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Crystal structure of transcriptional regulator protein from *Thermotoga maritima*

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The crystal structure of a transcriptional regulator protein from *Thermotoga maritima* TM1030 was determined by modified single-wavelength anomalous dispersion method at 2.0Å. Protein crystallized in orthorhombic space group $P2_12_12$ (a = 56.04 Å, b = 65.68 Å and c = 55.694 Å) with one monomer in the asymmetric unit, corresponding to solvent content of 42%. This 24kD helical protein belongs to a TetR family. Despite the low sequence similarity, the three-dimensional structure of TM1030 is closely related to known structures of 10 proteins that function as multidrug binding transcriptional repressors. TM1030 contains a large exposed pocket similar to the drug-binding pockets present in these repressors. The study of complexes with various antibiotic agents is under way. The comparison of the structure with other transcriptional regulator proteins will be presented.