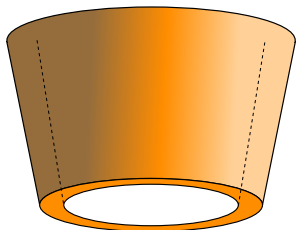
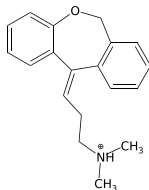
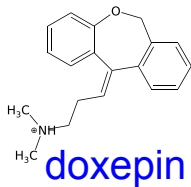


Revealing ligand-receptor interaction NMR titration

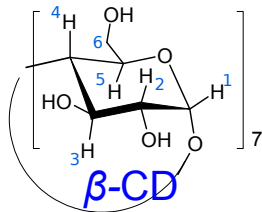
Martin Novák, Jan Novotný

May 4, 2016

Introduction of reacting partners

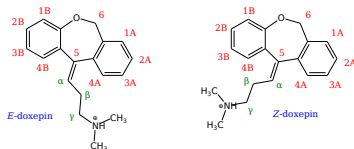


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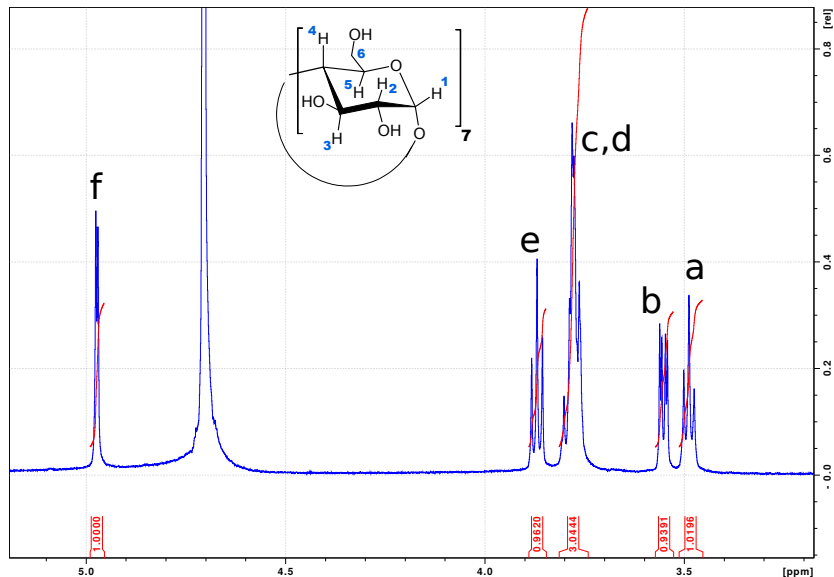


Recommended procedure

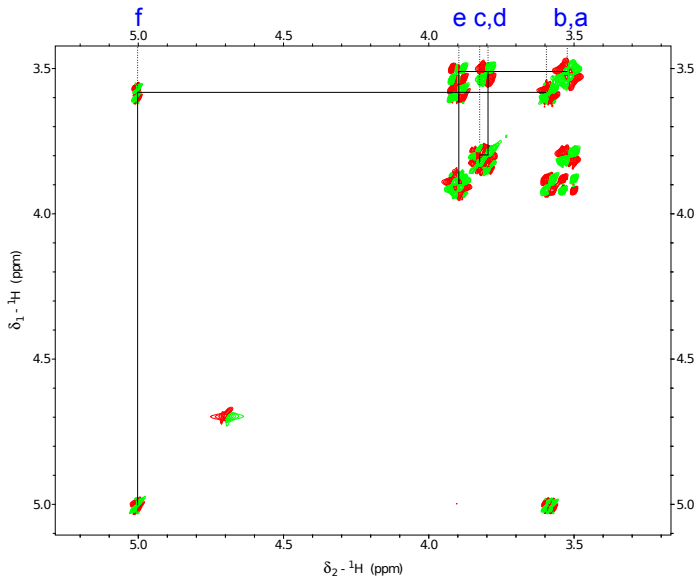
- 1 Assignment of free receptor - β -cyclodextrine (1D ^1H , DQF-COSY)
- 2 Assignment of free ligand - doxepin (1D ^1H , DQF-COSY, NOESY)
 - Identification of proton resonances of ring A and B
 - Determination of major and minor conformation of doxepin
- 3 1D NMR titration - rearrangement of β -cyclodextrine resonances upon interaction \Rightarrow identification of inner protons
- 4 1D NMR titration - rearrangement of doxepin resonances upon complexation \Rightarrow estimation of binding mode
- 5 ROESY spectrum of complex: ROE intermolecular contacts
- 6 Fitting the titration isotherm



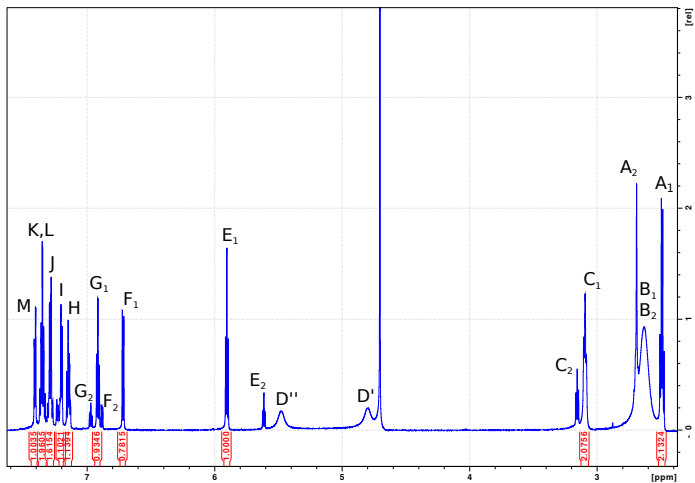
1D ^1H of β -cyclodextrine in D_2O



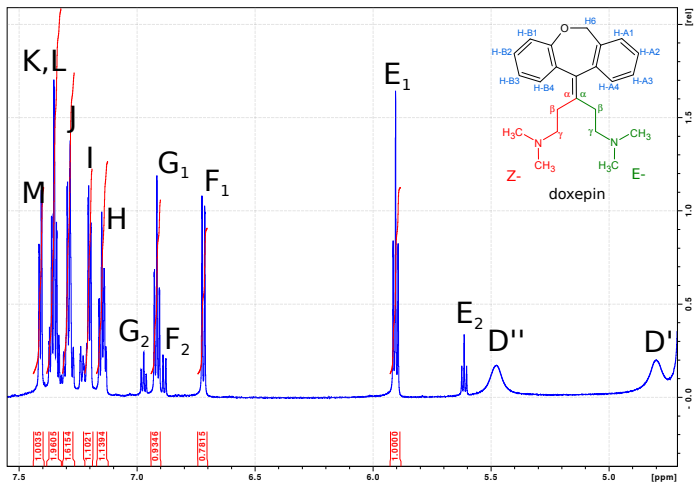
DQF-COSY of β -cyclodextrine in D_2O



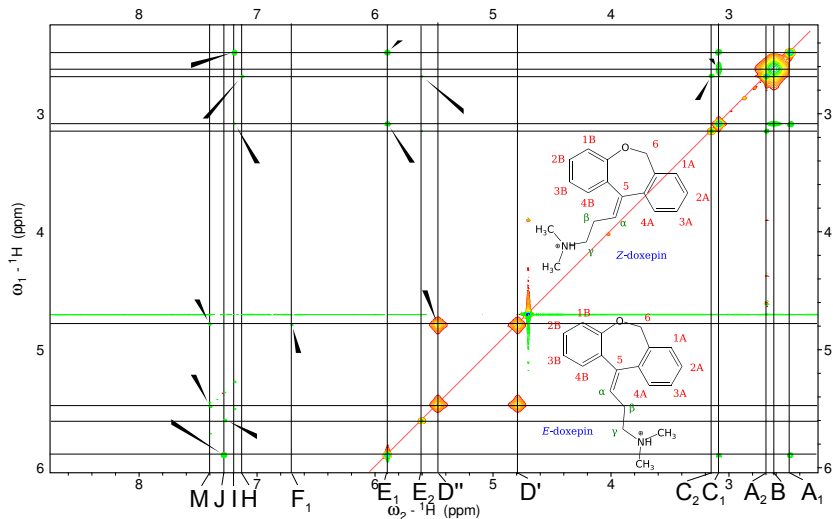
1D ^1H of doxepin in D_2O



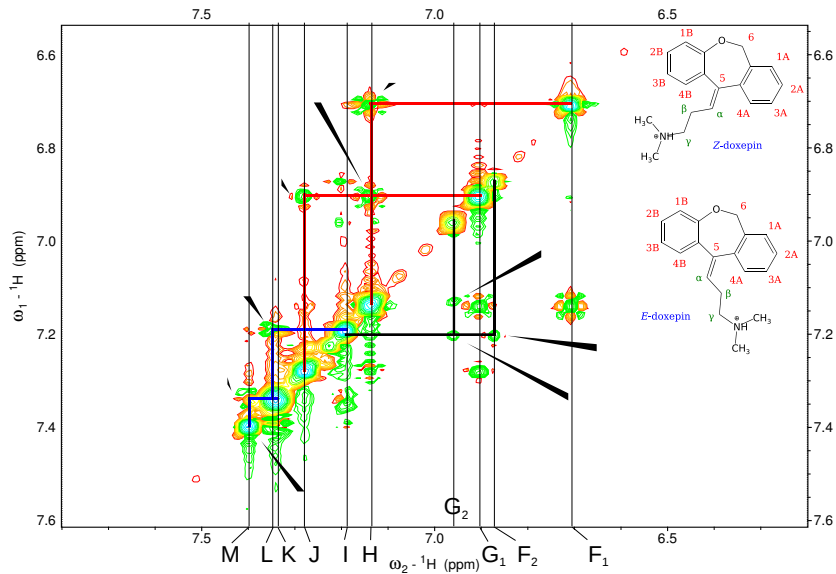
1D ^1H of doxepin in D_2O



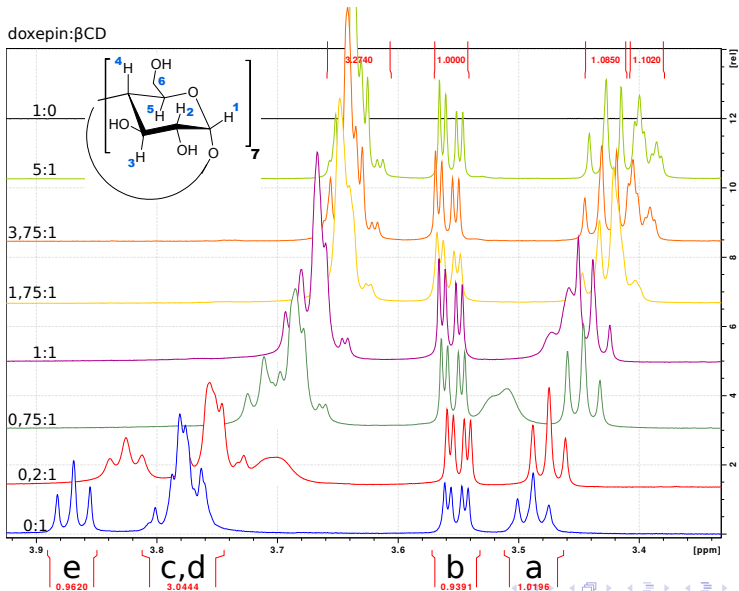
NOESY 700ms of doxepin in D₂O



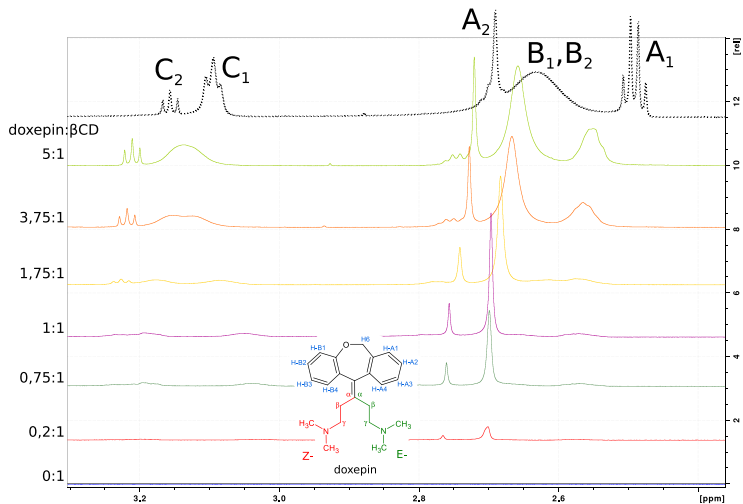
NOESY 700ms of doxepin in D₂O



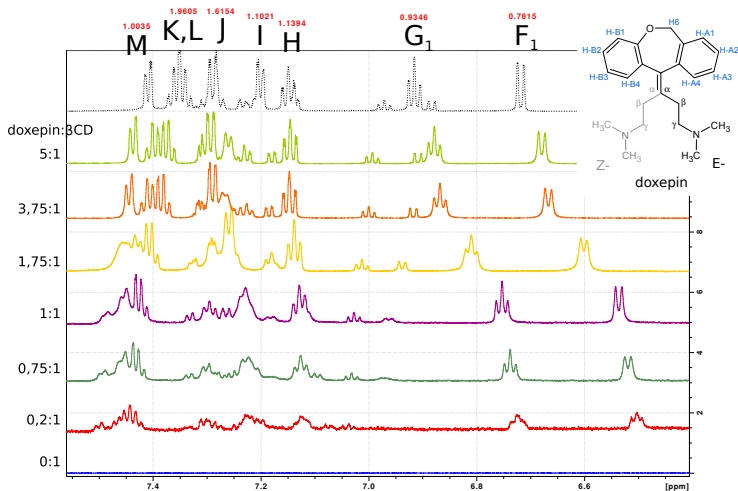
1D ^1H NMR titration: β -cyclodextrine



1D ^1H NMR titration: doxepin



1D ^1H NMR titration: doxepin



Find the most perturbed resonances and estimate the time regime of interaction:

ROESY 300ms - doxepin: β -cyclodextrine=5:1

