



Salted proteins: the molecular basis of protein halotolerance

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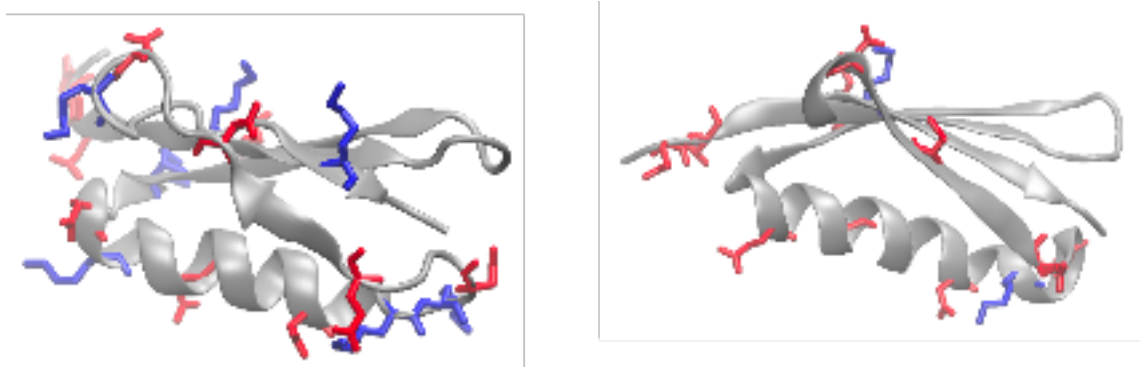


Figure: (Left) Wild type protein L, with similar number of acidic (red) and basic (blue) amino acids. (right) Kx5E mutant of protein L, rich in acidic amino acids.

Aqueous environments like the Dead Sea, with multimolar concentrations of NaCl, are far from dead. They are rich with uni- and multicellular organisms that thrive under conditions that would kill most other organisms on the planet. To counterbalance the large osmotic pressure that accompanies multimolar salt solutions, many halophilic organisms accumulate KCl in their cytoplasm also up to multimolar concentrations. The proteins of halophilic organisms are thus folded and active under KCl concentrations that would inactivate your typical set of proteins. This ability has been correlated with the unusual composition of halophilic proteins: richer in negative and polar amino acids, poorer in positive and hydrophobic amino acids relative to typical proteins. In this talk I will describe our recent work using molecular dynamics simulations to mechanistically clarify, at the atomistic level, the role played by acidic amino acids in protein tolerance to high salt concentrations.