

NMR characterization of XXX*

PSB platform

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Name : XXX

Sample : XXX

Molecular weight : 19 kDa

Label : 15N

Buffer : tris pH8 50 mM, NaCl 100 mM, betaME 2 mM

Sample concentration : 0,016 mM

Experiments: 2D SOFAST (fig 1) and 1D HETSOFAST (fig 3)

Temperature: 25°C

- The protein contains well folded regions (fig 1) and regions that are more flexible (20-30%)
- The λ_{NOE} parameter of 0.35 (fig 3) reveals a high proton density and thus well folded regions. This value could be smaller at lower pH since the protons involved in flexible regions may rather be exchanged with the solvent at pH=8.
- The peak line widths look a bit broad for a monomeric protein of 19kD (fig 1). Optimization of the sample condition (pH, temperature, salts...) may lead to a NMR spectrum with a better resolution.

*Please, add the following acknowledgment in your posters or publications: *"We thank Eric Condamine and/or Adrien Favier, from the IBS platform of the Partnership for Structural Biology and the Institut de Biologie Structurale in Grenoble (PSB/IBS), for the NMR access and the support provided."*

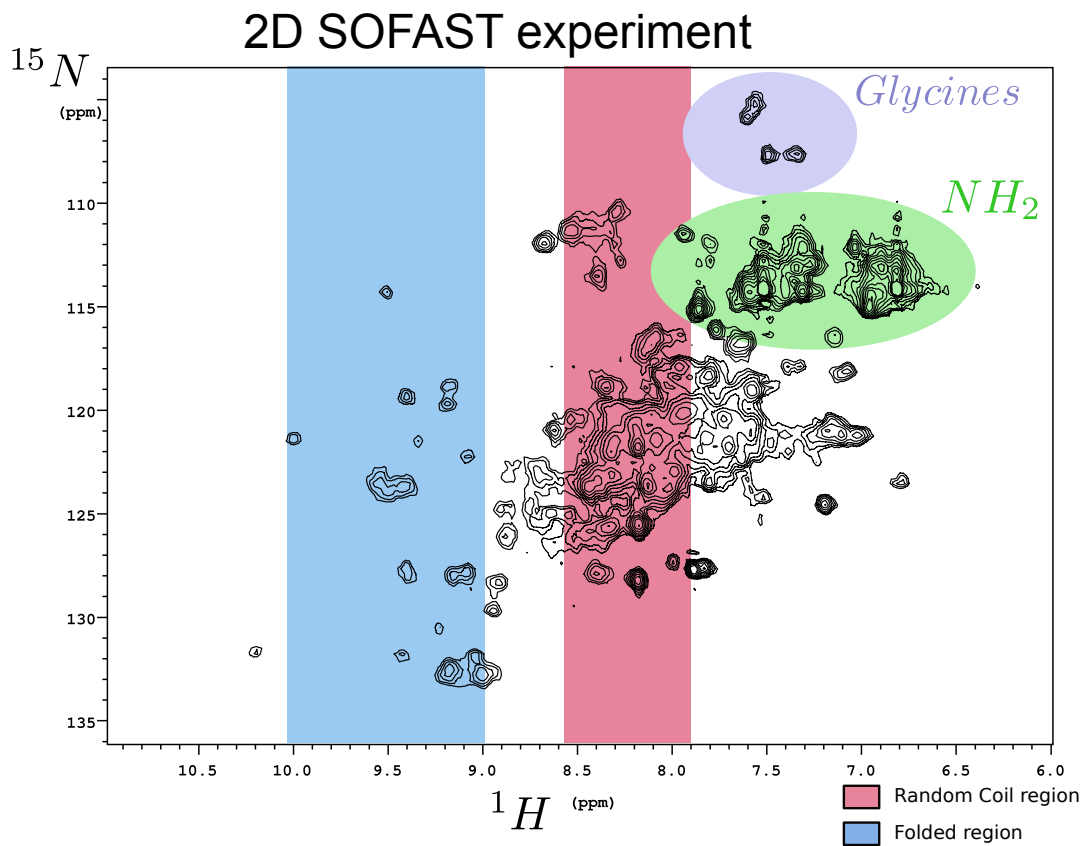
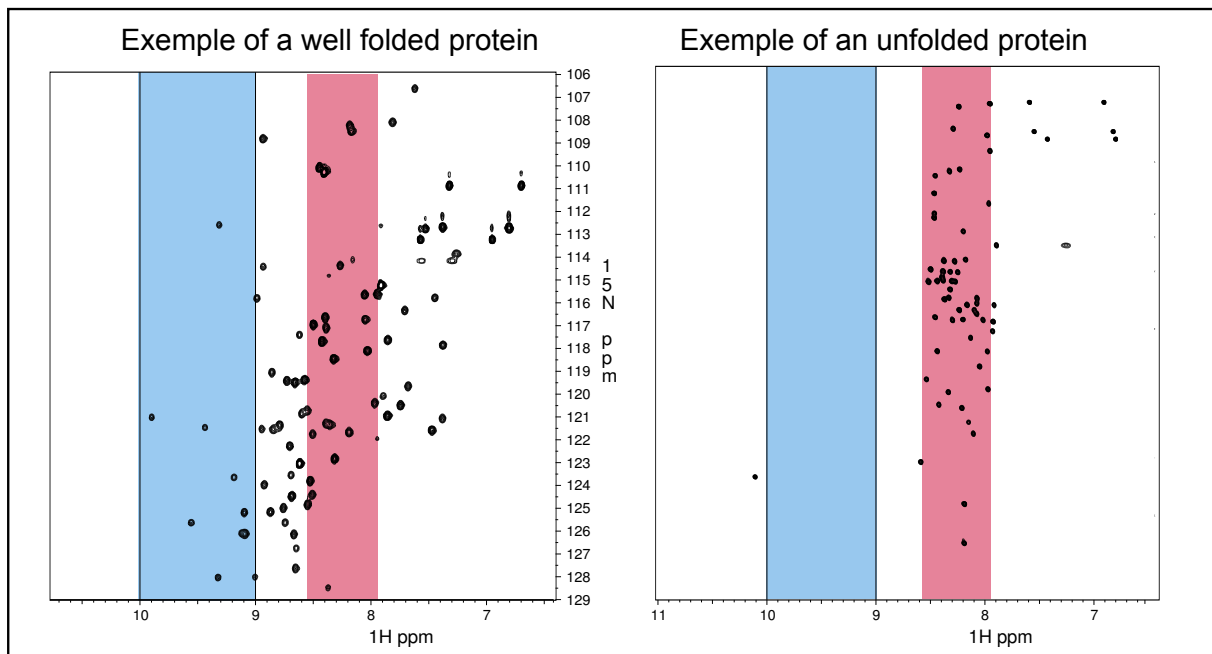


Figure 1: $^1H - ^{15}N$ correlation experiment of XXX (1) . Each peak corresponds to a NH pair of the protein.



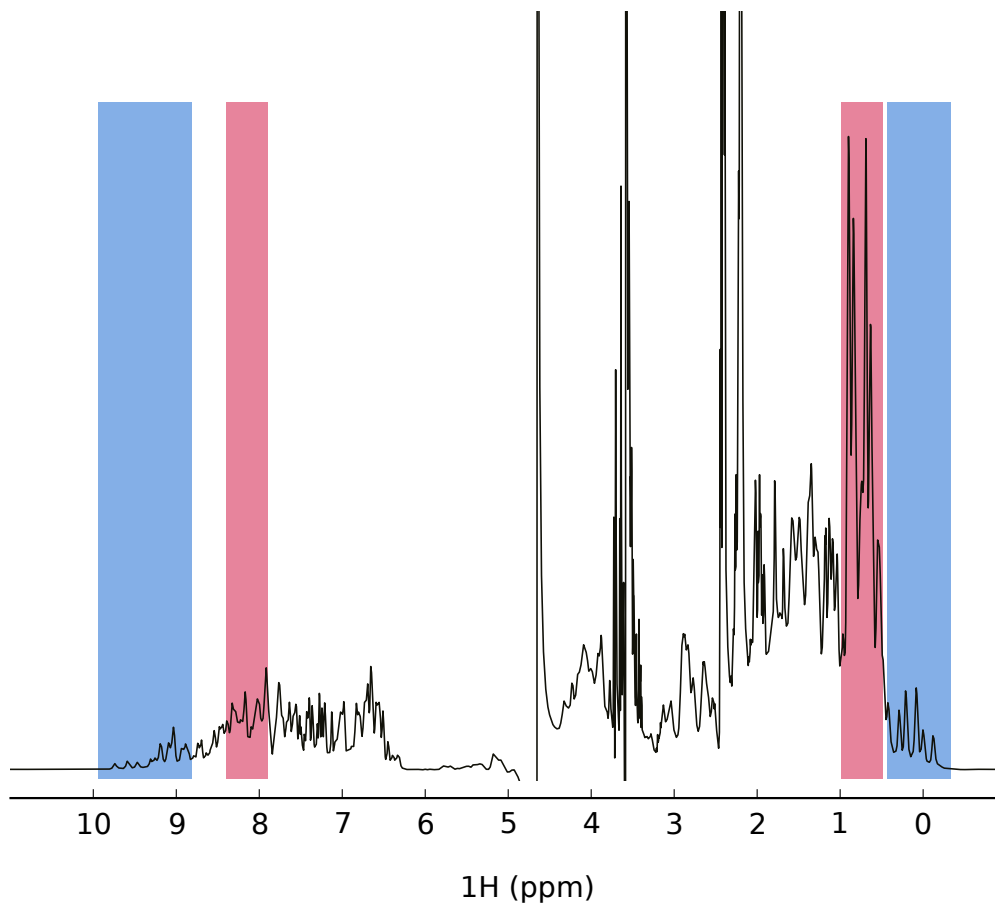
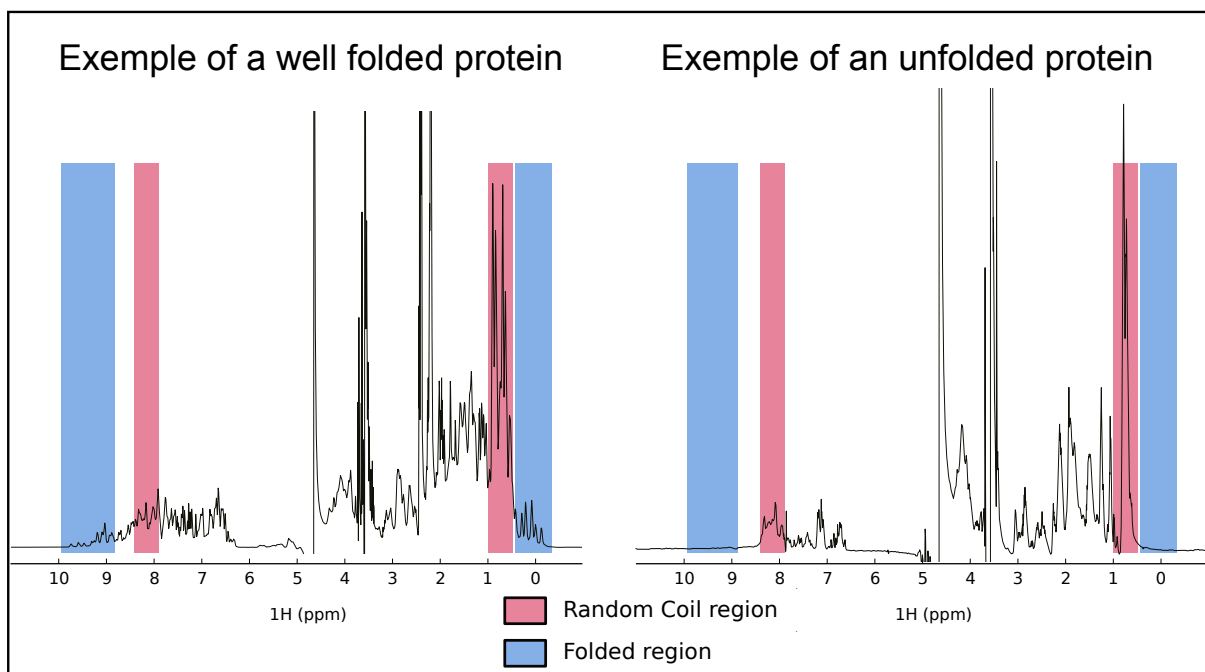


Figure 2: Standart 1D spectrum of XXX.



1D HETSOFAST experiment

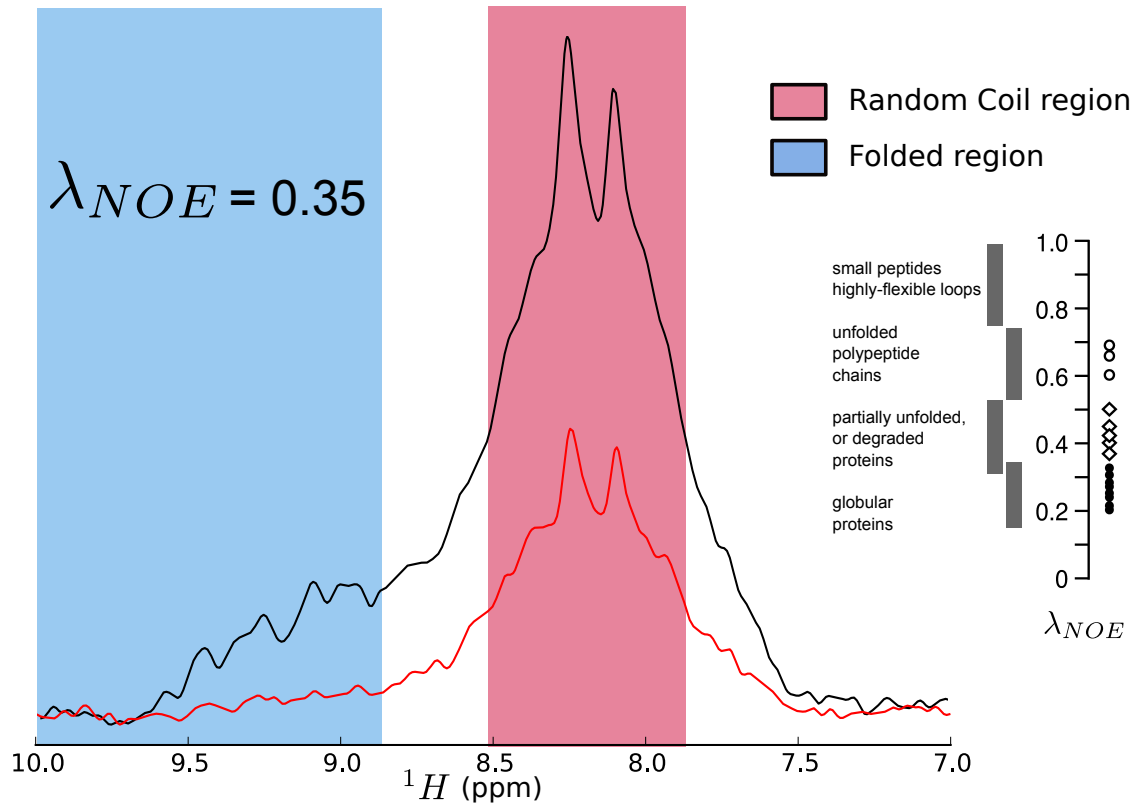
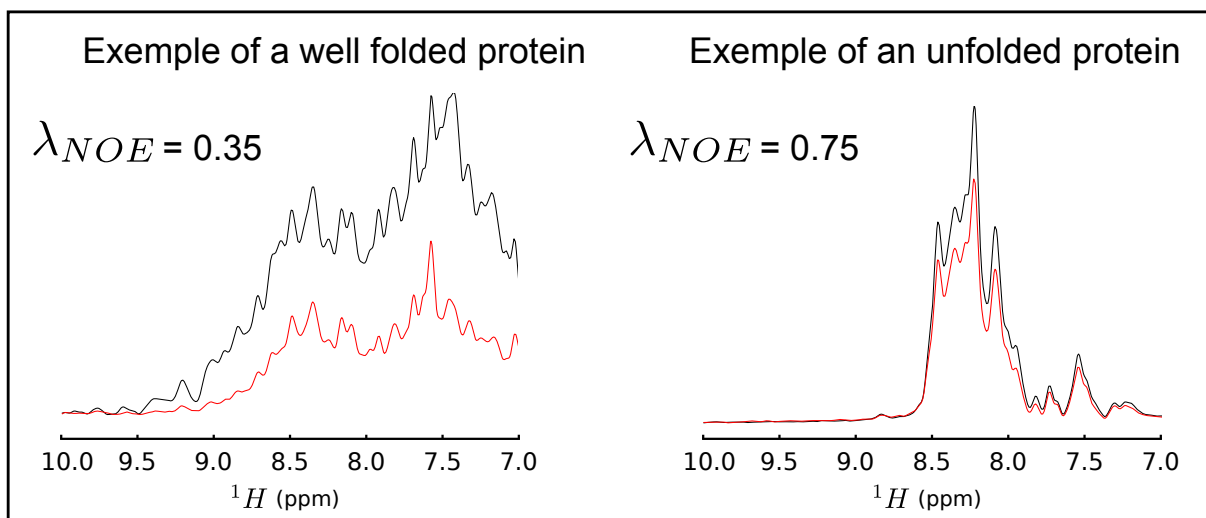


Figure 3: This experiment measures the “compactness” of XXX (2).



References

- [1] Brutscher B Schanda P, Kupce E. Sofast-hmqc experiments for recording two-dimensional heteronuclear correlation spectra of proteins within a few seconds. *J Biomol NMR*, 33:199–211, 2005.
- [2] Brutscher B Schanda P, Forge V. Het-sofast nmr for fast detection of structural compactness and heterogeneity along polypeptide chains. *Magn Reson Chem*, 44 Spec No:S177–84, 2006.