Towards predictive protein separations: Can physical chemistry solve a $100,000,000,000 problem?

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Abstract

Recent efforts by our group and others have shown the promise of applying single-molecule methods to link mechanistic detail about protein adsorption to macroscale observables. When we study one molecule at a time, we eliminate ensemble averaging, thereby accessing underlying heterogeneity. However, we must develop new methods to increase information content in the resulting low density and low signal-to-noise data and to improve space and time resolution.

I will highlight recent advances in super-localization microscopy for quantifying the physics and chemistry that occur between target proteins and stationary phase supports during chromatographic separations. My discussion will concentrate on the newfound ability of single-protein tracking to inform theoretical parameters by quantification of adsorption-desorption dynamics, protein unfolding, and nano-confined transport. Additionally, I will discuss using phase manipulation to encode temporal, 3D spatial, and orientational information, and briefly introduce new materials that could lead to bio-inspired active separations.