

# Dynamical networks in tRNA:protein complexes

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**Community network analysis derived from molecular dynamics simulations is used to identify and compare the signaling pathways in a bacterial glutamyl-tRNA synthetase (GluRS):tRNA<sup>Glu</sup> and an archaeal leucyl-tRNA synthetase (LeuRS):tRNA<sup>Leu</sup> complex. Although the 2 class I synthetases have remarkably different inter-**

**established. This study demonstrates that nucleotides in the tRNA as well as residues within the aaRS are essential for information transduction in the protein:RNA complex. Although contact maps based on the static structure of the complex give an initial approximation to the physical communication**