The antimicrobial peptide Cn-AMP1 was isolated from coconut water of Cocos nucifera L. and it have presented considerable action against Gram-positive and Gram-negative bacteria and fungi. Its primary structure is composed by linear chain containing 9 amino acid residues (SVAGRAQGM). In order to relate structure and interactions in this study were synthesized CnAMP1 besides two analogs, with were achieved substituting the methionine residue in the C-terminal region by tryptophan ([Trp9]Cn-AMP1) and Glycine ([Gly9]Cn-AMP1) residues. Peptides were obtained by solid phase peptide synthesis using Fmoc strategy. Purification was carried out by high performance liquid chromatography in reverse phase (RP-HPLC) and characterization by mass spectrometry (MALD-TOF). Structural studies were performed by circular dichroism (CD) at different biomimetic and physiological environments. Studies of hydrodynamic diameter (Dh) changes on the large unilamellar vesicles (LUVs) of distinct compositions were fulfilled by dynamic light scattering (DLS). CD studies of Cn-AMP1, [Trp9]Cn-AMP1 and [Gly9]Cn-AMP1 showed α-helix structure only in TFE solution or SDS micelles, although the last one has presented the minor helicity degree at both media. Whereas [Trp9]Cn-AMP1 present helix conformation in almost entire peptide chain, [Gly9]CnAMP-1 has an extend conformation and poor secondary structure in N-termini, as observed by NMR experiments. Nevertheless, it’s possible observe a subtle fold in C-termini which suggests a partial insertion of Trp-9 residue and, consequently, anchoring [Trp9]Cn-AMP1 on the micelle surface. The effect of peptides on the Dh of POPC and POPC:POPG (3:1) LUVs was evaluated by DLS and Potential Zeta measurements and showed great Dh changes by adding Cn-AMP1 and [Trp9]Cn-AMP1 as well. However, no significant changes were observed by [Gly9]Cn-AMP1 addition, suggesting less affinity for
either zwitterionic or negative LUVs. These results reveals that presence of a hydrophobic residue and large side chains (Met-9 and Trp-9) are essential for contribute to better interaction where exercise their action mechanisms.

**Keywords:** NMR, Peptide-membrane interaction, Structure.