Dynamics of biomolecules by means of NMR relaxometry - from aminoacids to proteins

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NMR relaxation studies performed versus magnetic field (resonance frequency) give access (in a single experiment) to dynamical processes on different time scales (from ms to ns). The shape of relaxation dispersion profiles (relaxation rate versus frequency) can be treated as a fingerprint of the mechanism of motion leading to the relaxation process – the shape is determined by Fourier transform of a correlation function characterizing the motion. In this way, NMR relaxometry probes not only the time scale of the dynamical processes, but also their nature.
This unique potential of NMR relaxometry will be demonstrated for a series of biological systems, including solid aminoacids and proteins of various kinds and their solutions. Dynamics of the system will be discussed on the basis of a detailed analysis of the relaxation data. The focus of the analysis is to identify generous features of spin relaxation processes in biomolecules in connection to their specific dynamics. Theoretical models describing the relaxation processes will be presented pointing out their validity regimes and underlying assumptions. Special attention will be put to sub-diffusive processes in solutions of biomolecules.
The presented NMR relaxation results have been complemented by Dielectric Spectroscopy data that give access to rotational dynamics. Comparison between the two methods and joint analysis of the data significantly broadens our understanding of the mechanisms of motion in biological systems.

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