The Ribosome: A Window in Time

<u>K.A. Lanier</u>¹, N.A. Kovacs, A.S. Petrov and L.D. Williams² ¹School of Chemistry and Biochemistry, Georgia Institute of Technology, Atlanta, GA 303302

* klanier@gatech.edu

The ribosome, in analogy with a tree, contains a record of its history, spanning 4 billion years of life on earth. The information contained within ribosomes connects us to the prehistory of biology. Details of ribosomal RNA variation, observed by comparing three-dimensional structures of ribosomes across the tree of life, form the basis of our molecular level model of the origins and evolution of the translational system. We have used information within ribosomes to reconstruct much of the emergence of the universal translational machinery and to understand the evolution of biopolymers. Using a 3D comparative method, we present a molecular-level model for the origin and evolution of the translation system. In this model, the ribosome evolved by accretion, recursively-adding expansion segments, iteratively growing, subsuming, and freezing the ribosomal RNA. The ribosome is also imprinted with a detailed molecular chronology of the origins and early evolution of proteins. When arranged by evolutionary phase of ribosomal evolution, ribosomal protein segments reveal an atomic level history of protein folding. Our models predict that appropriate rRNA fragments have inherited local autonomy of folding and local autonomy of assembly with ribosomal proteins, and that the ribosomal proteins and rRNAs are cochaperones. We have biochemically and computationally resurrected the ancestral oligomers and polymers predicted by the Accretion Model. We have synthesized the rRNAs described by early steps in the early accretion process and have experimentally explored their properties, focusing on their folding and stabilities. We have measured and computed the thermodynamic stabilities of theses models and experimentally probed their structures. We have also experimentally shown that rRNA can serve as a protein chaperone, aiding in the conversion of random coil peptide oligomers into β - β motifs, which would then collapse to globular domains, supporting previous models in which RNA preceded aboriginal proteins. Our results support a model in which protein folding was an emergent phenomenon of interactions with RNA, and that the evolution of the ribosome was the maturation of the symbiotic relationship between RNA and protein.