

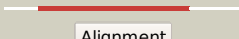
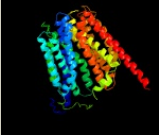
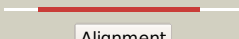


















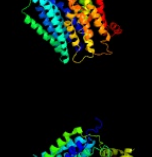


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1877 (- )_2125911_2127974
Date	Fri Aug 2 13:30:49 BST 2019
Unique Job ID	2f06680256a1159f

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4zp0A_</a>	 Alignment		100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug transporter mdfa; <b>PDBTitle:</b> crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate
2	<a href="#">d1pw4a_</a>	 Alignment		100.0	15	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> Glycerol-3-phosphate transporter
3	<a href="#">c3wdoA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> mfs transporter; <b>PDBTitle:</b> structure of e. coli yajr transporter
4	<a href="#">c6e9oA_</a>	 Alignment		99.9	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-galactonate transport; <b>PDBTitle:</b> e. coli d-galactonate:proton symporter mutant e133q in the outward2 substrate-bound form
5	<a href="#">c6g9xB_</a>	 Alignment		99.9	17	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> major facilitator superfamily mfs_1; <b>PDBTitle:</b> crystal structure of a mfs transporter at 2.54 angstrom resolution
6	<a href="#">c4ldsB_</a>	 Alignment		99.9	20	<b>PDB header:</b> transport protein, membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bicyclomycin resistance protein tcb; <b>PDBTitle:</b> the inward-facing structure of the glucose transporter from2 staphylococcus epidermidis
7	<a href="#">c6ei3A_</a>	 Alignment		99.9	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> proton-dependent oligopeptide transporter family protein; <b>PDBTitle:</b> crystal structure of auto inhibited pot family peptide transporter
8	<a href="#">c6gs7A_</a>	 Alignment		99.9	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptide and tripeptide permease a; <b>PDBTitle:</b> crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer
9	<a href="#">c2gfpA_</a>	 Alignment		99.9	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance protein d; <b>PDBTitle:</b> structure of the multidrug transporter emrd from2 escherichia coli
10	<a href="#">c6exsA_</a>	 Alignment		99.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptide abc transporter permease; <b>PDBTitle:</b> crystal structure of a pot family transporter in complex with2 thioalcohol conjugated peptide.
11	<a href="#">c4apsB_</a>	 Alignment		99.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> di- or tripeptide h+ symporter; <b>PDBTitle:</b> crystal structure of a pot family peptide transporter in an inward2 open conformation.

12	<a href="#">c6h7dA</a>	Alignment		99.9	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar transport protein 10; <b>PDBTitle:</b> crystal structure of a. thaliana sugar transport protein 10 in complex2 with glucose in the outward occluded state
13	<a href="#">c3o7pA</a>	Alignment		99.9	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-fucose-proton symporter; <b>PDBTitle:</b> crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
14	<a href="#">c4ikyA</a>	Alignment		99.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> di-tripeptide abc transporter (permease); <b>PDBTitle:</b> crystal structure of peptide transporter pot (e310q mutant) in complex2 with sulfate
15	<a href="#">c2xutC</a>	Alignment		99.9	11	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> proton/peptide symporter family protein; <b>PDBTitle:</b> crystal structure of a proton dependent oligopeptide (pot) family2 transporter.
16	<a href="#">c4cl5B</a>	Alignment		99.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nitrate transporter 1.1; <b>PDBTitle:</b> crystal structure of the nitrate transporter nrt1.1 from2 arabidopsis thaliana in complex with nitrate.
17	<a href="#">c4w6vA</a>	Alignment		99.9	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> di-/tripeptide transporter; <b>PDBTitle:</b> crystal structure of a peptide transporter from yersinia2 enterocolitica at 3 a resolution
18	<a href="#">c5c65A</a>	Alignment		99.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> structure of the human glucose transporter glut3 / slc2a3
19	<a href="#">c4pypA</a>	Alignment		99.9	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> crystal structure of the human glucose transporter glut1
20	<a href="#">c4q65A</a>	Alignment		99.9	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptide permease d; <b>PDBTitle:</b> structure of the e. coli peptide transporter ybgh
21	<a href="#">c4ybgB</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transport protein/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> rat glut5 with fv in the outward-open form
22	<a href="#">c4gbzA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-xylose-proton symporter; <b>PDBTitle:</b> the structure of the mfs (major facilitator superfamily) proton:xylose2 symporter xyle bound to d-glucose
23	<a href="#">c4j05A</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate transporter; <b>PDBTitle:</b> crystal structure of a eukaryotic phosphate transporter
24	<a href="#">c5aynA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 39 (iron-regulated transporter); <b>PDBTitle:</b> crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state
25	<a href="#">c4lepB</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> proton:oligopeptide symporter pot family; <b>PDBTitle:</b> structural insights into substrate recognition in proton dependent2 oligopeptide transporters
26	<a href="#">d1pv7a</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> LacY-like proton/sugar symporter
27	<a href="#">c1pv7B</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lactose permease; <b>PDBTitle:</b> crystal structure of lactose permease with tdg
28	<a href="#">c5aymA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 39 (iron-regulated transporter); <b>PDBTitle:</b> crystal structure of a bacterial homologue of iron

						transporter2 ferroportin in outward-facing state with soaked iron <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite extrusion protein 2; <b>PDBTitle:</b> crystal structure of a membrane transporter (selenomethionine2 derivative)
29	<a href="#">c4iu8A_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite extrusion protein 2; <b>PDBTitle:</b> crystal structure of a membrane transporter (selenomethionine2 derivative)
30	<a href="#">c4iu9A_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite extrusion protein 2; <b>PDBTitle:</b> crystal structure of a membrane transporter
31	<a href="#">c6ob7A_</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> equilibrative nucleoside transporter 1; <b>PDBTitle:</b> human equilibrative nucleoside transporter-1, dilazep bound
32	<a href="#">c4m64D_</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> melibiose carrier protein; <b>PDBTitle:</b> 3d crystal structure of na+/melibiose symporter of salmonella2 typhimurium
33	<a href="#">c2nyxB_</a>	Alignment	not modelled	98.6	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
34	<a href="#">c5zc2B_</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> flavoprotein <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)
35	<a href="#">d1lnwa_</a>	Alignment	not modelled	98.3	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
36	<a href="#">c2x4hA_</a>	Alignment	not modelled	98.2	21	<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 sulfolobus solfataricus
37	<a href="#">d1s3ja_</a>	Alignment	not modelled	98.1	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
38	<a href="#">d2a61a1</a>	Alignment	not modelled	98.0	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
39	<a href="#">c3e6mD_</a>	Alignment	not modelled	98.0	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.
40	<a href="#">c4yifE_</a>	Alignment	not modelled	98.0	19	<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
41	<a href="#">c2fa5B_</a>	Alignment	not modelled	98.0	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
42	<a href="#">c2rdpA_</a>	Alignment	not modelled	98.0	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
43	<a href="#">c3bj6B_</a>	Alignment	not modelled	97.9	14	<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
44	<a href="#">d2hr3a1</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
45	<a href="#">c4fhtA_</a>	Alignment	not modelled	97.9	21	<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
46	<a href="#">c5hsmA_</a>	Alignment	not modelled	97.9	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator rv2887; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis marr family protein2 rv2887
47	<a href="#">c3bpxB_</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
48	<a href="#">c3zplE_</a>	Alignment	not modelled	97.9	14	<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
49	<a href="#">c3zmdD_</a>	Alignment	not modelled	97.9	15	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of abs, a marr family transcriptional2 regulator from streptomyces coelicolor
50	<a href="#">c3oopA_</a>	Alignment	not modelled	97.8	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2960 protein; <b>PDBTitle:</b> the structure of a protein with unknown function from listeria innocua2 clip11262
51	<a href="#">c4xrfA_</a>	Alignment	not modelled	97.8	16	<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
52	<a href="#">c3k0IA_</a>	Alignment	not modelled	97.8	15	<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
53	<a href="#">d2fbia1</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

54	<a href="#">c4fx0A_</a>	Alignment	not modelled	97.8	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional repressor protein; <b>PDBTitle:</b> crystal structure of m. tuberculosis transcriptional regulator mosr
55	<a href="#">c3g3zA_</a>	Alignment	not modelled	97.8	18	<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
56	<a href="#">c6jbxB_</a>	Alignment	not modelled	97.8	12	<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
57	<a href="#">c3boqB_</a>	Alignment	not modelled	97.8	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 uncharacterized marr family transcriptional regulator from2 silicibacter pomeroyi
58	<a href="#">c4mnuA_</a>	Alignment	not modelled	97.7	15	<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
59	<a href="#">c3bjaA_</a>	Alignment	not modelled	97.7	14	<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
60	<a href="#">c3f3xA_</a>	Alignment	not modelled	97.7	15	<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 sulfobolus solfataricus
61	<a href="#">c2gxgA_</a>	Alignment	not modelled	97.7	13	<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 sulfobolus tokodaii strain7
62	<a href="#">c3ecoB_</a>	Alignment	not modelled	97.7	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> meprr; <b>PDBTitle:</b> crystal structure of meprr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
63	<a href="#">c5aiqD_</a>	Alignment	not modelled	97.7	12	<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
64	<a href="#">d1lj9a_</a>	Alignment	not modelled	97.7	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
65	<a href="#">c2nnnB_</a>	Alignment	not modelled	97.7	21	<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
66	<a href="#">c3nrvC_</a>	Alignment	not modelled	97.7	12	<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
67	<a href="#">d2bv6a1</a>	Alignment	not modelled	97.6	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
68	<a href="#">d2etha1</a>	Alignment	not modelled	97.6	21	<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="#">d2fbha1</a>	Alignment	not modelled	97.6	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
70	<a href="#">c2pexA_</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator ohrr; <b>PDBTitle:</b> structure of reduced c22s ohrr from xanthomonas campestris
71	<a href="#">c4b8xB_</a>	Alignment	not modelled	97.6	20	<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
72	<a href="#">d3broa1</a>	Alignment	not modelled	97.6	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
73	<a href="#">c3hrmA_</a>	Alignment	not modelled	97.6	14	<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
74	<a href="#">d2fbka1</a>	Alignment	not modelled	97.5	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
75	<a href="#">c3fm5D_</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> x-ray crystal structure of transcriptional regulator (marr family)2 from rhodococcus sp. rha1
76	<a href="#">c5yhxB_</a>	Alignment	not modelled	97.5	12	<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 zitrr, wild type
77	<a href="#">c1fx7C_</a>	Alignment	not modelled	97.4	21	<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
78	<a href="#">c5eriA_</a>	Alignment	not modelled	97.4	14	<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

79	<a href="#">c6c28C</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> transcriptional repressor, cour, bound to p-coumaroyl-coa
80	<a href="#">c3cjnA</a>	Alignment	not modelled	97.4	21	<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
81	<a href="#">c3kp3B</a>	Alignment	not modelled	97.4	13	<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
82	<a href="#">d3deua1</a>	Alignment	not modelled	97.4	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
83	<a href="#">c1f5tA</a>	Alignment	not modelled	97.3	18	<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
84	<a href="#">c2qwwB</a>	Alignment	not modelled	97.3	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
85	<a href="#">c5e1xA</a>	Alignment	not modelled	97.3	11	<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
86	<a href="#">d1jgsa</a>	Alignment	not modelled	97.3	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
87	<a href="#">c3deuB</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator slya; <b>PDBTitle:</b> crystal structure of transcription regulatory protein slya from2 salmonella typhimurium in complex with salicylate ligands
88	<a href="#">d1z91a1</a>	Alignment	not modelled	97.3	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
89	<a href="#">c3s2wB</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> the crystal structure of a marr transcriptional regulator from2 methanosarcina mazei go1
90	<a href="#">c3cdhB</a>	Alignment	not modelled	97.3	20	<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
91	<a href="#">c4q77B</a>	Alignment	not modelled	97.2	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator rot; <b>PDBTitle:</b> crystal structure of rot, a global regulator of virulence genes in2 staphylococcus aureus
92	<a href="#">c1g3wA</a>	Alignment	not modelled	97.2	21	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> cd-cys102ser dtxr
93	<a href="#">c2it0A</a>	Alignment	not modelled	97.2	18	<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
94	<a href="#">c3bddD</a>	Alignment	not modelled	97.0	11	<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
95	<a href="#">c4o6jA</a>	Alignment	not modelled	97.0	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent transcription repressor related protein; <b>PDBTitle:</b> crystal sturcture of t. acidophilum ider
96	<a href="#">c4hblA</a>	Alignment	not modelled	97.0	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of abfr of staphylococcus epidermidis
97	<a href="#">c5cviB</a>	Alignment	not modelled	97.0	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> slor; <b>PDBTitle:</b> structure of the manganese regulator slor
98	<a href="#">c4em1A</a>	Alignment	not modelled	97.0	15	<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
99	<a href="#">c3hruA</a>	Alignment	not modelled	96.9	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> metalloregulator scar; <b>PDBTitle:</b> crystal structure of scar with bound zn2+
100	<a href="#">c3jw4C</a>	Alignment	not modelled	96.8	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, marr/emrr family; <b>PDBTitle:</b> the structure of a putative marr family transcriptional regulator from2 clostridium acetobutylicum
101	<a href="#">c2h09A</a>	Alignment	not modelled	96.8	16	<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
102	<a href="#">c5jbrA</a>	Alignment	not modelled	96.8	15	<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
103	<a href="#">d2fxaa1</a>	Alignment	not modelled	96.7	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
104	<a href="#">d1p4xa2</a>	Alignment	not modelled	96.7	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
105	<a href="#">c1p4xA_</a>	Alignment	not modelled	96.6	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> staphylococcal accessory regulator a homologue; <b>PDBTitle:</b> crystal structure of sars protein from staphylococcus aureus
106	<a href="#">c2ev5B_</a>	Alignment	not modelled	96.4	19	<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
107	<a href="#">c3tgnA_</a>	Alignment	not modelled	96.3	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> adc operon repressor adcr; <b>PDBTitle:</b> crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
108	<a href="#">d2frha1</a>	Alignment	not modelled	96.3	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
109	<a href="#">c3nqoB_</a>	Alignment	not modelled	96.3	15	<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
110	<a href="#">d1ub9a_</a>	Alignment	not modelled	96.1	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
111	<a href="#">d1sfxa_</a>	Alignment	not modelled	96.0	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
112	<a href="#">c5jlsA_</a>	Alignment	not modelled	96.0	12	<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)
113	<a href="#">c3r0aB_</a>	Alignment	not modelled	95.5	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
114	<a href="#">c6o5cB_</a>	Alignment	not modelled	95.3	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative metal-dependent transcriptional regulator; <b>PDBTitle:</b> x-ray crystal structure of metal-dependent transcriptional regulator2 mtrsr
115	<a href="#">d1p4xa1</a>	Alignment	not modelled	95.3	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
116	<a href="#">d2obpa1</a>	Alignment	not modelled	95.3	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ReutB4095-like
117	<a href="#">c2fxaB_</a>	Alignment	not modelled	95.2	20	<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.
118	<a href="#">d1hsja1</a>	Alignment	not modelled	95.0	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="#">c4gcvD_</a>	Alignment	not modelled	95.0	22	<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
120	<a href="#">c4a5mH_</a>	Alignment	not modelled	94.7	13	<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