Michelle Zhou
CAID 40716486

Inconsistencies in the Published Rabbit Ribosomal rRNAs: A Proposal for Uniformity in Sequence and Site Numbering

Examination of all publicly available *Oryctolagus cuniculus* (rabbit) ribosome cryo-EM structures reveals numerous confusing inconsistencies. First, multiple single nucleotide differences exist among the rabbit 28S and 18S rRNA structures. Second, two nucleotides are absent from the NCBI Reference Sequence for the 18S rRNA gene. The discrepancies we have found have profound implications for structural biology. Inaccurate and inconsistent rRNA sequences in published PDB entries can lead to misinterpretations of ribosome structure and function, potentially affecting the validity of many downstream research findings and applications. The propagation of incorrect sequences through successive studies exacerbates these issues, leading to a cascade of errors and misannotations. To address these challenges, we propose that all future rabbit ribosome models use the numbering and sequence from the Broad Institute's rabbit genome sequencing project to reduce modeling ambiguity and improve consistency between ribosome models. Although rabbits possess multiple cistrons for their rRNAs just like many other organisms, potentially introducing sequence variability (Martin-DeLeon, 1980; Hori et al., 2023; Rothschild et al., 2024), our study provides a crucial foundation for understanding ribosome structure and function by establishing a consensus sequence. In this way, our study enables more accurate and meaningful interpretations of structural results, ultimately advancing our understanding of ribosome biology. We are also depositing the sequence-corrected 28S and 18S structures into the RCSB PDB to facilitate the use of correct sequences by the field. These sequence-corrected structures will also maintain consistency in numbering important ribosomal subunit sites between rabbit and human ribosomes. By adopting rigorous sequence verification and correction practices and utilizing trusted template sequences, we can ensure more accurate and reliable models, advancing our understanding of ribosome structure.