# Dynamics of solid proteins by means of Nuclear Magnetic Resonance Relaxometry

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Fast Field-Cycling relaxometry is an NMR technique used to determine the spin-lattice relaxation rates ($R_1$) of samples as a function of resonant frequency (or, equivalently, magnetic field strength). When studied over wide range of frequencies, $R_1(\omega)$ (the relaxation dispersion profile) provides information on molecular dynamics of the system under investigation.

Due to the presence of $^{14}$N nuclei in the structure of amide groups, $^{1}H$ spin-lattice relaxation dispersion profiles of proteins are described in terms of a sum of homonuclear $^{1}H$-$^{1}H$ and heteronuclear $^{1}H$-$^{14}N$ contributions. Standard quantitative analysis relies on formulae including power-laws or Cole-Davidson spectral density functions for the homonuclear contribution and Lorentzian or Gaussian functions for the heteronuclear counterpart [1,2]. In the present studies we make an attempt to describe the relaxation dispersion profiles of proteins by employing: 1) multi rotational-like dynamics for $^{1}$H-$^{1}$H interactions and 2) quadrupolar relaxation enhancement of $^{1}$H relaxation originating from $^{1}$H-$^{14}$N dipole-dipole interactions [3, 4].

Thorough quantitative analysis of relaxation data obtained for solid proteins: elastin, lysozyme and albumin shows, that the homonuclear contribution to the NMRD profile can be described in terms of three rotational-like dynamical processes occurring on a different time scales, ranging from µs to ns, and frequency independent term A. Despite structural differences between the investigated systems, the parameters characterising $^{1}$H-$^{1}$H dipolar interactions (coupling constants and correlation times) , $^{1}$H-$^{14}$N couplings ($^{1}$H-$^{14}$N distances and $^{1}$H-$^{14}$N bond orientations) and $^{14}N$ quadrupolar interactions (coupling constants, asymmetry parameters) are similar.

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