Chemical kinetics and microfluidic approaches for the analysis of protein properties in bioprocessing

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Protein stability towards unfolding and aggregation plays a key role in the development of a range of important biotechnological products such as therapeutic proteins, vaccines, enzymes and food proteins. During storage and manufacturing, proteins can self-assemble via several possible multi-step processes, which are challenging to characterize and rationalize. Here we show the application of two emerging methods to address this challenge: a) a chemical kinetic platform to identify protein aggregation path-ways at the molecular level; b) novel microfluidic techniques that enable the measurement of sizes and viscosities of polydisperse protein samples under native conditions and on a timescale of few seconds.

We demonstrate the potential of these approaches by analyzing the aggregation mechanisms of different model proteins (IgGs, human insulin, peptides) and we discuss the implications of these methods for monitoring and designing product quality during bioprocessing.

[1] P. Arosio et al., *ACS Nano*, **2016**, 10, 333-341.
[2] P. Arosio, et al., *Analytical Chemistry*, **2016**, 3488-3493.
[3] P. Arosio, et al., *Nature Communications*, **2016**, 7:10948.