Poster Presentation

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Microfluidic dialysis on the beamline: experiment and theory

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Biological small angle x-ray solution scattering requires sufficient sample concentration to yield good signal while at the same time avoiding interparticle interference or the formation of unwanted oligomers or aggregates. The mere act of concentrating some samples risks rendering them unfit for SAXS measurements and the limit to which a sample may be concentrated before problems occur is often unknown a priori; aggregation is not generally regarded as a reversible process. At the same time, sample behavior at high concentrations is increasingly important not just for characterization of equilibria, or e.g. applications in the pharmaceutical industry, but also for understanding potential molecular crowding effects. We have constructed a microfluidic dialysis setup that permits on-demand concentration of protein samples at the beamline. Rather than generating dilution series to explore concentration effects, this approach produces true "concentration series", efficiently working from dilute sample upward. We experimentally demonstrate that useful concentrations can be achieved on practical timescales and that buffer exchange can be performed. Convection-diffusion modeling shows that the dialysis chip may actually retard aggregates, thus resulting in some degree of incidental sample purification. Based on model projections, the theoretical limits and potential of chip-dialysis will be described.

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