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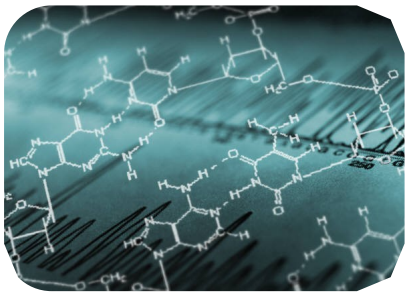
RNA Analysis Via Purified Lariat Populations



Brief Description:
A new method to analyze RNA lariats by employing the high-throughput sequencing of purified RNA lariat populations.

Invention Description:
UMKC Researchers have developed a new technology for the analysis of RNA lariats called Lariat-seq, which is high-throughput sequencing of purified RNA lariat populations. Lariat-seq can be used to investigate gene structure, identify alternative splicing patterns, map intron RNA branch points, compare gene transcription levels, and identify small RNAs encoded within intron lariats. In addition, Lariat-seq can identify the presence of other (non-lariat) covalent modifications in RNAs.
Lariat-seq increases the accuracy of genome annotation and simplifies the process of identifying lariat RNA branch points and the sites of some other covalent modifications of RNA. These advances will speed the development of diagnostics and drugs that target RNA features related to intron splicing as well as RNA covalent modifications that are not due to an RNA branch. Lariat-seq is a very sensitive method for basic and applied researchers to identify introns, branch point sequences , alternative splicing events, as well as the presence of covalent modifications in RNAs that are not due to an RNA branch. The sensitivity can be greatly enhanced by reducing RNA lariat debranching activity in the cells that are the source of the experimental RNA.

Advantages:
- Increased sensitivity
- Increased accuracy

The sensitivity of Lariat-seq is an improvement over other methods for identifying introns and alternative splicing events. Furthermore, Lariat-seq is the only way to globally identify the lariat RNA branch point sequences within a heterogenous RNA population. Current methods require evaluation of one branch point at a time. Lariat-seq is also the only way to globally identify sites of covalent RNA modifications that are not due to an RNA branch within a heterogenous RNA population.

IP Status:
Patent Pending

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