

# Using Rapid Kinetics and Molecular Dynamics Simulations to Study Biomolecular Information Processing and Design

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Translation, the ribosome dependent synthesis of proteins, is the last step of gene expression. It is targeted by a large number of antibiotics that modulate, in one way or the other, the dynamic properties of the involved biomolecules. Protein synthesis is a highly conserved multi-step process facilitated by a large ribonucleoprotein complex (the ribosome) acting as a biomolecular assembler, converting genetic information provided as RNA transcripts (mRNA) into proteins. This process occurs with high speed and incredible accuracy within any living system (1). As such, accuracy is the key to maintaining the integrity of the genetic information to be reflected in the resulting proteins. The underlying design principles that enable the translation machinery to achieve these performance characteristics is of great interest for a large number of fields and applications, naming antibiotics design and the rational engineering of biomolecular machines just as two examples.

The following article, based on this talk, is published in the article section of this issue, see page 74.

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