

**POSTER 18****DIRECT PROBING OF RNA TRANSPORT ELEMENT STRUCTURES BY SHAPE, SOLUTION X-RAY SCATTERING AND 3D MASS SPECTROMETRY**

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Functional RNA motifs are typically too large for resolution by NMR and/or are refractory to crystallization. Our goal is to develop efficient and reliable biochemical and biophysical methodologies to complement more established techniques for high-resolution RNA structure determination, and apply them to solve the secondary and tertiary structures of essential human retroviral RNAs. SHAPE (Selective 2'-Hydroxyl Acylation analyzed by Primer Extension) is one such methodology, providing a rapid and quantitative distinction between constrained and flexible domains of RNA with single nucleotide resolution. In addition, small-angle X-ray scattering (SAXS) data contain information about the overall shape of RNAs and can be utilized to define the interface of subdomains of RNAs. Furthermore, the tertiary interaction in RNAs can also be analyzed precisely by Mass Spectrometric three-dimensional (MS3D) approach. Electrospray ionization (ESI) Fourier Transform Mass Spectrometry (FTMS) with crosslinking method to obtain information about the spatial relationship of contiguous domains in folded structures. RNA is exported by proteins binding to RTEs that is able to replace Rev-responsive element (RRE) regulation in human immunodeficiency virus type 1. The structures of RNA Transport Elements (RTEs) and Rev-responsive elements (RRE) were investigated using SHAPE, SAXS and MS3D. In conclusion, our data indicated that the combination of SHAPE, SAXS and MS3D would be a useful tool to solve the tertiary and secondary structures of various RNAs.