

# Aminoacyl-tRNA Synthetases Dynamics: A Comparison between Coarse-grained and All-atom Simulations

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Aminoacyl-tRNA synthetases are a group of multi-domain enzymes responsible for catalyzing the covalent attachment of an amino acid to its corresponding tRNA forming an aminoacyl-tRNA. A characteristic of these enzymes is the large-scale conformational changes they undergo during catalysis. Recent studies in our lab<sup>1-3</sup> show that coarse-grained as well as atomistic simulations can provide reliable results in predicting global dynamics encompassing larger domains. However, these studies also pose serious questions about their abilities in predicting substrate-induced local changes. In order to evaluate the effectiveness of coarse-grained approaches in studying dynamics of large protein systems like aminoacyl-tRNA synthetases, we performed a systematic study to compare the performances of coarse-grained vs. all-atom simulations. Two types of coarse-grained analyses were performed: normal mode calculations and molecular dynamics simulations, each using one-bead per residue elastic network model. For all-atom simulations, regular molecular dynamics was performed using CHARMM forcefield. Herein, we will present the comparative results of this study on three aminoacyl-tRNA synthetases: *Escherichia coli* methionyl-tRNA synthetase, *Thermus thermophilus* leucyl-tRNA synthetase, and *Enterococcus faecium* prolyl-tRNA synthetase.

## References

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