ABSTRACT

Structures alone cannot explain protein functions and biochemical data. Studying dy- namics on different timescales play an important role in understanding protein func- tions. NMR relaxation experiments provides wealth of information about molecular dynamics in macromolecules and uids.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(R1;R2;NOE) within the model free formalism (Clore et al.1990; Lipari and Sizabo,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.