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INFLUENCE OF POSTTRANSCRIPTIONAL MODIFICATIONS ON RNA STRUCTURES: CRYSTALLOGRAPHIC AND THERMODYNAMIC ANALYSIS

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The ubiquity of the RNA's functions comes from its structural richness derived from four nucleotides (A, C, G, U) and their canonical pairing. Posttranscriptional modifications of nucleotides expand RNA folding possibilities, and thus the spectrum of structural variations. Among modifications, pseudouridine (Ψ) is the most abundant across all RNA classes and three domains of life[1]. The N1-methylpseudouridine (m1Ψ) has been identified in eucaryotic rRNA, and in archaeal tRNA and rRNA[1]. It has also been incorporated into COVID-19 mRNA vaccines to improve their efficiency[2]. Comparison of the 3D models of modified sequences to their 'native'counterparts can help describe the impact of the modification on RNA structure and function. Hence, more crystallographic studies on RNA molecules is crucial, especially given their limited number.
Here, we present the crystallographic and thermodynamic analysis of unmodified RNA model structures (RNA1-U;RNA2-U;RNA3-U), which serve as references for modified (RNA1-Ψ;RNA2-Ψ;RNA3-Ψ;RNA1-m1Ψ;RNA2-m1Ψ;RNA3-m1Ψ) crystal models. Moreover, the UV-melting analysis and DSC were employed to calculate the thermodynamic parameters of native RNA duplexes.

Field

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