

Effect of peptide architecture on the self-assembly properties of tripeptide based anionic surfactants issued from two different peptide sequences: Ala-Ala-Val and Ala-Pro-Val in aqueous media (pH 7.4)

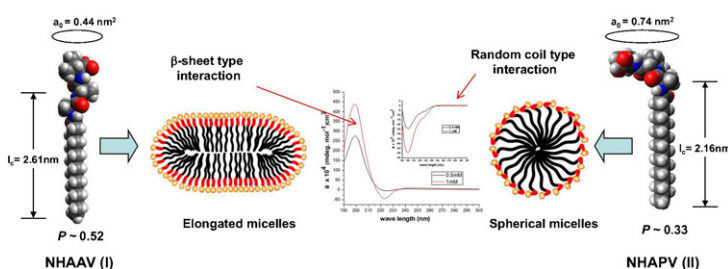
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HIGHLIGHTS

- ▶ Peptide segment architecture influences on the morphology of the self assemblies.
- ▶ β -Sheet network at peptide segment triggers elongated micelle formation.
- ▶ Proline at the central amino acid destabilize the formation of β -sheet type network.
- ▶ Structural change at the peptide level affects self assembly behavior.

GRAPHICAL ABSTRACT



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ABSTRACT

Structurally different tripeptide based surfactants issued from two different peptide sequences: Ala-Ala-Val (**I**) and Ala-Pro-Val (**II**) were synthesized and their self assembly properties were characterized using various physicochemical experiments (tensiometry, fluorimetry, anisotropy, fluorescence lifetime, DLS, CD, TEM) in aqueous media (pH 7.4). The results reveal that, architectural change of the tripeptide sequence on the surfactant backbone affects their self assembly properties remarkably. The replacement of alanine by proline residue in the middle of the tripeptide sequence affects the intermolecular H-bonding interaction operative at the peptide segment (β -sheet for **I** and random coil for **II**) which seemingly affects the molecular aggregation as well as the self assembly properties of the surfactants. Such architectural change at the peptidic level induces a larger curvature that results to a micellar type aggregates for **II** whereas, a β -sheet type interaction prevailing in **I** does not affect much towards the packing of the surfactants tails rather helps in formation of elongated micelles. Micellar growth was also found to be more pronounced in case of **I**. Higher CMC values and lower aggregation number for **II** compared to **I** also describes that an increase in hydrophilic character takes place in **II**. Formation of micellar aggregates in presence or absence of H-bonding network suggest that hydrophobic effect is the driving force behind the self assembly process but not the H-bonding interaction, however the physicochemical properties of the self assemblies are affected by H-bonding interaction of the peptide segment.

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1. Introduction

Self-organized molecular assemblies of peptide derived amphiphiles have attracted extensive research interest in recent

times for their propensity to self-assemble into well-defined nanostructures [1]. Due to their additional intermolecular non-covalent interactions, including hydrogen bonding, van der Waals forces, electrostatic interactions, hydrophobicity, and π - π interactions, operative at the peptidic segment, self assembly of many such peptide amphiphiles tends to generate diverse nanostructures like, nanofibers [1–6], nano-tubes [7], nano-taps [8,9] and structurally similar to cylindrical and spherical aggregates [10,11].

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