### **NOESY and EXSY Experiments**

Correlation through incoherent magnetization transfer

## Pulse Sequence for the NOESY and EXSY Experiment



coherence path for absolute value spectra acquired with EXORCYCLE

there is a further 90 pulse with respect to COSY. It has a phase difference of 180 respect to the previous one Assuming  $B_1$  along y':

the former pulse carries the magnetizatins of the A and B nuclei to the x' axis of the rotating frame

during  $t_1$  the transverse magnetization vectors precess with angular frequency  $\Omega_{\rm A}$  and  $\Omega_{\rm B}$ 

![](_page_2_Figure_3.jpeg)

The components of the magnetization vector:

$$M_{Ax'} = M_{A0} \cos(\Omega_A t_1)$$

$$M_{Ay'} = M_{A0} sin(\Omega_A t_1)$$

$$\begin{split} \mathsf{M}_{\mathsf{Bx'}} &= \mathsf{M}_{\mathsf{B0}}\mathsf{cos}(\Omega_{\mathsf{B}}\mathsf{t}_1)\\ \mathsf{M}_{\mathsf{By'}} &= \mathsf{M}_{\mathsf{B0}}\mathsf{sin}(\Omega_{\mathsf{B}}\mathsf{t}_1) \end{split}$$

The latter pulse, again with  $B_1$  along y', carries the components  $M_{Ax'}$  and  $M_{Bx'}$  up to -z, whereas it leaves unchanged the y' components. The latter components are deleted either by a phase cycle or by defoccussing by means of a pulsed gradient

![](_page_3_Figure_1.jpeg)

During  $\tau_{mix}$  the **exchange** of the nucleus from the A to the B site can occur (either intermolecular exchange or conformational conversion): EXSY

or magnetization **transfer** from B to A by (transient) **NOE**: NOESY The last pulse, with B<sub>1</sub> along –y', carries the magnetization, which was along –z at the end of the mixing time, along x' thus becoming responsible for the signal, which is acquired by receiver.

The magnetization, which was precessing with  $\Omega_A$  in  $t_1$  and during  $\tau_{mix}$  was transferred to B, precesses in  $t_2$  with  $\Omega_B$ , thus it originates a cross peak. The reciprocal holds for  $B \rightarrow A$ 

The NOESY phase sensitive spectra are advantageous because:

✓ the EXSY cross-peaks have the same sign of the diagonal peaks

✓ the NOESY cross peaks have opposite sign with respect to the diagonal peaks for positive NOE

- the NOESY cross peaks have the same sign of the diagonal peaks for a negative NOE
- the ROESY spectra are obtained applying a spin-lock during the mixing time
- the ROESY cross-peaks have always opposite sign with respect of diagonal peaks because ROE is always positive

### ROESY

rotating frame Overhauser effect spectroscopy

![](_page_6_Figure_2.jpeg)

Spinlock = mixing time, should not exceed 300 ms, best between  $T_2/2$  and  $T_2$ 

The strength of the ROE signal is proportional to the inverse sixth power of the distance between the atoms. The sensitivity is increased by choosing low-viscosity solvents and/or removing dissolved oxygen from the sample.

Prof. Jenny

# Study of protein folding under native conditions by rapidly switching the hydrostatic pressure inside an NMR sample cell

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![](_page_7_Figure_3.jpeg)

![](_page_8_Figure_0.jpeg)

Schematic timing diagram of the pulse sequence.

At the end of a high-pressure equilibration period (12 s), the <sup>1</sup>H magnetization is transferred to <sup>15</sup>N z magnetization by a refocused **INEPT** pulse scheme.

Conversion to transverse <sup>15</sup>N magnetization and subsequent  $t_1$  evolution, followed by a pulse that stores a  $cos(\omega_N t_1)$  fraction of this magnetization back to z, is initiated at time  $\tau d$  after the pressure drop, thereby encoding the <sup>15</sup>N frequencies present at  $\tau d$ .

At a fixed time, T, after the pressure drop, this encoded <sup>15</sup>N magnetization is transferred back to the amide proton for <sup>1</sup>H detection. T is chosen sufficiently long (330 ms) that most of the protein has folded at the time of detection

![](_page_9_Figure_0.jpeg)

(B–F) Small regions of the HSQC
spectra, recorded on a 280 μM
<sup>2</sup>H/<sup>15</sup>N/<sup>13</sup>C-enriched ubiquitin sample
at indicated τd delay durations after
the pressure drop.

All spectra correlate the frequency of the detected amide proton in the folded protein to the <sup>15</sup>N frequency of either the unfolded (red) or folded (blue) protein, with resonance intensities proportional to the fractions populating the unfolded and native states. Note that colors have been added manually. Residues are labeled by their one-letter residue code and number, with U and F denoting the unfolded and native state, respectively. (G) Time dependence of the resonance intensities observed in B–F. Fitted time constants show faster disappearance of resonances of the unfolded state than appearance of the folded final spectrum