

# NMR tools for the structural studies of IDPs

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Intrinsically disordered proteins, IDPs can be associated with a range of functions, and they play a main role in protein interaction networks. This has brought an increased interest in characterizing it. X-ray crystallography can not be used to characterize IDPs as their mobility prevents the formation of suitable crystals. NMR spectroscopy emerges as the unique tool to obtain structural and dynamic information at atomic resolution.

Chemical shifts and J-coupling constants are a valuable source of structural information. Sequential assignment of NMR spectra of proteins is a prerequisite to obtain these parameters. NMR assignment of IDPs by conventional HN-detected methods is hampered by the small dispersion of the amide protons chemical shifts and exchange broadening of amide proton signals. Therefore alternative assignment strategies are needed. We have proposed an approach based on the acquisition of two <sup>13</sup>C-detected experiments to directly correlate the chemical shifts of two consecutive <sup>13</sup>C'-<sup>15</sup>N groups in proteins<sup>1</sup>.

On the other hand, although chemical shifts are highly useful for identifying transiently populated secondary structure elements in intrinsically disordered proteins (IDPs), further evidence can be obtained from the analysis of J couplings. A coupling that may be useful in this sense is <sup>2</sup>J<sub>N(i)Ca(i-1)</sub>. The <sup>2</sup>J<sub>N(i)Ca(i-1)</sub> coupling has been proposed as a valuable indicator to identify secondary structure elements in folded proteins<sup>[2]</sup> and has proven to be useful for characterizing structures of IDPs. Here we present an approach based on the acquisition of <sup>13</sup>C-detected experiments and Non Uniform Sampling methodology to measure it.

This approach has been tested with different IDPs, Nupr1 (93 residues), IF7 (86 residues), hCPEB-Nt (128 residues).

## References

1.-Pantoja-Uceda D and Santoro J., *J. Biomol. NMR*, 43-50 (2014)

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