



Human Alpha-C domain of Fibrinogen, 300uM, pbs buffer pH=6. Disordered protein with important potential in understanding blood clotting

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Field strength: 600 MHz

Why is this your favorite spectrum?

Alpha-C domain of human fibrinogen is a mostly disordered protein with over 200 residues which makes it increasingly important to have good resolution in NMR spectra. After acquiring 2D ^{15}N - ^1H HSQC, the data is processed either as usual "red" or using non-uniform sampling zero filling (NUS Zero-Filling) "blue." The overlay shows how the resolution of the spectrum is enhanced with using NUS Zero-filling as an alternative to linear prediction.

Comments: Using this simple trick enhances the quality of data which is extremely beneficial for disordered proteins where the resolutions is usually an issue.

J. Ying, F. Delaglio, D.A. Torchia, and A. Bax: Sparse Multidimensional Iterative Lineshape-Enhanced (SMILE) Reconstruction of Both Non-Uniformly Sampled and Conventional NMR Data, *J Biomol NMR*, 68, 101-118 (2017).