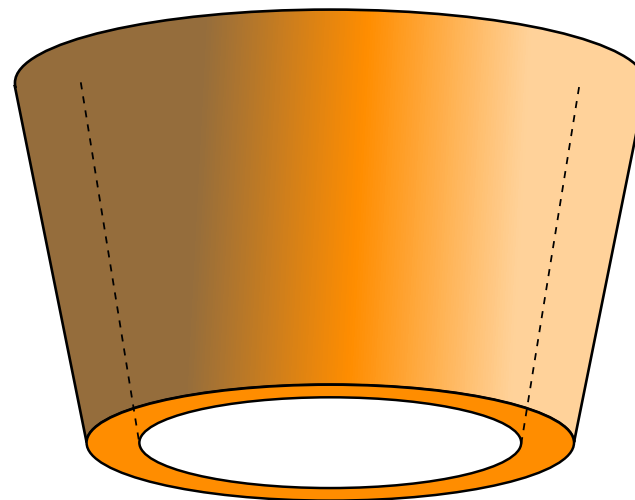
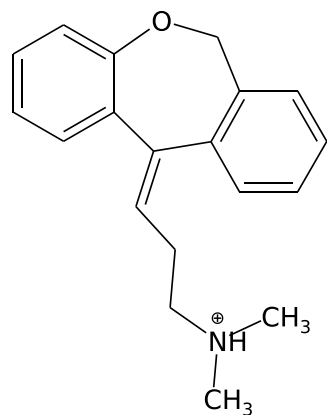
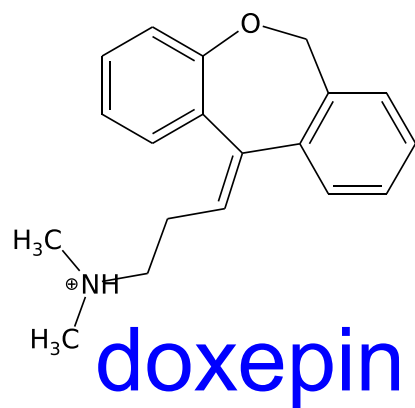
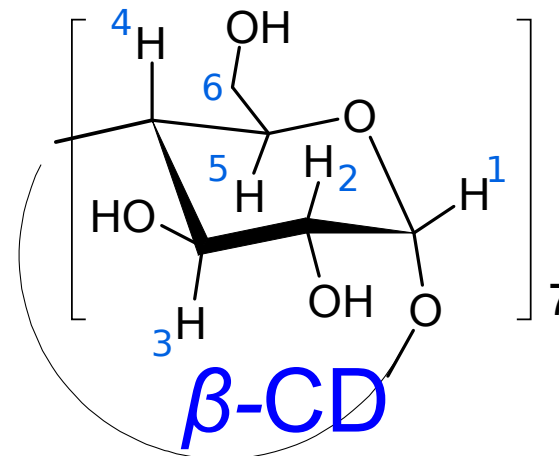


Introduction of reacting partners

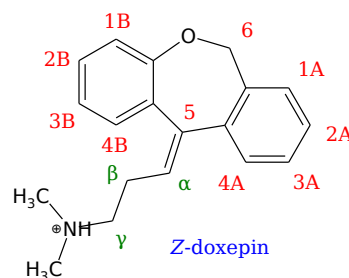
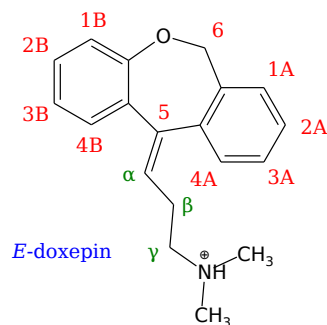


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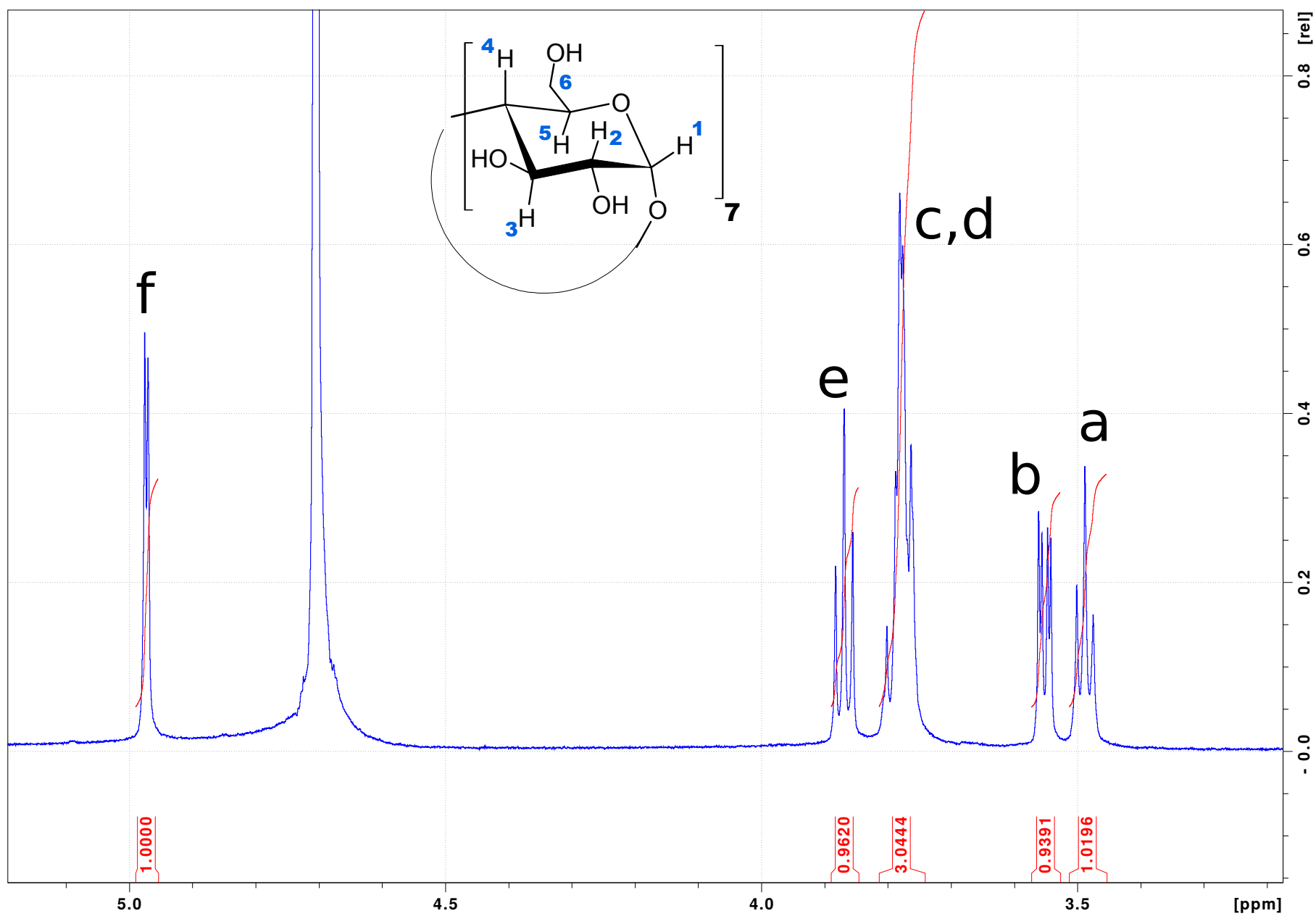


Recommended procedure

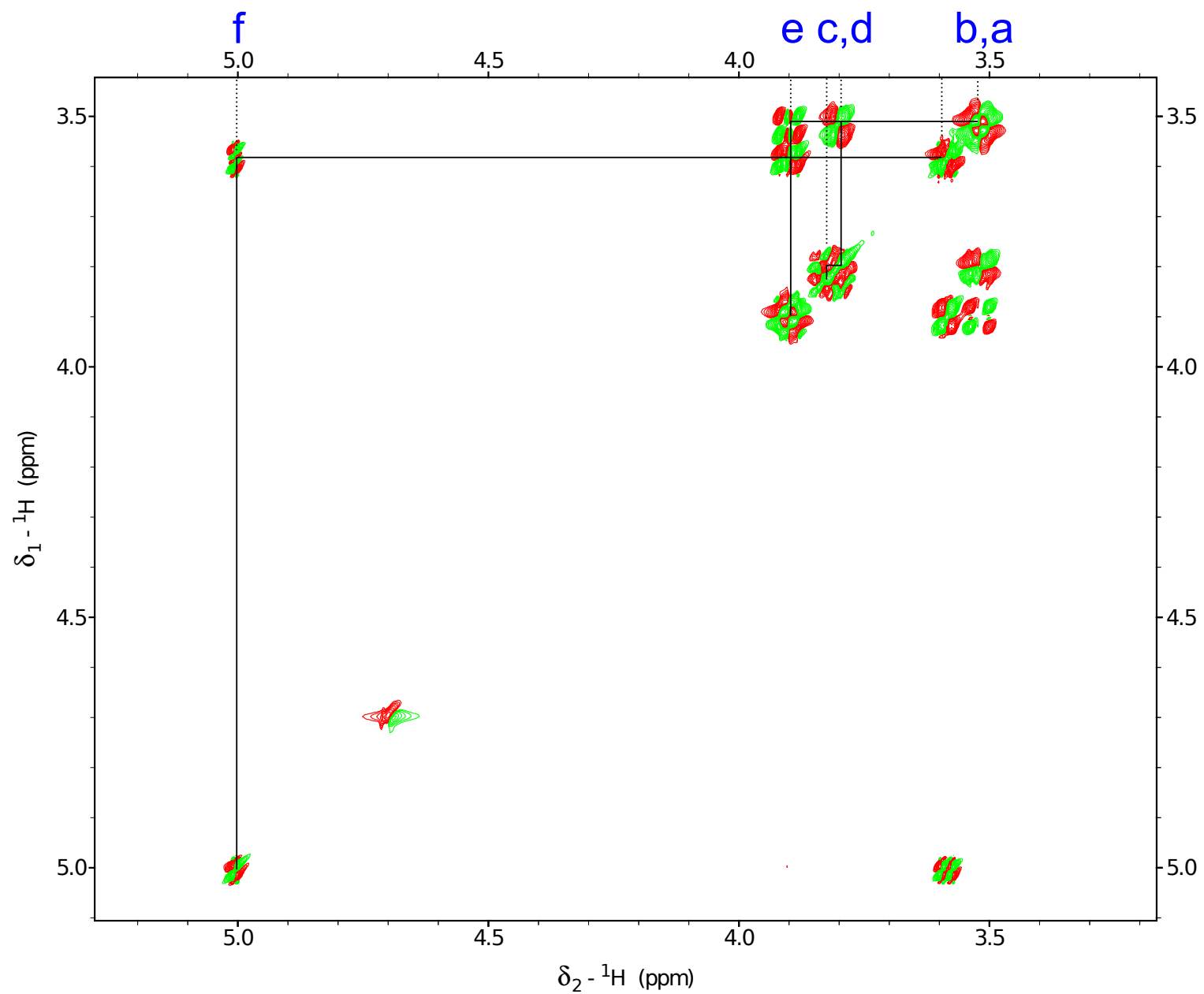
- 1 Assignment of free receptor: β -cyclodextrine (1D ^1H , DQF-COSY)
- 2 Assignment of free ligand: doxepine (1D ^1H , DQF-COSY, NOESY)
 - Identification of proton resonances of ring A and B
 - Determination of major and minor conformation of doxepin
- 3 1D NMR titration: rearrangement of β -cyclodextrin resonances upon interaction \Rightarrow identification of perturbed 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



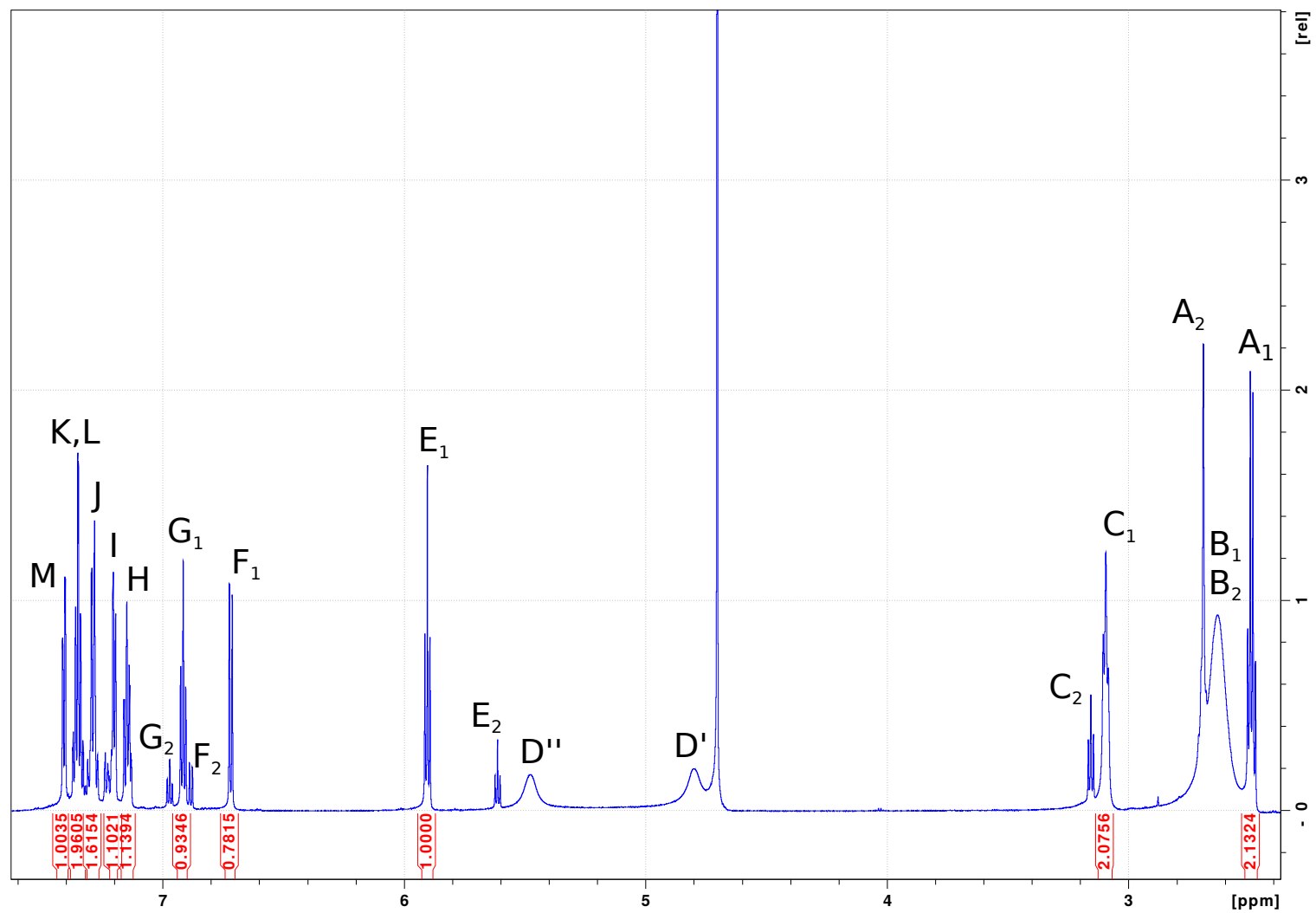
1D ^1H of β -cyclodextrin in D_2O



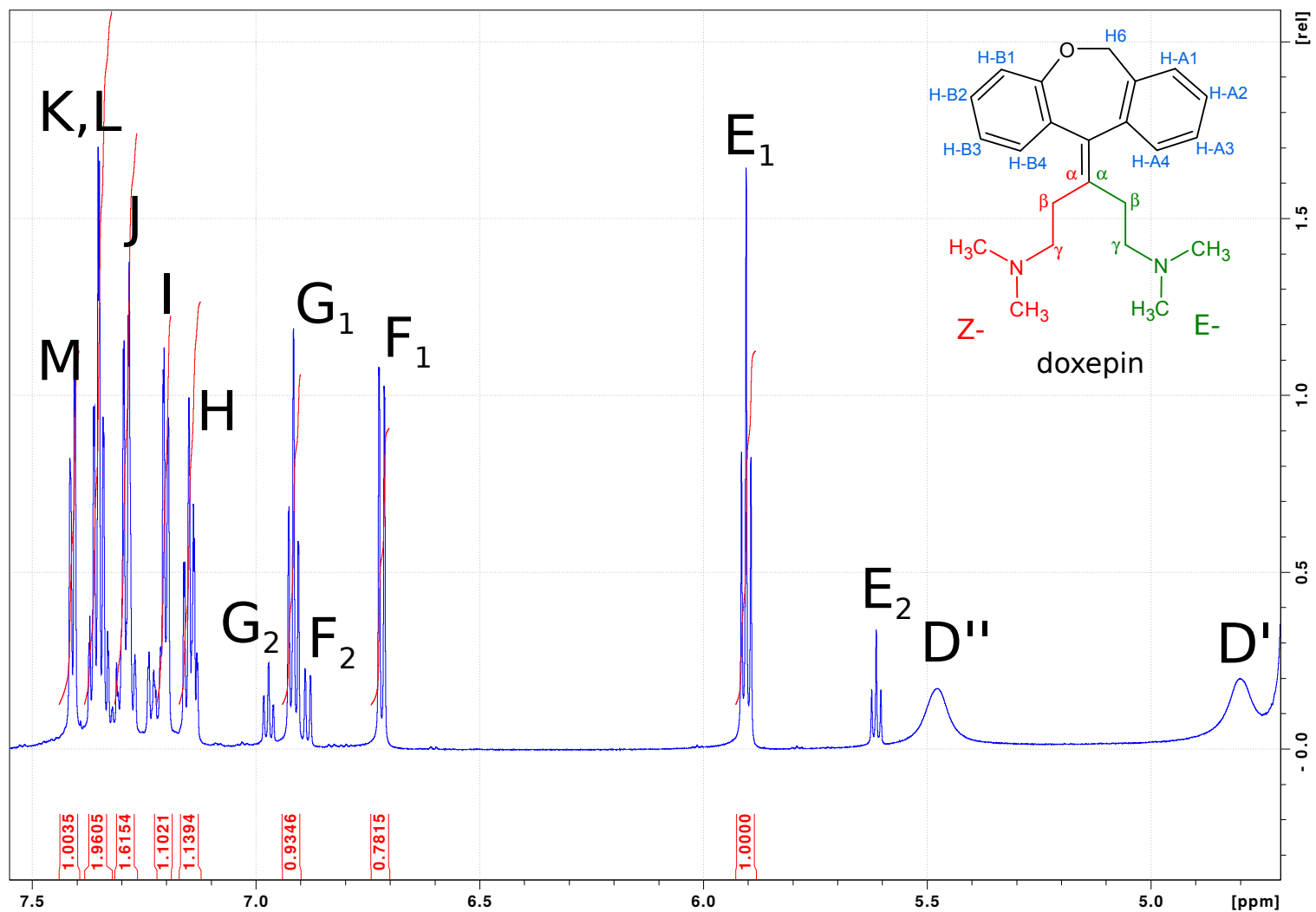
DQF-COSY of β -cyclodextrin in D_2O



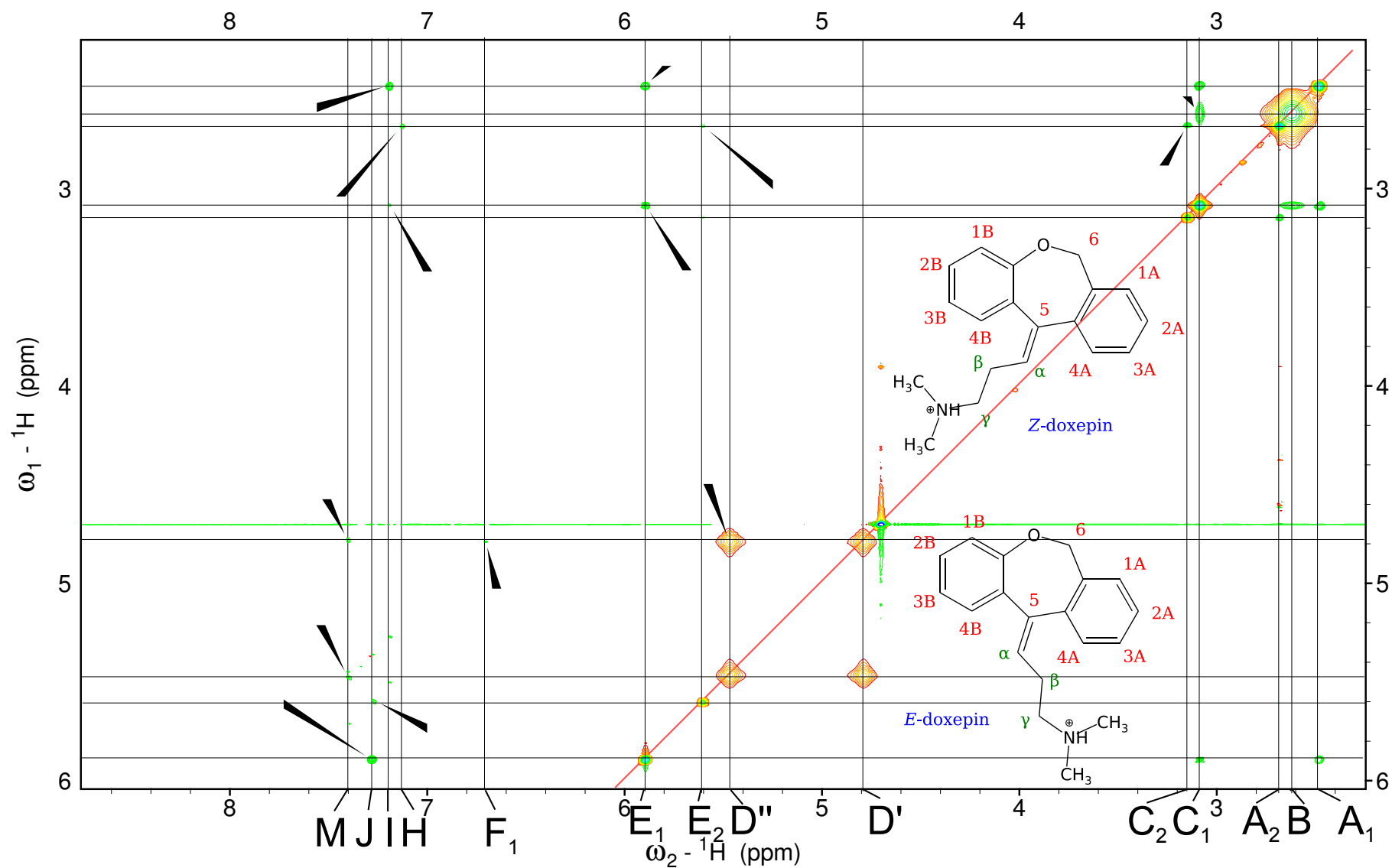
1D ^1H of doxepin in D_2O



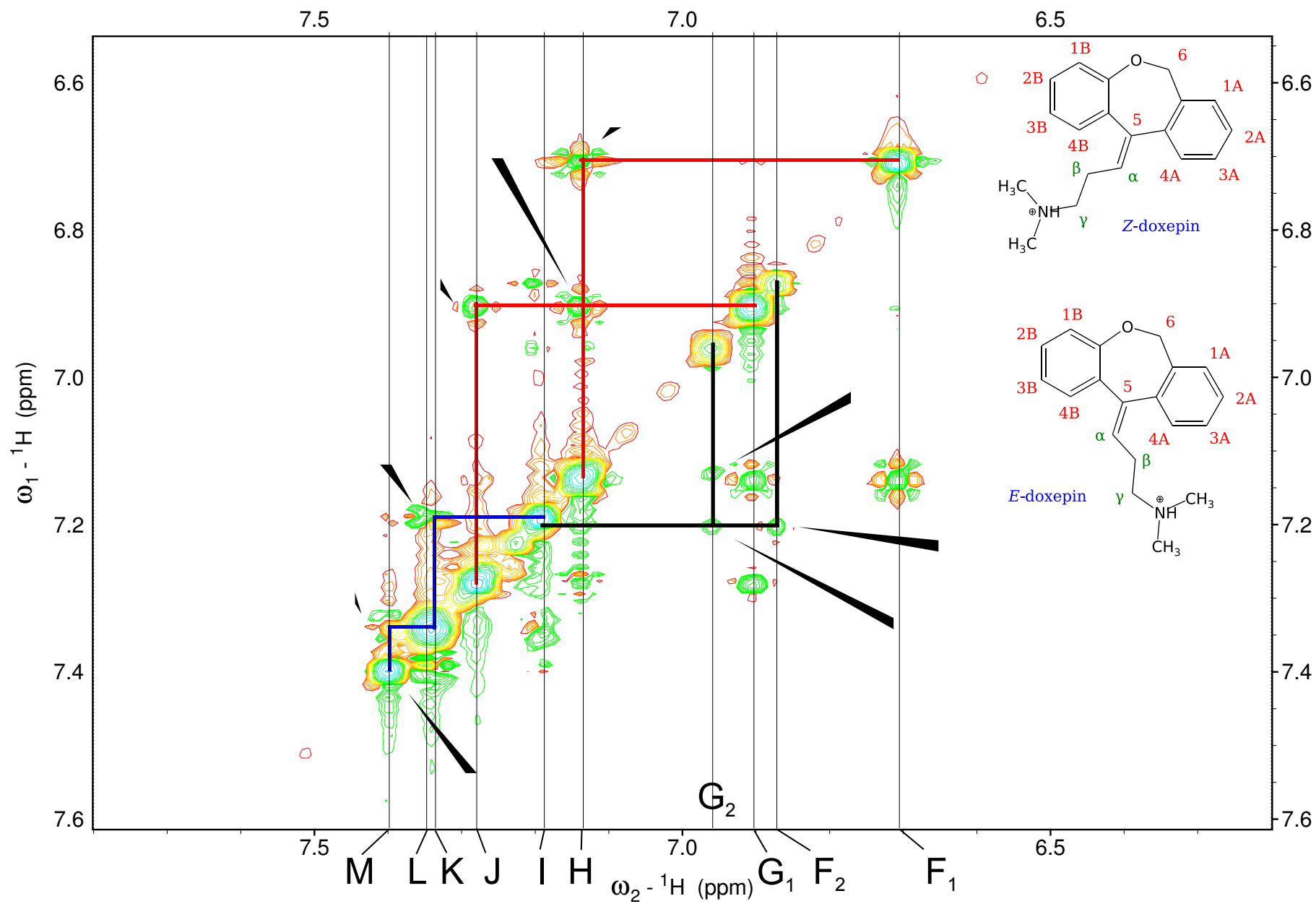
1D ^1H of doxepin in D_2O



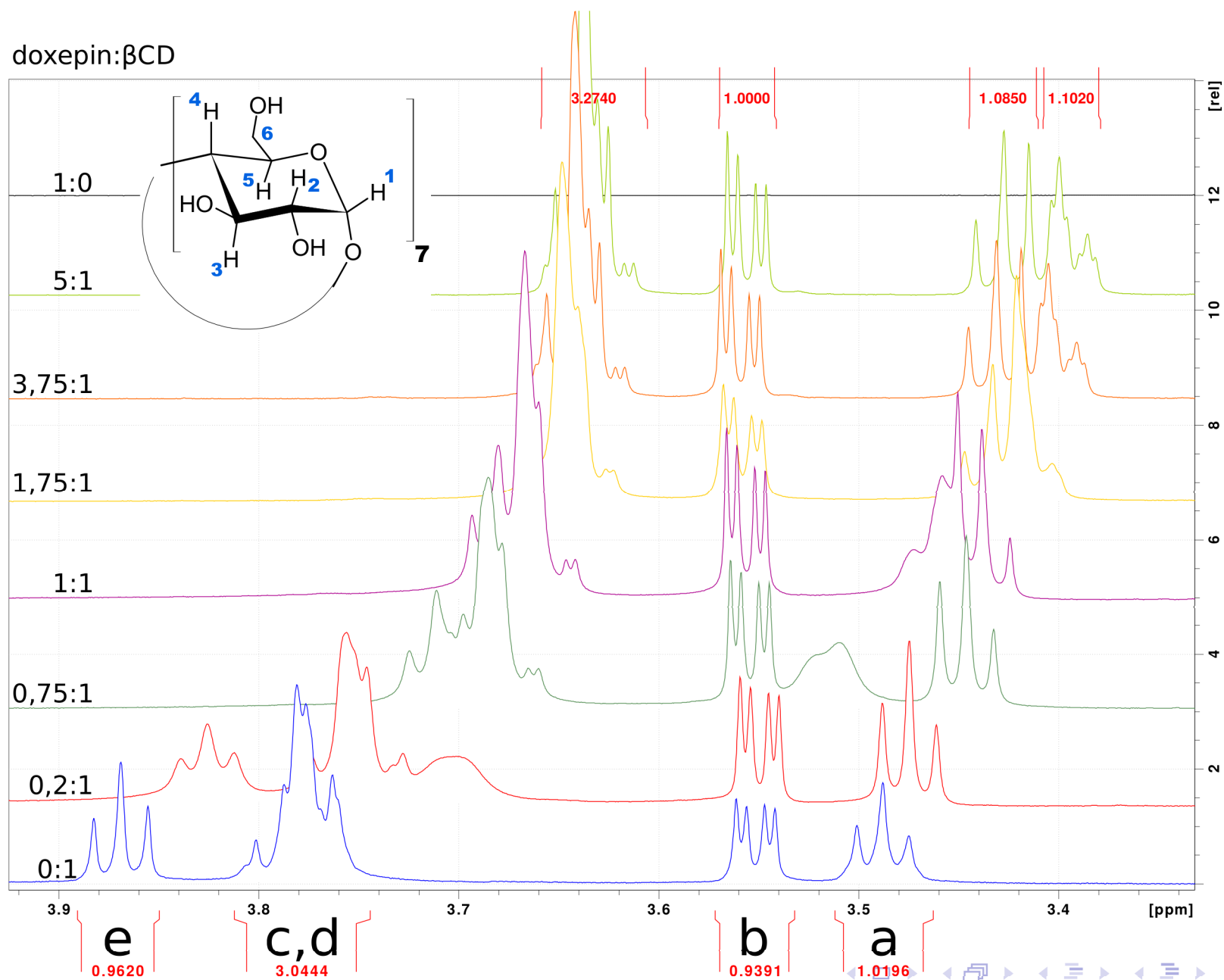
NOESY 700ms of doxepin in D₂O



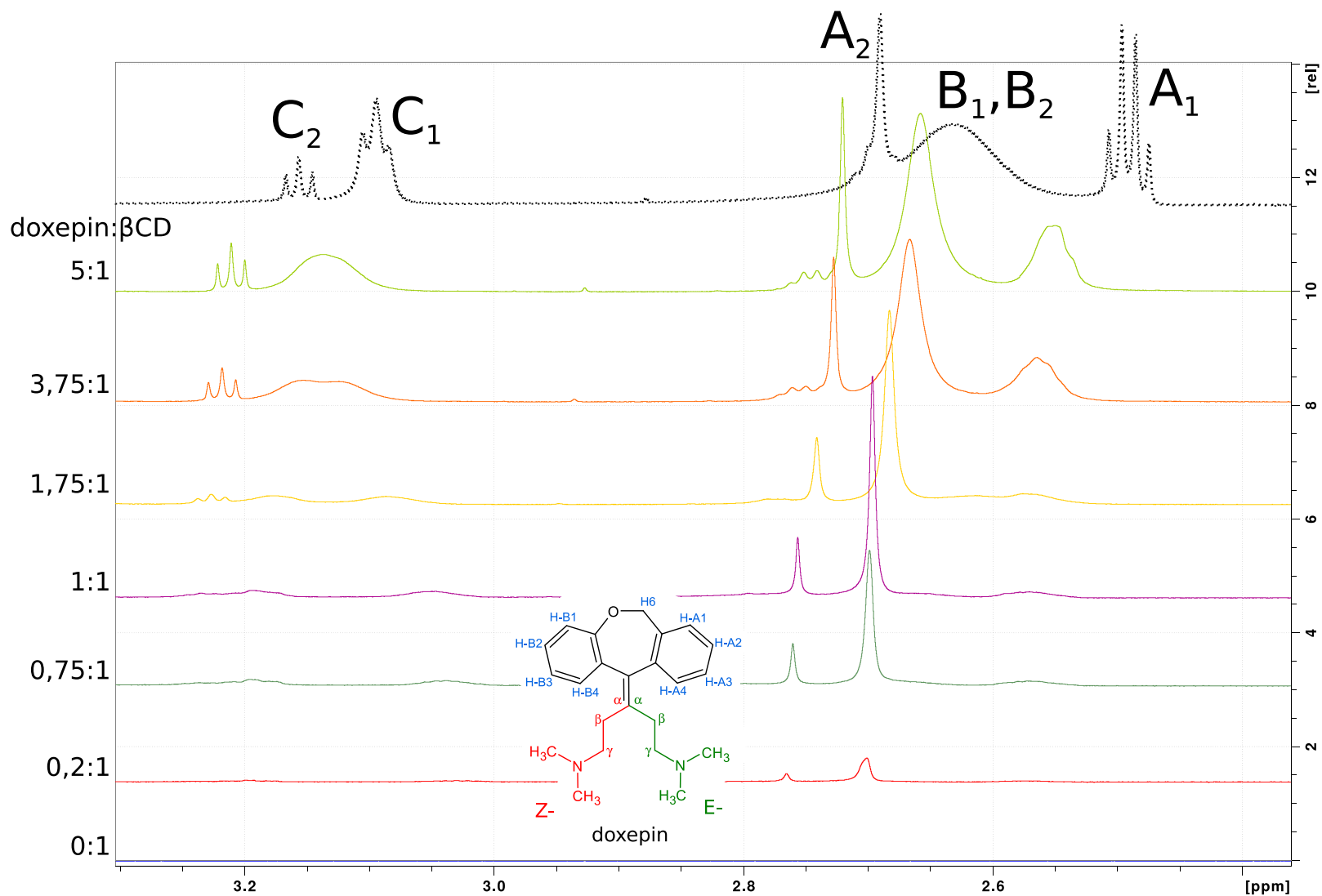
NOESY 700ms of doxepin in D₂O



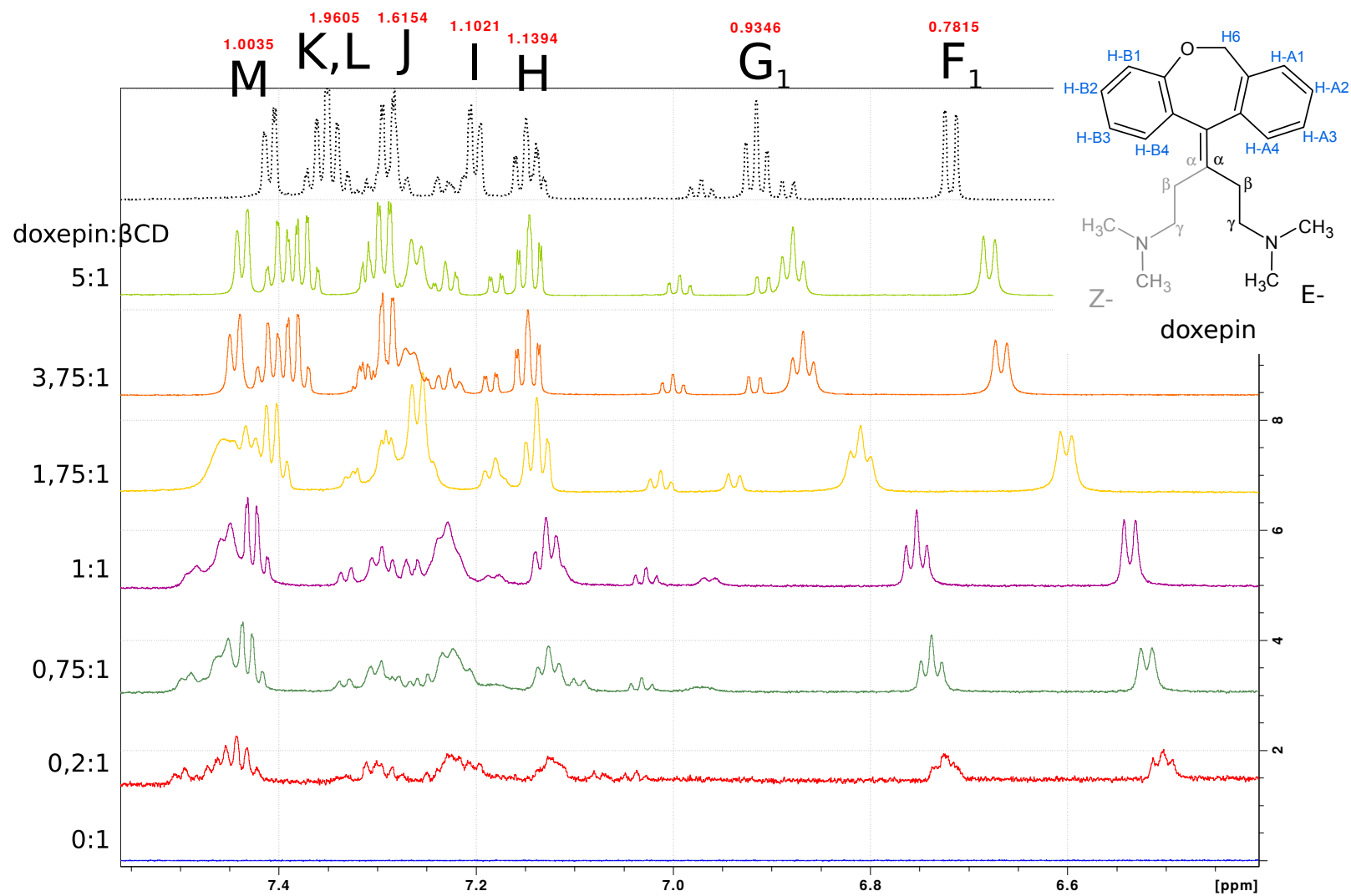
1D ^1H NMR titration: β -cyclodextrin



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 -cyclodextrin=5:1

