**Identification of Trm7 residues required for Trm732 and Trm734 binding for tRNA methyltransferase in yeast**

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Transfer RNAs (tRNAs) undergo post-transcriptional modifications at or near the anticodon loop and are necessary for protein synthesis. In *Saccharomyces cerevisiae,* Trm7 is required for 2’-*O*-methylation of tRNA and requires interaction with Trm732 and Trm734 for modifications at positions 32 and 34, respectively. The Trm7, Trm732, and Trm734 proteins are widely conserved in numerous eukaryotes, indicating that Trm7 proteins may universally require binding partners for methyltransferase activity. In humans, mutations in FTSJ1, a Trm7 ortholog, can cause non-syndromic X-linked intellectual disability. The particular Trm7 residues associated with Trm732 or Trm734 binding are still unknown. To identify these residues, sequences of evolutionarily diverse Trm7 homologs were compared to identify possible regions required for binding to Trm732 and Trm734. Candidate residues were modeled on the Trm7:Trm734 crystal structure to identify possible interactions. Trm7 variants were generated by site-directed mutagenesis, and a yeast growth assay was conducted to analyze the selected Trm7 amino acid variants. Through a series of yeast mutants that required Trm7 interaction with Trm732 or Trm734 for proper growth, we have identified Trm7 residues required for both Trm732 and Trm734 binding interactions. Through this study, understanding how these proteins interact will later facilitate the study of conserved homologs in humans.