

P005 Self-assembly behaviour of surfactant-like peptides with systematically varied sequence motifs

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We investigate the self-assembly behaviour of cationic surfactant-like peptides with systematically varied tail regions. Two positively charged amino acids give the polar head, and the hydrophobic tail is formed by a repetitive sequence of one apolar amino acid. Polypeptides regulate many biophysical processes by interaction with or translation through the cell membrane and model peptide-membrane systems are thus of high interest.

This approach enables us to investigate the effects of variations in the tail composition on the self-assembly behaviour of the monomers at different concentrations in aqueous solutions under various pH and ionic strength conditions. So far, we analyzed the behaviour of Ac-Ile₆Lys₂-NH₂ (I6K2). The assemblies were characterized using static (SLS) and dynamic (DLS) light scattering, transmission electron microscopy (TEM) and atomic force microscopy (AFM). We can show that the peptides assemble into mostly micellar fibres depending on concentration and ionic strength. With SLS we found that the aggregate size increases with decreasing peptide concentration. Now we perform investigations using frozen-hydrated TEM to elucidate the shape of the assembled structures in a “near solution” state. We also study interaction of the peptide and peptide assemblies with different substrates (eventually supported lipid membranes) using AFM and Quartz Crystal Microbalance with Dissipation monitoring (QCM-D).