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DYNAMICS OF *GRAMICIDIN A* DEDUCED FROM HIGH-RESOLUTION MAGIC-ANGLE SPINNING NMR

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Early attempts to obtain high-resolution solid-state NMR spectra of peptides and proteins in liquid-crystalline membranes were unsuccessful because of problems associated with the dynamics of the molecules. All subsequent studies have avoided them altogether by performing the experiments at very low temperatures, where motion is frozen. Recent experiments performed in our laboratory have given more insight on the nature of this perturbation, namely the interference of some molecular motion with high-power ^{1}H-decoupling. We are now able to quantitate it, to devise ways to circumvent it and, most importantly, to extract relevant data concerning the dynamics of the observed molecules.

Such effects are demonstrated here and studied in great detail for the case of a membrane peptide, Gramicidin A, in an hydrated lipid bilayer. The study has been performed over a broad temperature range, on different ^{13}C,^{15}N,^{2}H-labeled peptides. Several dynamical models and a comparison with previously published results will be presented. Various ways to obtain high-resolution Magic-Angle Spinning ^{1}H, ^{13}C and ^{15}N-NMR spectra of peptides in membranes will also be discussed.