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Title: Characterization of Molecular Motions in Proteins Using Relaxation Data

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Abstract: Structures alone cannot explain protein functions and biochemical data. Studying dynamics on different timescales play an important role in understanding protein functions. NMR relaxation experiments provides wealth of information about molecular dynamics in macromolecules and aids. To get the meaningful explanation of NMR relaxation data, Model free approach for analysis of the data is used. We analyse the spin-relaxation experimental data (R_1 ; R_2 ; NOE) within the model free formalism (Clare et al. 1990; Lipari and Szabo, 1982) to study and analyse molecular dynamics with atomic resolution of biomolecules like Ubiquitin, RNase and 14-mer RNA using the program FAST-Model free for the fully automated, high throughout analysis of NMR spin relaxation data.

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