RNAsack: Integrated Multi-RNA Analytics Platform for Transcriptome-Wide Regulatory Intelligence

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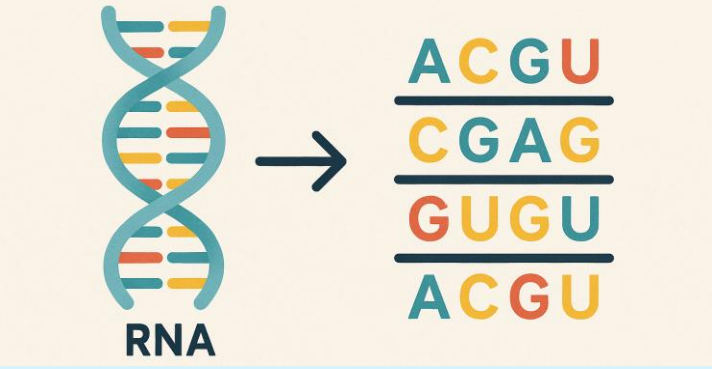
About the Technology: RNAsack is a unified, computer implemented platform that enables simultaneous analysis of mRNA, lncRNA, circRNA, and miRNA from RNA-seq data within a single standardized workflow. It incorporates a built-in transcriptome wide RNA–RNA interaction engine, generating harmonized, machine-readable outputs for downstream biological interpretation and AI/ML integration.

Technology ID: PM-TT-IM-2026-Mar-41
Lead Inventor: Dr. Deepak Modi
Institute: ICMR - National Institute For Research in Reproductive and Child Health
Technology Domain: Bioinformatics, Multi-omics analytics, Digital health
Disease Area (Broad): Cross-disease applications (research)

Need and utility of the Technology from Public health perspective: RNA-seq analyses rely on fragmented tools, manual integration, and high bioinformatics expertise, limiting reproducibility and scalability. Asl RNAsack enables standardized, reproducible, and unified multi-RNA analysis

Technology Readiness level (TRL):

TRL-4: Validated at in house laboratory



Validation Status and Study Outcome:

- Inhouse Validation –Complete
- Efficacy Outcome: Successful generation of integrated multi-RNA profiles and RNA–RNA interaction networks

Market Potential: Growing need for integrated, standardized transcriptomics platforms to support precision diagnostics, biomarker discovery

Unmet need: RNAsack fills a key gap by offering a scalable, easy-to-use alternative to fragmented RNA analysis tools and is ready for commercialization.

Publication: NA

IP Filing: NA