



## International Journal of Advanced Research

### Publisher's Name: Jana Publication and Research LLP

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#### REVIEWER'S REPORT

Manuscript No.: IJAR-52107 Date: 05/05/2025

Title: MicroRNAs in Hypertension: Molecular Mechanisms and Therapeutic Perspectives - A Bioinformatics Analysis

Recommendation:	Rating _	Excel.	Good	Fair	Poor
✓ Accept as it is	Originality		<b>√</b>		
Accept after minor revision	Techn. Quality		<b>✓</b>		
Accept after major revision	Clarity		<b>\</b>		
Do not accept (Neusons below)	Significance	<			

Reviewer Name: Dr. S. K. Nath

Date: 07/05/2025

#### **Reviewer's Comment for Publication:**

This research offers valuable structural insights into key miRNAs implicated in hypertension by leveraging advanced bioinformatics tools. It successfully elucidates the molecular architecture and network interactions of these miRNAs, highlighting their roles in vascular remodeling and hypertensive pathophysiology. However, the lack of experimental validation limits the immediate translational application of these findings. Future research should aim to experimentally validate these structural predictions and explore their functional significance in biological systems. Overall, this study advances our understanding of miRNA regulatory networks in hypertension and lays a foundation for potential multi-target therapeutic strategies.

#### Reviewer's Comment / Report

#### **Strengths**

- 1. **Comprehensive Structural Analysis:** The study provides an in-depth analysis of the secondary and tertiary structures of five key microRNAs (miR-21, miR-126, miR-133a, miR-155, and miR-181a), offering detailed insights into their molecular architectures and potential functional roles in hypertension.
- 2. **Systems-Level Understanding:** It presents a systems-level view of miRNA regulatory networks involved in hypertension, emphasizing the central role of miR-21 and its interactions with other miRNAs, which could be pivotal for future therapeutic strategies.
- 3. **Integration of Multiple Bioinformatics Tools:** The use of various bioinformatics tools (RNAfold, RNAComposer, ChimeraX, MolProbity) enhances the reliability of structural predictions and provides multi-faceted insights into miRNA functions.
- 4. **Potential for Therapeutic Advances:** By identifying specific miRNA interactions and networks, the research points towards multi-target therapeutic approaches and personalized medicine strategies for hypertension management.

#### Weaknesses

- 1. Lack of Experimental Validation: The study is primarily computational and structural, with no experimental validation (e.g., in vitro or in vivo experiments) to confirm the predicted miRNA interactions or their functional impact in hypertension.
- 2. **Limited Functional Data:** While structural features are well-characterized, there is limited discussion on the direct functional implications of these structures in biological processes or disease mechanisms, which could strengthen the translational relevance.
- 3. **Sample and Validation Details:** The manuscript lacks detailed information about sample selection, experimental conditions, or validation datasets used for structure predictions, which are critical for assessing the robustness of the findings.

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4. **Potential Oversimplification:** The complexity of miRNA regulatory networks in vivo may exceed the computational models' capabilities, and the study doesn't address the potential influence of cellular context or additional regulatory factors.