

# CRYSTAL STRUCTURE OF tRNA(m<sup>1</sup>G37)METHYLTRANSFERASE

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tRNA(m<sup>1</sup>G37)methyltransferase (TrmD) catalyzes the transfer of a methyl group from S-adenosyl-L-methionine (AdoMet) to G<sup>37</sup> within a subset of bacterial tRNA species, which have a residue G at 36<sup>th</sup> position. The modified guanosine is adjacent to and 3' of the anticodon and is essential for the maintenance of the correct reading frame during translation. We have determined the first crystal structure of TrmD from *Haemophilus influenzae*, as a binary complex with either AdoMet or S-adenosyl-L-homocysteine (AdoHcy), as a ternary complex with AdoHcy/phosphate, and as an apo form. The structure indicates that TrmD functions as a dimer (Figure 1). It also suggests the binding mode of G<sup>36</sup>G<sup>37</sup> in the active site of TrmD and catalytic mechanism. The N-terminal domain has a trefoil knot, in which AdoMet or AdoHcy is bound in a novel, bent conformation. The C-terminal domain shows a structural similarity to DNA binding domain of *trp* or *tet* repressor. We propose a plausible model for the TrmD<sub>2</sub>-tRNA<sub>2</sub> complex, which provides insights into recognition of the general tRNA structure by TrmD (Figure 2).

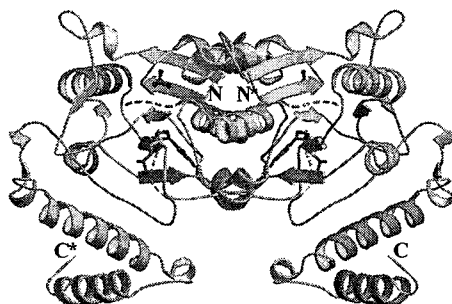


Figure 1. TrmD dimer (ternary complex with AdoHcy and phosphate)

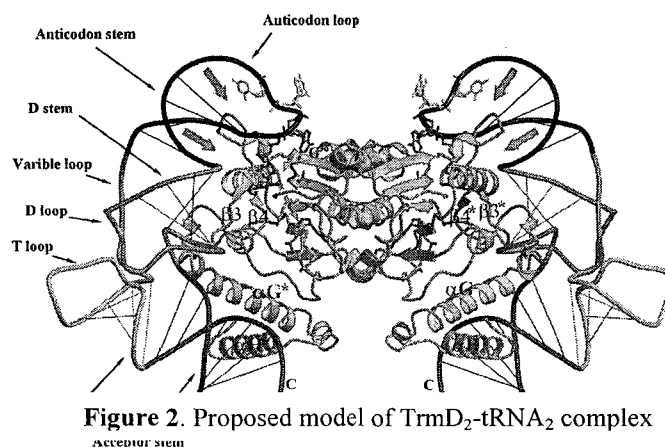


Figure 2. Proposed model of TrmD<sub>2</sub>-tRNA<sub>2</sub> complex

Reference: Ahn *et al.* (2003) *EMBO J.* 22, 000-000. (in press)