

Biochemical and computational analysis of protein:RNA interactions  
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Aminoacyl-tRNA synthetases (aaRSs) catalyze the attachment of amino acids to their cognate tRNAs as the first chemical step of peptide bond formation. As with most protein:RNA interactions, conformational changes are observed in both aaRS and tRNA upon complex formation. We are interested in the intramolecular signaling that occurs when tRNA identity elements (such as anticodon nucleotides) are bound by their protein recognition motifs at sites distant from the enzyme's catalytic center. We are using biochemical methods as well as molecular dynamic simulations to probe contributions of both tRNA and protein to efficient tRNA aminoacylation.