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# Frozen In Time: The History of the Ribosome

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Translation provides a window into the essential nature of biology. Translation is characterized by: **(1) Ubiquity**: Translation dominates the Universal Gene Set of Life; sequences that encode translational components are found in every organism on earth. **(2) Conservation**: Structures of macromolecular assemblies of the translational system are conserved in three dimensions in every organism on earth. (3) **Communication**: The translation system dominates biological interaction networks in centrality, size and complexity. (4) **Abundance**: Ribosomal components are the most abundant biological polymers in the known universe. (5) **Consumption**: Translation is the largest consumer of cellular resources. (5) **Complexity**: The complexity of translation predicts organismal complexity.

Structures of ribosomes in three dimensions contain molecular records of the history of biopolymers. We have developed a three-dimensional comparative method that shows that the ribosome evolved by accretion, recursively adding rRNA expansion segments, iteratively growing and 'freezing'. When relative ages of rRNA are mapped onto the ages of rProtein segments, the genesis of protein folding is revealed. The data support a model in which aboriginal polypeptides evolved into globular proteins in a hierarchical step-wise process. (i) Short random coil peptides bound to rRNA, and (ii) lengthened over time and coalesced into β-β secondary elements. Polypeptide secondary elements (iii) accreted and collapsed, primarily into β-domains. Domains (iv) accumulated and gained complex super-secondary structures composed of mixtures of a-helices and b-strands. Protein evolution was guided and accelerated throughout this process by interactions with rRNA. rRNA stabilized immature and intermediate polypeptide species, bypassing the immense space of unproductive sequences. The broad diversity of proteins in nature descended from prototypes that were created by the ribosome, on the ribosome and for the ribosome. Protein folding from random coil peptides to functional polymeric domains was an emergent property of rRNA-polypeptide interactions. The co-evolution of RNA and protein was accomplished in the context of the ribosome, which was therefore the cradle of early evolution.