

¹H longitudinal relaxation enhancement in ¹³C detected NMR experiments on IDPs

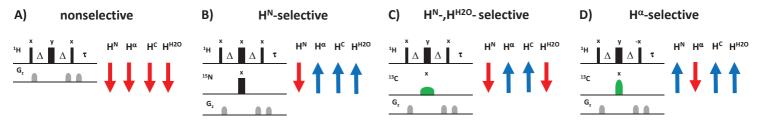


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Exclusively heteronuclear NMR experiments based on ¹³C direct detection ¹⁻³ now provide a valuable tool to study intrinsically disordered proteins. ¹H is often used as a starting polarization source to increase the sensitivity of the experiments offering the possibility of easily manipulating different sets of ^{1}H spins (H^{N} , H^{α} , H^{C} , H^{H2O}) to achieve longitudinal relaxation enhancement^{2,3}. We would like here to evaluate the various contributions to longitudinal relaxation enhancement in the case of IDPs, using as a model protein a paradigmatic one, α-synuclein. The results provide useful information to design more complex multidimensional NMR experiments as well as to characterize the compactness and/or solvent accessibility of different parts of the polypeptide chain

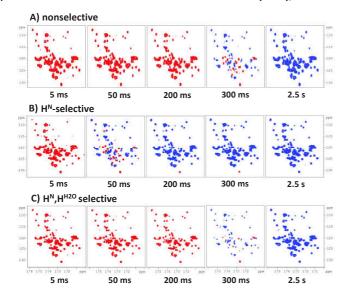
¹H-flip variants to invert different sets of ¹H spins (H^N, H^α, H^C, H^{H2O})



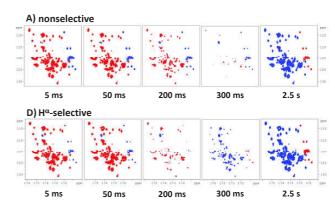
The ¹H-flip approach^{2,3} can be easily used to invert different pools of spins, exploiting the large one-bon proton-heteronucleus cuplings (2Δ=1/JHX). The different ¹H-flip approach^{2,3} can be easily used to invert different pools of spins, exploiting the large one-bon proton-heteronucleus cuplings (2Δ=1/JHX). The different ¹H-flip approach^{2,3} can be easily used to invert different pools of spins, exploiting the large one-bon proton-heteronucleus cuplings (2Δ=1/JHX). The different ¹H-flip approach^{2,3} can be easily used to invert different pools of spins, exploiting the large one-bon proton-heteronucleus cuplings (2Δ=1/JHX). flip variants illustrated above can be exploited to control the recovery of H^N and H^α polarization to the equilibrium value under different initial conditions.

2D CON maps to monitor ¹H inversion recovery-profiles

The different ¹H-flip variants were included in the beginning of HN-flip CON³ and Hα-flip CON² 2D experiments. These are well suited as ¹H are only used as an initial polarization source. The experiments are demonstrated on α-synuclein (1 mM, pH 7.4, 297 K, [Pi] 20 mM, [NaCl] 200 mM). The 2D maps acquired with the different ¹Hflip variants are shown as a function of the inversion recovery delay, τ. It can be easily recognized the T_{null} for the different ¹H-flip variants.

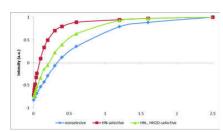


(A) nonselective, (B) HN- and (C) HN-,HH2O- selective 13C-detected 2D 1H-flip HNCO experiments of α -synuclein with different inversion recovery delays τ .

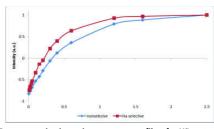


(A) nonselective and (D) Hα-selective 13C-detected 2D 1H-flip HCACON experiments of α -synuclein with different inversion recovery delays τ .

Different contributions to ¹H longitudinal relaxation enhancement on α-synuclein



Representative inversion recovery profiles for HN proton spins under different initial conditions



Representative inversion recovery profiles for H^{α} proton spins under different initial conditions.

As an example the different inversion recovery profiles of 118 Val are shown for HN and Ha proton spins.





sion recovery profiles were analysed with Dynamics Center 2.0



