain containing transcriptional regulator; <b>PDBTitle:</b> crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution

12	<a href="#">c1t6sB_</a>	 Alignment		67.7	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of a conserved hypothetical protein from chlorobium2 tepidum
13	<a href="#">c2qufB_</a>	 Alignment		66.3	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor pf0095; <b>PDBTitle:</b> crystal structure of transcription factor axxa-pf0095 from pyrococcus2 furiosus
14	<a href="#">c2nyxB_</a>	 Alignment		60.8	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulatory protein, rv1404; <b>PDBTitle:</b> crystal structure of rv1404 from mycobacterium tuberculosis
15	<a href="#">c3cjnA_</a>	 Alignment		60.1	4	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
16	<a href="#">c2k4bA_</a>	 Alignment		59.5	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> copr repressor structure
17	<a href="#">d2fbia1</a>	 Alignment		59.2	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
18	<a href="#">c3f6vA_</a>	 Alignment		58.1	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family <b>PDBTitle:</b> crystal structure of possible transcriptional regulator for2 arsenical resistance
19	<a href="#">c3mwmA_</a>	 Alignment		54.2	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal uptake regulation protein; <b>PDBTitle:</b> graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
20	<a href="#">c2xigA_</a>	 Alignment		54.1	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
21	<a href="#">c2o03A_</a>	 Alignment	not modelled	53.6	10	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> probable zinc uptake regulation protein furb; <b>PDBTitle:</b> crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
22	<a href="#">d1mzba_</a>	 Alignment	not modelled	51.5	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> FUR-like
23	<a href="#">c3g3zA_</a>	 Alignment	not modelled	49.8	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
24	<a href="#">c1u5tA_</a>	 Alignment	not modelled	49.2	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> appears to be functionally related to snf7; <b>PDBTitle:</b> structure of the escrt-ii endosomal trafficking complex
25	<a href="#">d1lnwa_</a>	 Alignment	not modelled	48.6	3	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
26	<a href="#">c3bpbB_</a>	 Alignment	not modelled	48.3	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
27	<a href="#">d2g9wa1</a>	 Alignment	not modelled	47.9	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
28	<a href="#">d1lj9a_</a>	 Alignment	not modelled	47.5	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators

29	<a href="#">d1lvaa3</a>	Alignment	not modelled	47.0	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal fragment of elongation factor SelB
30	<a href="#">c1r22B_</a>	Alignment	not modelled	46.7	16	<b>PDB header:</b> transcription repressor <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor smtb; <b>PDBTitle:</b> crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
31	<a href="#">c2w57A_</a>	Alignment	not modelled	45.1	12	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains
32	<a href="#">d2bv6a1</a>	Alignment	not modelled	44.2	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
33	<a href="#">c2hoeA_</a>	Alignment	not modelled	43.2	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylglucosamine kinase; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
34	<a href="#">d2a61a1</a>	Alignment	not modelled	43.1	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
35	<a href="#">c3hhhA_</a>	Alignment	not modelled	42.6	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, padr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator, a member of padr2 family, from enterococcus faecalis v583
36	<a href="#">c2aj6A_</a>	Alignment	not modelled	41.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein mw0638; <b>PDBTitle:</b> crystal structure of a putative gnat family acetyltransferase (mw0638)2 from staphylococcus aureus subsp. aureus at 1.63 a resolution
37	<a href="#">d2etha1</a>	Alignment	not modelled	41.6	3	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
38	<a href="#">d1okra_</a>	Alignment	not modelled	41.5	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
39	<a href="#">c2plyB_</a>	Alignment	not modelled	41.4	9	<b>PDB header:</b> translation/rna <b>Chain:</b> B: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
40	<a href="#">c2fe3B_</a>	Alignment	not modelled	39.9	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> peroxide operon regulator; <b>PDBTitle:</b> the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
41	<a href="#">c3iz6V_</a>	Alignment	not modelled	39.7	13	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 40s ribosomal protein s25 (s25e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
42	<a href="#">d1s3ja_</a>	Alignment	not modelled	39.5	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
43	<a href="#">c3hrmA_</a>	Alignment	not modelled	39.3	7	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator sarz; <b>PDBTitle:</b> crystal structure of staphylococcus aureus protein sarz in sulfenic2 acid form
44	<a href="#">d1p6ra_</a>	Alignment	not modelled	39.1	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
45	<a href="#">c3nrvC_</a>	Alignment	not modelled	39.1	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> putative transcriptional regulator (marr/emrr family); <b>PDBTitle:</b> crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1
46	<a href="#">c3e6mD_</a>	Alignment	not modelled	39.0	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> marr family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
47	<a href="#">c3k0lA_</a>	Alignment	not modelled	37.1	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein; <b>PDBTitle:</b> crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
48	<a href="#">d1ub9a_</a>	Alignment	not modelled	37.1	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
49	<a href="#">c2fa5B_</a>	Alignment	not modelled	35.7	9	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator marr/emrr family; <b>PDBTitle:</b> the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
50	<a href="#">c3bj6B_</a>	Alignment	not modelled	35.1	7	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcription regulator sp03579
51	<a href="#">d1i5za1</a>	Alignment	not modelled	34.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
52	<a href="#">d1ulya_</a>	Alignment	not modelled	34.3	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932
53	<a href="#">c3pqkD_</a>	Alignment	not modelled	34.0	24	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> biofilm growth-associated repressor; <b>PDBTitle:</b> crystal structure of the transcriptional repressor bigr from xylella2 fastidiosa
						<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat)

54	<a href="#">d2i6ca1</a>	Alignment	not modelled	33.8	8	<b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
55	<a href="#">d1g3wa1</a>	Alignment	not modelled	33.8	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
56	<a href="#">d2isya1</a>	Alignment	not modelled	33.6	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
57	<a href="#">c3cdhB_</a>	Alignment	not modelled	33.5	4	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of the marr family transcriptional regulator spo14532 from silicibacter pomeroyi dss-3
58	<a href="#">c2nnnB_</a>	Alignment	not modelled	33.2	8	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
59	<a href="#">d1ku9a_</a>	Alignment	not modelled	32.4	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DNA-binding protein Mj223
60	<a href="#">d3bz6a2</a>	Alignment	not modelled	32.4	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PSPTO2686-like
61	<a href="#">c2rdpA_</a>	Alignment	not modelled	32.4	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator marr; <b>PDBTitle:</b> the structure of a marr family protein from bacillus2 stearotherophilus
62	<a href="#">d1xd7a_</a>	Alignment	not modelled	32.0	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator Rrf2
63	<a href="#">c3bwgA_</a>	Alignment	not modelled	30.6	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator yydk; <b>PDBTitle:</b> the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
64	<a href="#">d1fp1d1</a>	Alignment	not modelled	30.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Plant O-methyltransferase, N-terminal domain
65	<a href="#">c2pjpA_</a>	Alignment	not modelled	30.5	15	<b>PDB header:</b> translation/rna <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> structure of the mrna-binding domain of elongation factor2 selb from e.coli in complex with secis rna
66	<a href="#">c3bjaA_</a>	Alignment	not modelled	30.4	4	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family, putative; <b>PDBTitle:</b> crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution
67	<a href="#">d1sd4a_</a>	Alignment	not modelled	29.8	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
68	<a href="#">c2zmeA_</a>	Alignment	not modelled	29.2	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar-sorting protein snf8; <b>PDBTitle:</b> integrated structural and functional model of the human escrt-ii2 complex
69	<a href="#">c2zkzC_</a>	Alignment	not modelled	28.2	5	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional repressor pagr; <b>PDBTitle:</b> crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
70	<a href="#">c3cuqA_</a>	Alignment	not modelled	28.2	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar-sorting protein snf8; <b>PDBTitle:</b> integrated structural and functional model of the human escrt-ii2 complex
71	<a href="#">c2huzB_</a>	Alignment	not modelled	27.8	19	<b>PDB header:</b> structural genomics, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glucosamine 6-phosphate n-acetyltransferase; <b>PDBTitle:</b> crystal structure of gnpmat1
72	<a href="#">d1n71a_</a>	Alignment	not modelled	27.7	13	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
73	<a href="#">d1wi9a_</a>	Alignment	not modelled	27.3	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PCI domain (PINT motif)
74	<a href="#">d2ev0a1</a>	Alignment	not modelled	27.2	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
75	<a href="#">c3kfwX_</a>	Alignment	not modelled	27.2	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> X: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> uncharacterized protein rv0674 from mycobacterium tuberculosis
76	<a href="#">c3edpB_</a>	Alignment	not modelled	27.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lin2111 protein; <b>PDBTitle:</b> the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clp11262
77	<a href="#">c2ev5B_</a>	Alignment	not modelled	26.5	10	<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
78	<a href="#">d2d1ha1</a>	Alignment	not modelled	25.3	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
79	<a href="#">d1se9a_</a>	Alignment	not modelled	25.1	13	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related

80	<a href="#">c1se9A</a>	Alignment	not modelled	25.1	13	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin family; <b>PDBTitle:</b> structure of at3g01050, a ubiquitin-fold protein from2 arabidopsis thaliana
81	<a href="#">c3bz6A</a>	Alignment	not modelled	25.1	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0502 protein pspto_2686; <b>PDBTitle:</b> crystal structure of a conserved protein of unknown function from2 pseudomonas syringae pv. tomato str. dc3000
82	<a href="#">d2aj6a1</a>	Alignment	not modelled	24.6	14	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
83	<a href="#">d2oz6a1</a>	Alignment	not modelled	24.5	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
84	<a href="#">c2oqgA</a>	Alignment	not modelled	24.4	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> arsr-like transcriptional regulator from rhodococcus sp. rha1
85	<a href="#">c3izbV</a>	Alignment	not modelled	23.9	15	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 40s ribosomal protein rps25 (s25e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
86	<a href="#">c3f6oB</a>	Alignment	not modelled	23.8	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulator, arsr family <b>PDBTitle:</b> crystal structure of arsr family transcriptional regulator,2 rha00566
87	<a href="#">d1z91a1</a>	Alignment	not modelled	23.8	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
88	<a href="#">c3bddD</a>	Alignment	not modelled	22.8	9	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein marr; <b>PDBTitle:</b> crystal structure of a putative multiple antibiotic-resistance2 repressor (ssu05_1136) from streptococcus suis 89/1591 at 2.20 a3 resolution
89	<a href="#">d3e5ua1</a>	Alignment	not modelled	22.5	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
90	<a href="#">d1qbic</a>	Alignment	not modelled	21.8	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Z-DNA binding domain
91	<a href="#">c3cuoB</a>	Alignment	not modelled	21.8	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator ygav; <b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
92	<a href="#">c2h09A</a>	Alignment	not modelled	21.7	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator mntr; <b>PDBTitle:</b> crystal structure of diphtheria toxin repressor like protein2 from e. coli
93	<a href="#">d1kyza1</a>	Alignment	not modelled	21.0	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Plant O-methyltransferase, N-terminal domain
94	<a href="#">c2wpwA</a>	Alignment	not modelled	20.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orf14; <b>PDBTitle:</b> tandem gnat protein from the clavulanic acid biosynthesis2 pathway (without accoa)
95	<a href="#">d2gaua1</a>	Alignment	not modelled	19.8	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
96	<a href="#">c2jscB</a>	Alignment	not modelled	19.8	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator rv1994c/mt2050; <b>PDBTitle:</b> nmr structure of the cadmium metal-sensor cmtr from mycobacterium2 tuberculosis
97	<a href="#">d2gxba1</a>	Alignment	not modelled	19.8	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Z-DNA binding domain
98	<a href="#">d1qgpa</a>	Alignment	not modelled	19.7	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Z-DNA binding domain
99	<a href="#">d1mkma1</a>	Alignment	not modelled	19.6	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator lclR, N-terminal domain