Primordial amino acid alphabets yield proteins that bind ATP and GTP
Matilda Newton*, Kun-Hwa Lee*, Celia Blanco**, Irene Chen**, and Burckhard Seelig*

*Department of Biochemistry, Molecular Biology and Biophysics and BioTechnology
Institute, University of Minnesota, St. Paul MN 55108

Imagine building a car with pieces of toy bricks. Building a well-functioning car with a full set of bricks may not be as challenging as to build one with only a handful of parts. Inside modern life forms, protein machineries are working as a dominant component in maintaining viability and essential cell function. Varieties of amino acid in the genetic code have been evolving from the simpler state. Considering the changes in the availability of the amino acids in the environment, it is highly likely that the early proteins have fulfilled necessary functions to a certain extent with a limited variety of amino acids. How these early proteins comprised of less diverse amino acids achieved their functions is a critical question in our journey to unearth the origin of life. In order to address this question, four reduced alphabet libraries were constructed to represent varying time points of alphabet evolution. High-throughput selection using mRNA display was done and resulting pools were deep sequenced for further analysis. The kinetics studies on the variants that showed great enrichment is ongoing to determine the functionality of the reduced amino acid alphabet.