























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1725c_(-)_1951048_1951758
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2fswa1</a>	 Alignment		100.0	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> HxIR-like
2	<a href="#">d1z7ua1</a>	 Alignment		100.0	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> HxIR-like
3	<a href="#">d2f2ea1</a>	 Alignment		100.0	36	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> HxIR-like
4	<a href="#">c4gcvD_</a>	 Alignment		100.0	34	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcription protein; <b>PDBTitle:</b> structure of a putative transcription factor (pa1374)from pseudomonas2 aeruginosa
5	<a href="#">c4a5mH_</a>	 Alignment		100.0	26	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator yybr; <b>PDBTitle:</b> redox regulator hypr in its oxidized form
6	<a href="#">c4hqeB_</a>	 Alignment		100.0	22	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator qsr; <b>PDBTitle:</b> the crystal structure of qsr-dna complex
7	<a href="#">d1yyva1</a>	 Alignment		99.9	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> HxIR-like
8	<a href="#">c3df8A_</a>	 Alignment		99.9	30	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> possible hxlr family transcriptional factor; <b>PDBTitle:</b> the crystal structure of a possible hxlr family transcriptional factor2 from thermoplasma volcanium gss1
9	<a href="#">c5hs9A_</a>	 Alignment		99.9	39	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator yodb; <b>PDBTitle:</b> crystal structure of the quinone-bound yodb from b. subtilis
10	<a href="#">d2hzta1</a>	 Alignment		99.9	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> HxIR-like
11	<a href="#">d2cfua1</a>	 Alignment		99.7	16	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> Alkylsulfatase C-terminal domain-like

12	<a href="#">d1ikta_</a>	Alignment		99.6	15	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> Sterol carrier protein, SCP
13	<a href="#">d1c44a_</a>	Alignment		99.6	13	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> Sterol carrier protein, SCP
14	<a href="#">c3bdqB_</a>	Alignment		99.6	16	<b>PDB header:</b> lipid transport <b>Chain:</b> B: <b>PDB Molecule:</b> sterol carrier protein 2-like 2; <b>PDBTitle:</b> room temperture crystal structure of sterol carrier protein-2 2 like-2
15	<a href="#">c4ueiA_</a>	Alignment		99.6	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sterol carrier protein 2/3-oxoacyl-coa thiolase; <b>PDBTitle:</b> solution structure of the sterol carrier protein domain 22 of helicoverpa armigera
16	<a href="#">c3bn8A_</a>	Alignment		99.5	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sterol carrier protein 2; <b>PDBTitle:</b> crystal structure of a putative sterol carrier protein type 2 (af1534)2 from archaeoglobus fulgidus dsm 4304 at 2.11 a resolution
17	<a href="#">c2yheD_</a>	Alignment		99.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> sec-alkyl sulfatase; <b>PDBTitle:</b> structure determination of the stereoselective inverting sec-2 alkylsulfatase pisa1 from pseudomonas sp.
18	<a href="#">c4nurB_</a>	Alignment		99.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> psdsa; <b>PDBTitle:</b> crystal structure of thermostable alkylsulfatase sdsap from2 pseudomonas sp. s9
19	<a href="#">c2cfuA_</a>	Alignment		99.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sdsa1; <b>PDBTitle:</b> crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
20	<a href="#">d1pz4a_</a>	Alignment		99.4	13	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> Sterol carrier protein, SCP
21	<a href="#">c4jgxB_</a>	Alignment	not modelled	99.4	10	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid-binding protein; <b>PDBTitle:</b> the structure of sterol carrier protein 2 from the yeast yarrowia2 lipolytica
22	<a href="#">c4pdxB_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alkyl/aryl-sulfatase yjcs; <b>PDBTitle:</b> crystal structure of escherchia coli uncharacterized protein yjcs
23	<a href="#">c3bkrA_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sterol carrier protein-2 like-3; <b>PDBTitle:</b> crystal structure of sterol carrier protein-2 like-3 (scp2-2 l3) from aedes aegypti
24	<a href="#">d1wfra_</a>	Alignment	not modelled	99.1	14	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> Sterol carrier protein, SCP
25	<a href="#">c2kkoB_</a>	Alignment	not modelled	99.0	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> possible transcriptional regulatory protein <b>PDBTitle:</b> 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.
26	<a href="#">c3f6oB_</a>	Alignment	not modelled	98.9	13	<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
27	<a href="#">c2oqgA_</a>	Alignment	not modelled	98.9	28	<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

28	<a href="#">d1r1ta_</a>	Alignment	not modelled	98.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
29	<a href="#">c2lkbB_</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, arsr family; <b>PDBTitle:</b> solution structure of apo-nmtr
30	<a href="#">c1r22B_</a>	Alignment	not modelled	98.8	19	<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="#">c3pqkD_</a>	Alignment	not modelled	98.8	30	<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
32	<a href="#">d1r1ua_</a>	Alignment	not modelled	98.7	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
33	<a href="#">c2jscB_</a>	Alignment	not modelled	98.7	25	<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
34	<a href="#">d1ub9a_</a>	Alignment	not modelled	98.7	19	<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="#">c4omzG_</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> nolr; <b>PDBTitle:</b> crystal structure of nolr from sinorhizobium fredii
36	<a href="#">c3f6vA_</a>	Alignment	not modelled	98.7	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> crystal structure of possible transcriptional regulator for arsenical2 resistance
37	<a href="#">c3f8fA_</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, padr-like family; <b>PDBTitle:</b> crystal structure of multidrug binding transcriptional regulator lmrr2 complexed with daunomycin
38	<a href="#">c3hhhA_</a>	Alignment	not modelled	98.6	28	<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
39	<a href="#">d1xmaa_</a>	Alignment	not modelled	98.5	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PadR-like
40	<a href="#">c1xmaA_</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> predicted transcriptional regulator; <b>PDBTitle:</b> structure of a transcriptional regulator from clostridium thermocellum2 cth-833
41	<a href="#">c3ri2B_</a>	Alignment	not modelled	98.5	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, padr-like family; <b>PDBTitle:</b> crystal structure of padr family transcriptional regulator from2 eggerthella lenta dsm 2243
42	<a href="#">c3cuoB_</a>	Alignment	not modelled	98.4	23	<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
43	<a href="#">c3jthA_</a>	Alignment	not modelled	98.4	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription activator hlyu; <b>PDBTitle:</b> crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
44	<a href="#">c6h6pA_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquinone biosynthesis protein ubij; <b>PDBTitle:</b> ubij-scp2 ubiquinone synthesis protein
45	<a href="#">d2p4wa1</a>	Alignment	not modelled	98.3	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF1790-like
46	<a href="#">c3l7wA_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.1704; <b>PDBTitle:</b> the crystal structure of smu.1704 from streptococcus mutans ua159
47	<a href="#">c5zhcA_</a>	Alignment	not modelled	98.3	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of the padr-family transcriptional regulator rv34882 of mycobacterium tuberculosis h37rv
48	<a href="#">c4esbA_</a>	Alignment	not modelled	98.3	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, padr family; <b>PDBTitle:</b> crystal structure of padr-like transcriptional regulator (bc4206) from2 bacillus cereus strain atcc 14579
49	<a href="#">c2nyxB_</a>	Alignment	not modelled	98.3	18	<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
50	<a href="#">c2qufB_</a>	Alignment	not modelled	98.2	15	<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
51	<a href="#">c6j05B_</a>	Alignment	not modelled	98.2	27	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
52	<a href="#">c6j0eB_</a>	Alignment	not modelled	98.2	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> arsenic responsive repressor arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
						<b>PDB header:</b> transcription

53	<a href="#">c2zkzC_</a>	Alignment	not modelled	98.2	19	<b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional repressor pagr; <b>PDBTitle:</b> crystal structure of the transcriptional repressor pagr of bacillus2 anthracis
54	<a href="#">c4esfA_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> padr-like transcriptional regulator; <b>PDBTitle:</b> crystal structure of padr-like transcriptional regulator (bce3449)2 from bacillus cereus strain atcc 10987
55	<a href="#">c2gxgA_</a>	Alignment	not modelled	98.2	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> 146aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
56	<a href="#">c5dymA_</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> padr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a padr family transcription regulator from2 hypervirulent clostridium difficile r20291 - cd padr_0991 to 1.893 angstrom resolution
57	<a href="#">c3f3xA_</a>	Alignment	not modelled	98.1	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family, putative; <b>PDBTitle:</b> crystal structure of the transcriptional regulator bldr from2 sulfolobus solfataricus
58	<a href="#">d3ctaa1</a>	Alignment	not modelled	98.1	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
59	<a href="#">d1lnwa_</a>	Alignment	not modelled	98.0	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
60	<a href="#">c5jlsA_</a>	Alignment	not modelled	98.0	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adhesin competence repressor; <b>PDBTitle:</b> crystal structure of adhesin competence repressor (adcr) from2 streptococcus pyogenes (c-terminally his tagged)
61	<a href="#">c3zplE_</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> E: <b>PDB Molecule:</b> putative marr-family transcriptional repressor; <b>PDBTitle:</b> crystal structure of sco3205, a marr family transcriptional regulator2 from streptomyces coelicolor, in complex with dna
62	<a href="#">c5eriA_</a>	Alignment	not modelled	98.0	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> marr family transcriptional regulator; <b>PDBTitle:</b> marr protein from peptoclostridium difficile da00132
63	<a href="#">c5h20A_</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative padr-family transcriptional regulatory protein; <b>PDBTitle:</b> x-ray structure of padr-like transcription factor from bacteroid2 fragilis
64	<a href="#">c3ctaA_</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin kinase; <b>PDBTitle:</b> crystal structure of riboflavin kinase from thermoplasma acidophilum
65	<a href="#">d1ulya_</a>	Alignment	not modelled	97.9	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Hypothetical protein PH1932
66	<a href="#">d1u2wa1</a>	Alignment	not modelled	97.9	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
67	<a href="#">c3bj6B_</a>	Alignment	not modelled	97.9	15	<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
68	<a href="#">d2etha1</a>	Alignment	not modelled	97.9	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
69	<a href="#">c6jbxB_</a>	Alignment	not modelled	97.9	11	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid biosynthesis transcriptional regulator; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae fabt in complex with dna
70	<a href="#">d2hr3a1</a>	Alignment	not modelled	97.9	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
71	<a href="#">d1jgsa_</a>	Alignment	not modelled	97.9	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
72	<a href="#">d1lj9a_</a>	Alignment	not modelled	97.9	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
73	<a href="#">c3k0IA_</a>	Alignment	not modelled	97.9	18	<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
74	<a href="#">c2rdpA_</a>	Alignment	not modelled	97.9	16	<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 stearothermophilus
75	<a href="#">d2fbia1</a>	Alignment	not modelled	97.9	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
76	<a href="#">c3bpxB_</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
77	<a href="#">c5xqpB_</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator rv0081; <b>PDBTitle:</b> crystal structure of m.tuberculosis rv0081 <b>PDB header:</b> flavoprotein

78	<a href="#">c5zc2B_</a>	Alignment	not modelled	97.9	11	<b>Chain:</b> B: <b>PDB Molecule:</b> p-hydroxyphenylacetate 3-hydroxylase, reductase component; <b>PDBTitle:</b> acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah).2 reductase component (c1)
79	<a href="#">c3bjaA_</a>	Alignment	not modelled	97.8	16	<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
80	<a href="#">d1s3ja_</a>	Alignment	not modelled	97.8	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
81	<a href="#">c3g3zA_</a>	Alignment	not modelled	97.8	13	<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
82	<a href="#">c3nqoB_</a>	Alignment	not modelled	97.8	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> marr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
83	<a href="#">c4b8xB_</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> possible marr-transcriptional regulator; <b>PDBTitle:</b> near atomic resolution crystal structure of sco5413, a marr family2 transcriptional regulator from streptomyces coelicolor
84	<a href="#">c4yifE_</a>	Alignment	not modelled	97.8	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> marr family protein rv0880; <b>PDBTitle:</b> crystal structure of rv0880
85	<a href="#">d2fbha1</a>	Alignment	not modelled	97.8	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
86	<a href="#">c3e6mD_</a>	Alignment	not modelled	97.8	13	<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.
87	<a href="#">c4fhtA_</a>	Alignment	not modelled	97.8	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> pcav transcriptional regulator; <b>PDBTitle:</b> crystal structure of the pcav transcriptional regulator from2 streptomyces coelicolor in complex with its natural ligand
88	<a href="#">c3nrvc_</a>	Alignment	not modelled	97.7	19	<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
89	<a href="#">c5zqhA_</a>	Alignment	not modelled	97.7	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> padr family transcriptional regulator; <b>PDBTitle:</b> crystal structure of streptococcus transcriptional regulator
90	<a href="#">c3zmdD_</a>	Alignment	not modelled	97.7	17	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of absc, a marr family transcriptional2 regulator from streptomyces coelicolor
91	<a href="#">d2a61a1</a>	Alignment	not modelled	97.7	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
92	<a href="#">c2fa5B_</a>	Alignment	not modelled	97.7	14	<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
93	<a href="#">c4em1A_</a>	Alignment	not modelled	97.7	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator sar2349; <b>PDBTitle:</b> staphylococcus aureus marr native
94	<a href="#">c2nnnB_</a>	Alignment	not modelled	97.7	15	<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
95	<a href="#">c5jbrA_</a>	Alignment	not modelled	97.7	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bcav_2135; <b>PDBTitle:</b> crystal structure of uncharacterized protein bcav_2135 from2 beutenbergia cavernae
96	<a href="#">d2ozga1</a>	Alignment	not modelled	97.7	11	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> EF1021 C-terminal domain-like
97	<a href="#">c3cjnA_</a>	Alignment	not modelled	97.6	18	<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
98	<a href="#">d2bv6a1</a>	Alignment	not modelled	97.6	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
99	<a href="#">c4xrfA_</a>	Alignment	not modelled	97.6	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of mepr like protein complexed with pseudoligands
100	<a href="#">d2d1ha1</a>	Alignment	not modelled	97.6	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
101	<a href="#">c5yhxH_</a>	Alignment	not modelled	97.6	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> zinc transport transcriptional regulator; <b>PDBTitle:</b> structure of lactococcus lactis zittr, wild type
102	<a href="#">c4mnuA_</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> slya-like transcription regulator; <b>PDBTitle:</b> crystal structure of uncharacterized slya-like transcription regulator2 from listeria monocytogenes
						<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein



103	<a href="#">c3l9fD_</a>	Alignment	not modelled	97.6	22	smu.1604c; <b>PDBTitle:</b> the crystal structure of smu.1604c from streptococcus mutans ua159
104	<a href="#">c2it0A_</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of a two-domain ider-dna complex crystal2 form ii
105	<a href="#">c1f5tA_</a>	Alignment	not modelled	97.6	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
106	<a href="#">c2qwwB_</a>	Alignment	not modelled	97.5	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
107	<a href="#">c4nb5D_</a>	Alignment	not modelled	97.5	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> dna binding protein; <b>PDBTitle:</b> crystal structure of a transcriptional regulator
108	<a href="#">c5dukA_</a>	Alignment	not modelled	97.5	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna binding protein; <b>PDBTitle:</b> n-terminal structure of putative dna binding transcription factor from2 thermoplasmatales archaeon scgc ab-539-n05
109	<a href="#">c3kp3B_</a>	Alignment	not modelled	97.5	11	<b>PDB header:</b> transcription regulator/antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator tcar; <b>PDBTitle:</b> staphylococcus epidermidis in complex with ampicillin
110	<a href="#">c5x11G_</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> G: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of bacillus subtilis padr in complex with operator2 dna
111	<a href="#">c3r1kA_</a>	Alignment	not modelled	97.5	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> enhanced intracellular survival protein; <b>PDBTitle:</b> crystal structure of acetyltransferase eis from mycobacterium2 tuberculosis h37rv in complex with coa and an acetamide moiety
112	<a href="#">c4g6qA_</a>	Alignment	not modelled	97.5	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein kfla_6221 from2 kribbella flavida dsm 17836
113	<a href="#">c2x4hA_</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sso2273; <b>PDBTitle:</b> crystal structure of the hypothetical protein sso2273 from2 sulfobolus solfataricus
114	<a href="#">c3b73A_</a>	Alignment	not modelled	97.4	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phih1 repressor-like protein; <b>PDBTitle:</b> crystal structure of the phih1 repressor-like protein from haloarcula2 marismortui
115	<a href="#">c2fxaB_</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> protease production regulatory protein hpr; <b>PDBTitle:</b> structure of the protease production regulatory protein hpr from2 bacillus subtilis.
116	<a href="#">c1fx7C_</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis
117	<a href="#">d2i00a1</a>	Alignment	not modelled	97.4	12	<b>Fold:</b> SCP-like <b>Superfamily:</b> SCP-like <b>Family:</b> EF1021 C-terminal domain-like
118	<a href="#">d3broa1</a>	Alignment	not modelled	97.4	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
119	<a href="#">c5aiqD_</a>	Alignment	not modelled	97.4	26	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of ligand-free nadr
120	<a href="#">c5e1xA_</a>	Alignment	not modelled	97.4	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of the organohalide sensing rdhr-cbdba16252 transcriptional regulator in the 3,4-dichlorophenol bound form