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**Electrostatic Potential of Aminoacyl-tRNA Synthetase Navigates tRNA on its Pathway to the Binding Site.**

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The aaRSs catalyzing the same overall aminoacylation reaction vary greatly in subunit organization, structural domain composition and amino acid sequence. The diffusion-controlled association of aaRS and tRNA was found to be governed by long-range electrostatic interactions when homogenous negative potential of tRNA fits to the patches of positive potential produced by aaRS: one patch for each tRNA substrate molecule. Considering aaRS as a molecule with anisotropic reactivity and based on the continuum electrostatics and Smoluchowski's theory, the reaction conditions for tRNA-aaRS diffusional encounters were formulated. The domains, categorized as enzymatically relevant, appeared to be nonessential for field sculpturing at long distances. On the other hand, set of complementary domains exerts primary control on the aaRS's isopotential surface formation. Subdividing the aaRS's charged residues into native, conservative and non-conservative subsets we evaluated the contribution of each group to long-range electrostatic potential (EP). Surprisingly, the EP landscapes generated by native and non-conservative subsets are fairly similar, thus suggesting the non-conservative subset being specifically developed for efficient tRNA attraction.