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# Sequential and dynamic RNA:RNA base-pairing interactions between U6atac and U12 snRNAs predicted to form Helix 1a and Helix 1b

Maitri Patel  
*Cleveland State University*

Jagjit Singh  
*Cleveland State University*

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***Sequential and dynamic RNA:RNA base-pairing interactions between U6atac and U12 snRNAs predicted to form Helix 1a and Helix 1b***

College of Sciences and Health Professions

**Student Researchers:** Maitri Patel and Jagjit Singh

**Faculty Advisor:** Girish C. Shukla

**Abstract**

In eukaryotes, pre-mRNA splicing is important step for gene expression. Splicing is a two-step process which is carried out by a multi-megadalton molecular weight ribonucleoprotein (RNP) machinery called spliceosome. Spliceosome converts pre-mRNA to mRNA by removing non-coding sequence (introns) and splice together coding sequence (exons). Mammalian pre-mRNA are spliced by two different class of spliceosomes which are known as U2- and U12- dependent spliceosomes. U12 dependent spliceosome is composed of five small nuclear RNAs (snRNA). As compared to U2-dependent spliceosome, there is very less known about the catalytic process of U12-dependent splicing. U6atac and U12 snRNA are central to U12-dependent splicing. Therefore, to understand importance of U6atac and U12 snRNA interaction during splicing we have created a series of 2<sup>nd</sup> site nucleotide mutations in both U6atac and U12 snRNA to test for their functionality in in vivo splicing assays. Our work will help to better understand the catalytic process of minor class spliceosome and involvement of these snRNA in mammalian gene expression and genetic disorders.