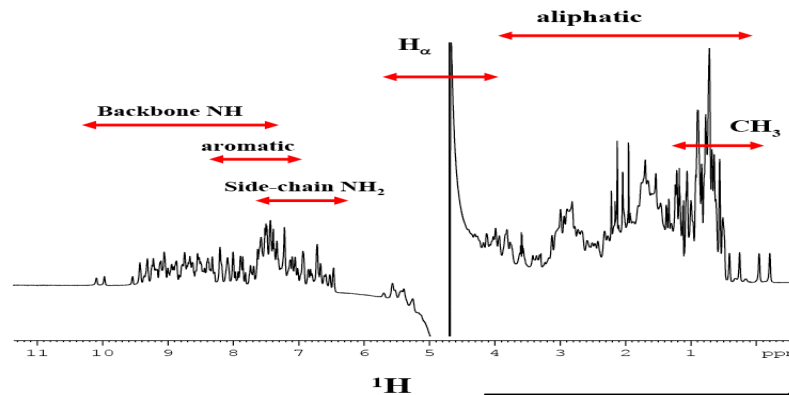
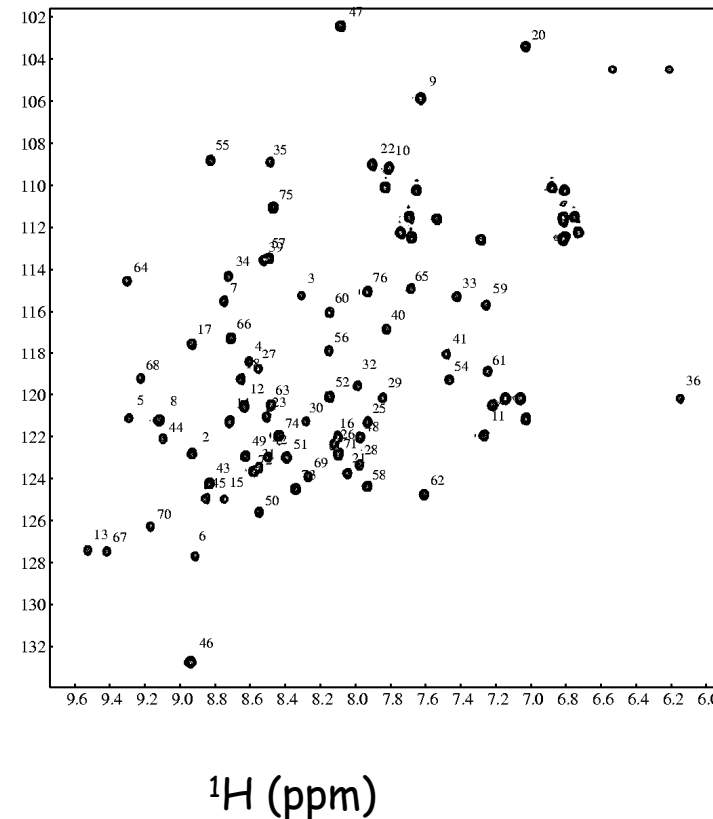
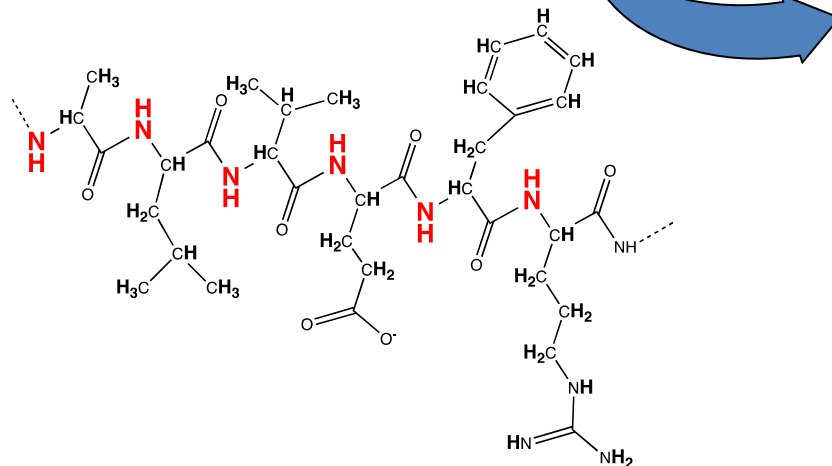


2D ^{15}N HSQC spectrum



- Selection of ^1H bound to ^{15}N
(covalent H-N bond)

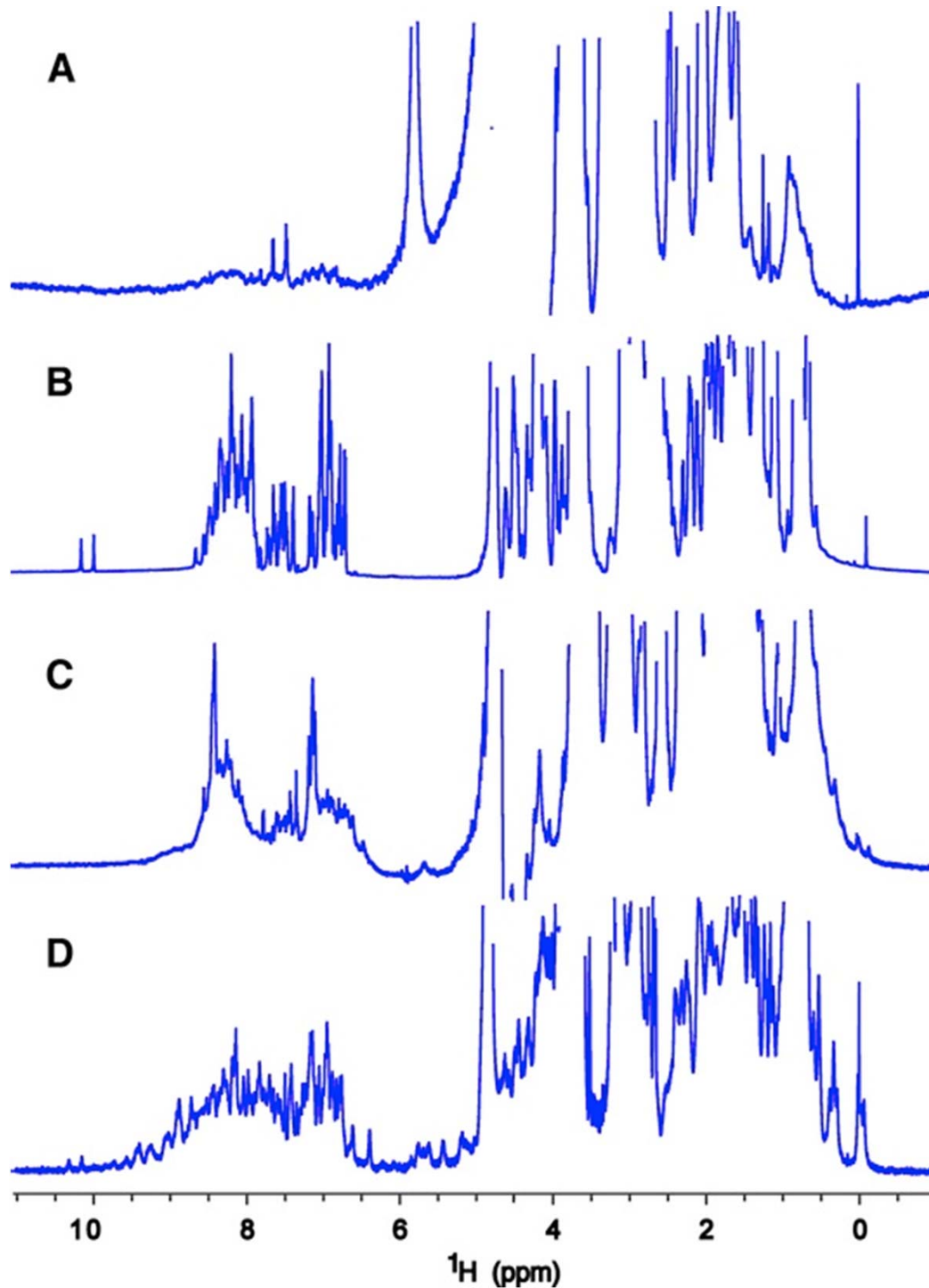
- Chemical shift edition ^1H and ^{15}N



^{15}N (ppm)

^1H (ppm)

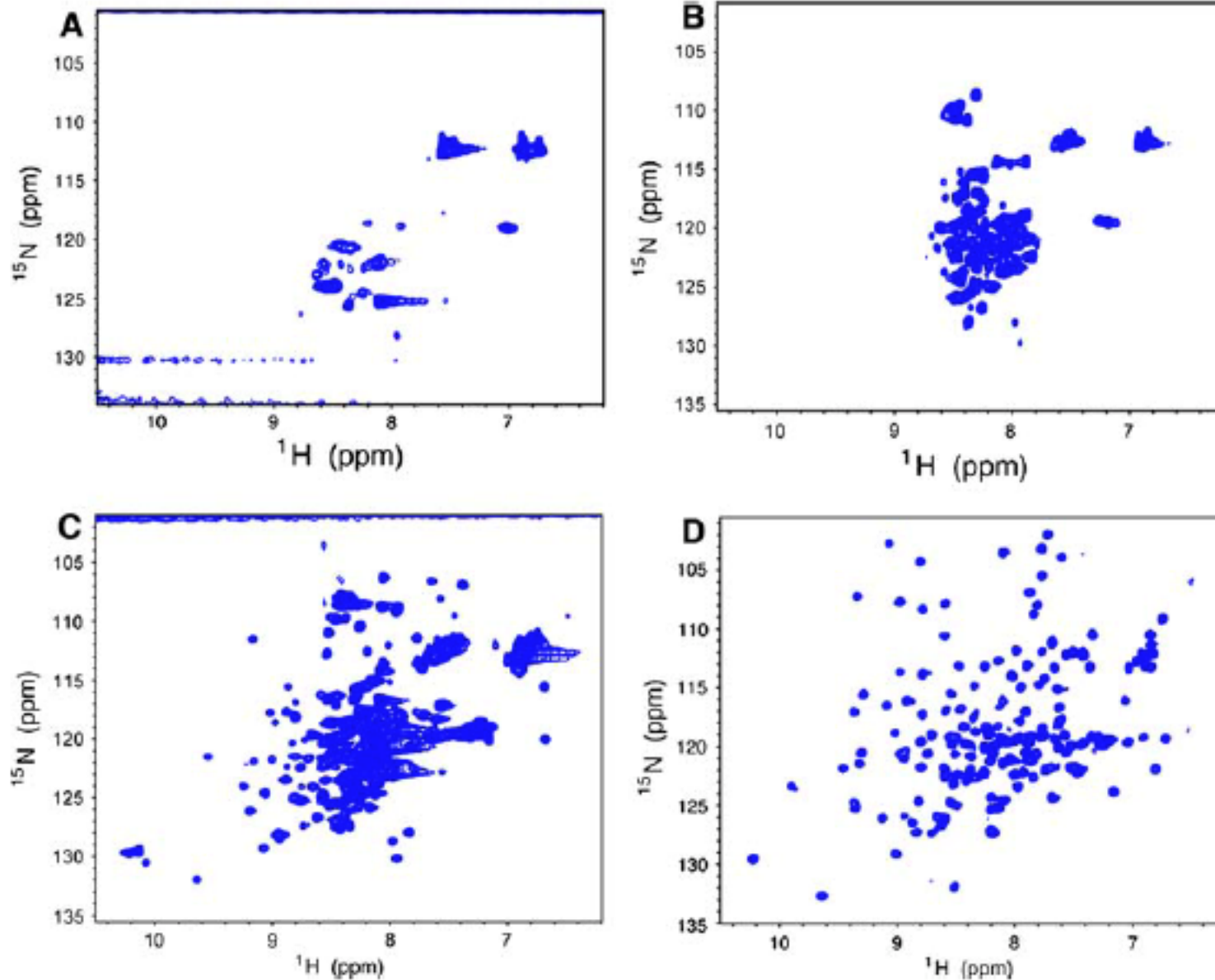
NMR spectrum and protein folding



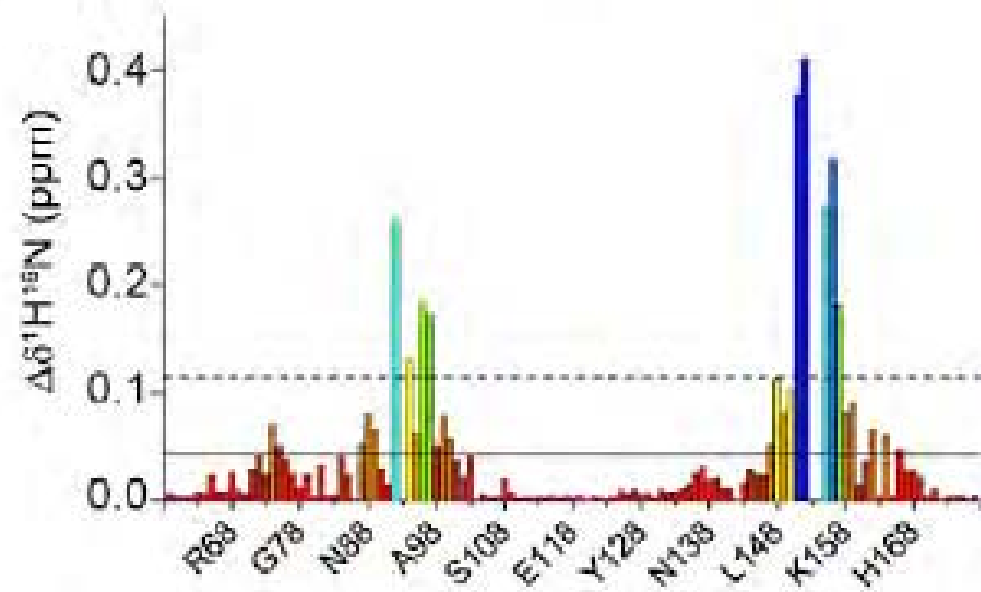
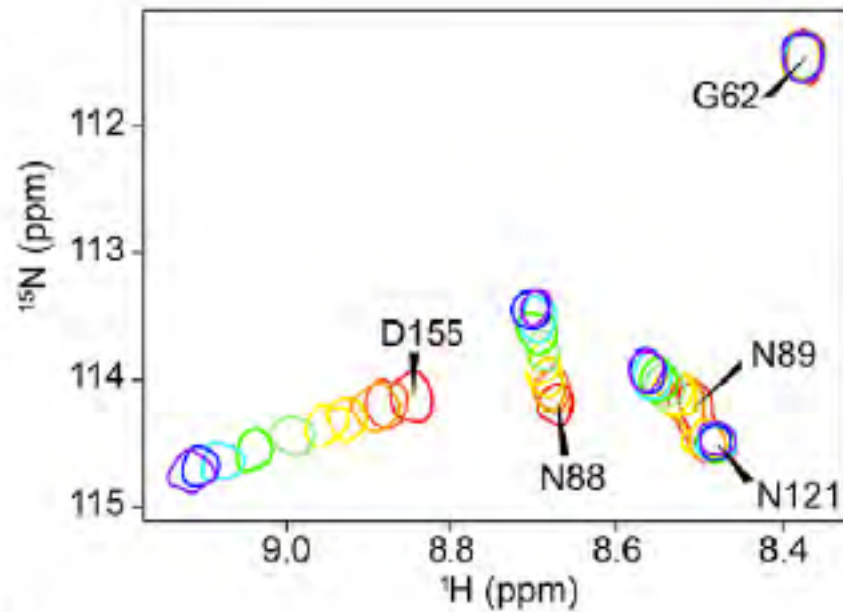
1D ^1H NMR spectra with H_2O presaturation of representative NESG targets obtained with a 1.7-mm micro NMR cryoprobe at 20°C with corresponding NESG target IDs. **A** HR3159A spectrum scores as “poor” on account of broad poorly dispersed resonances. **B** LmR69A spectrum scores “unfolded” due to sharp and poorly dispersed peaks in all regions. **C** EwR71A spectrum scores as “promising” with the presence of upfield-shifted methyl peaks but crowding of the amide region (7–9 ppm), and relatively broad peaks. **D** NsR431C spectrum scores “good” with sharp uniform intensity and upfield-shifted methyls

Rossi P. *et al.*
J. Biomol. NMR, **2009**,
46, 11-22

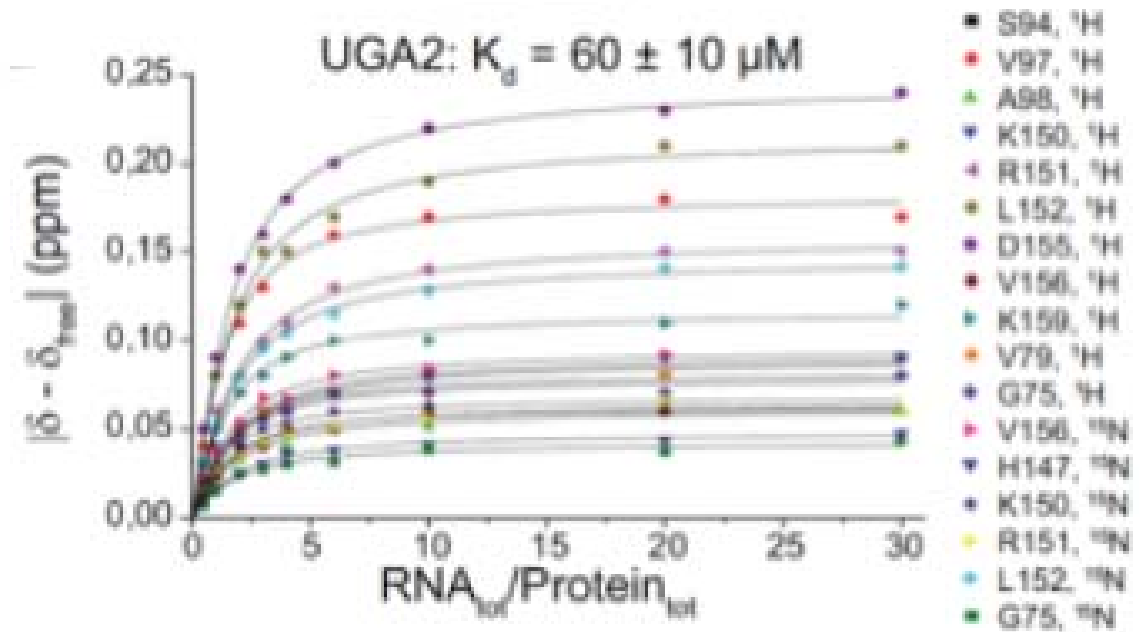
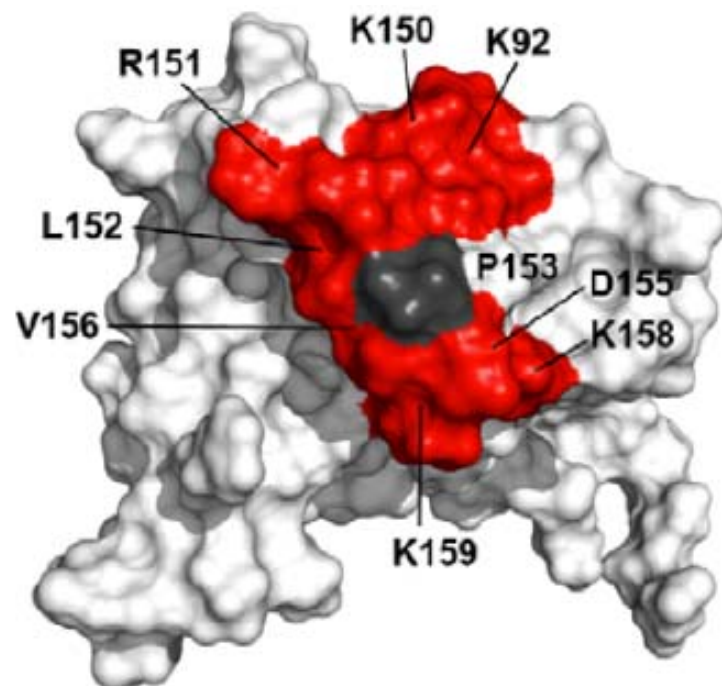
2D ^{15}N HSQC spectra



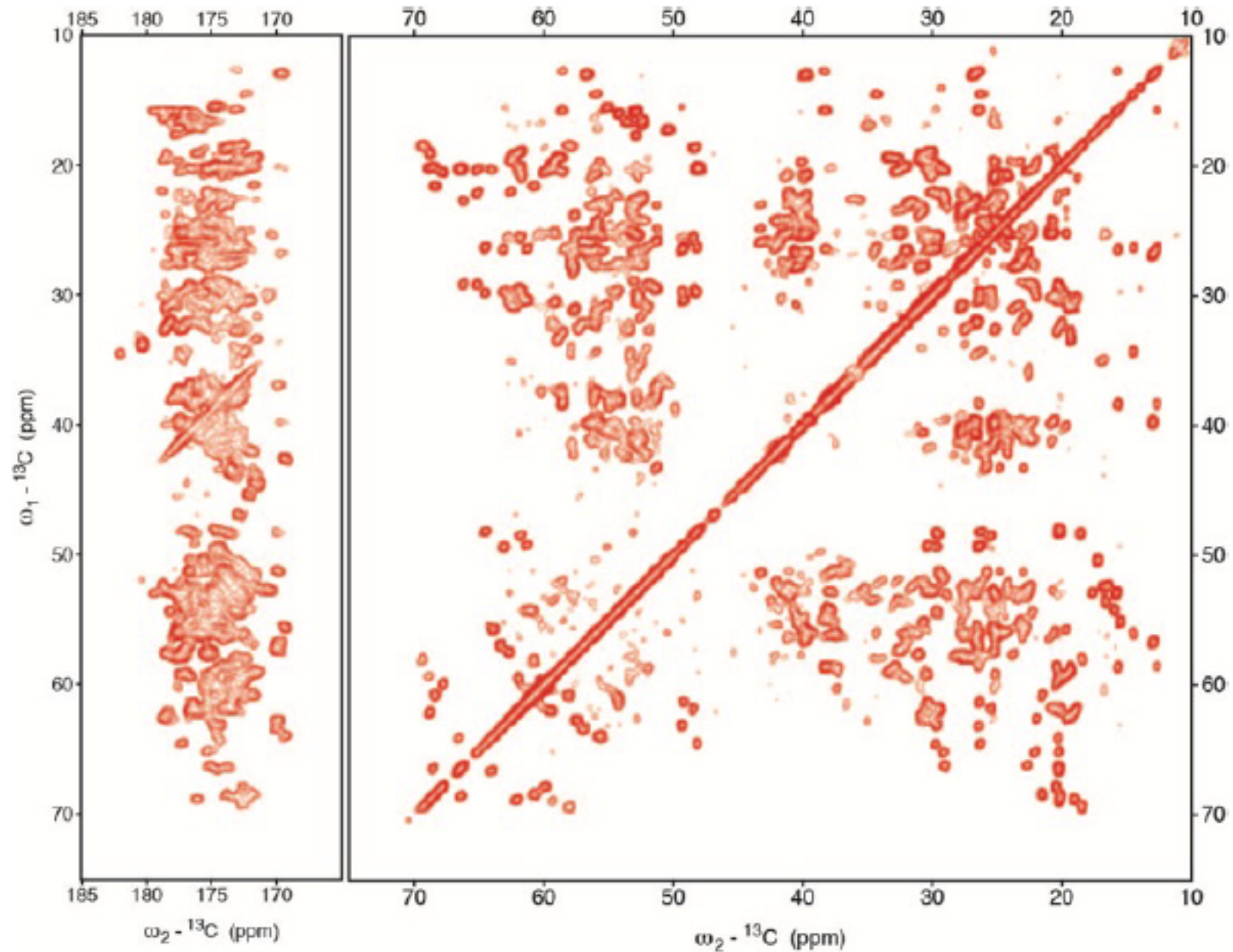
Following a binding event to extract Kd



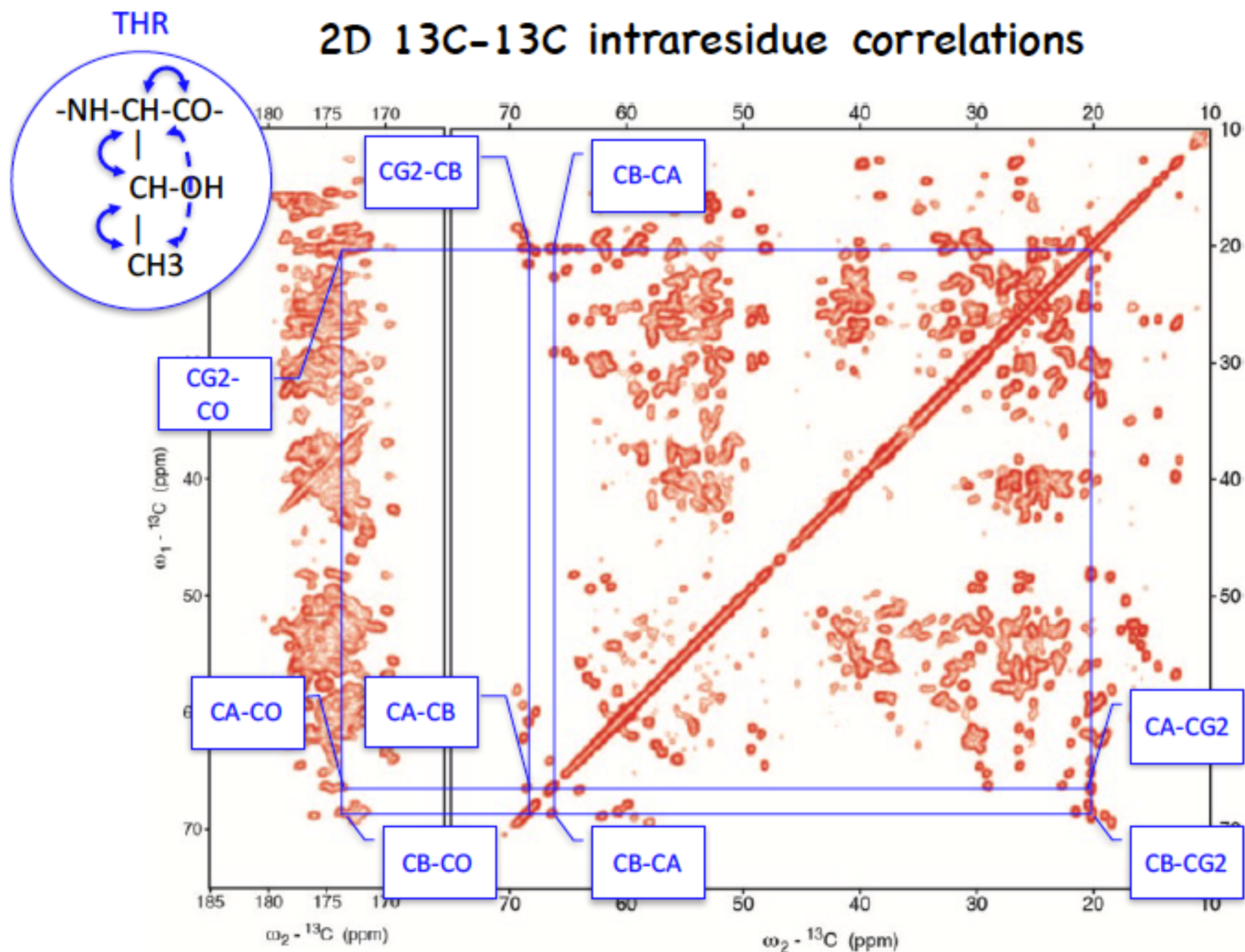
Following a binding event to extract K_d



2D ^{13}C - ^{13}C or ^{13}C - ^{15}N correlation spectrum



2D ^{13}C - ^{13}C intraresidue correlations



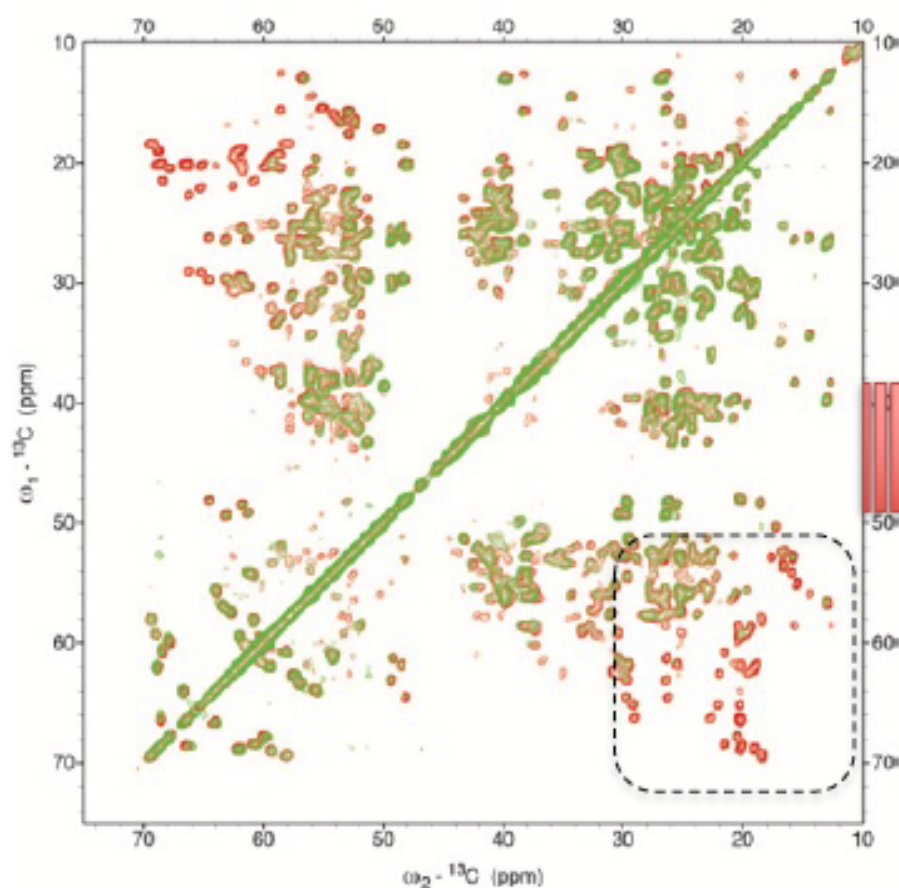
Is higher MAS frequency really beneficial ?

MAS 12 kHz

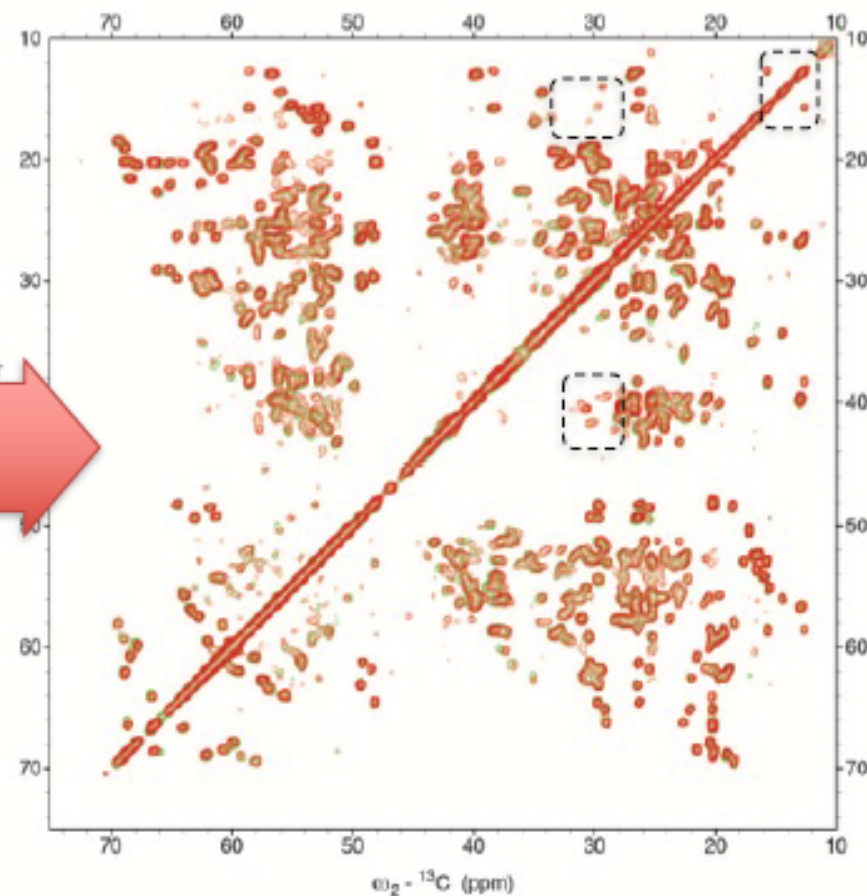
MAS 18 kHz

^{13}C - ^{13}C dipolar-based transfer efficiency

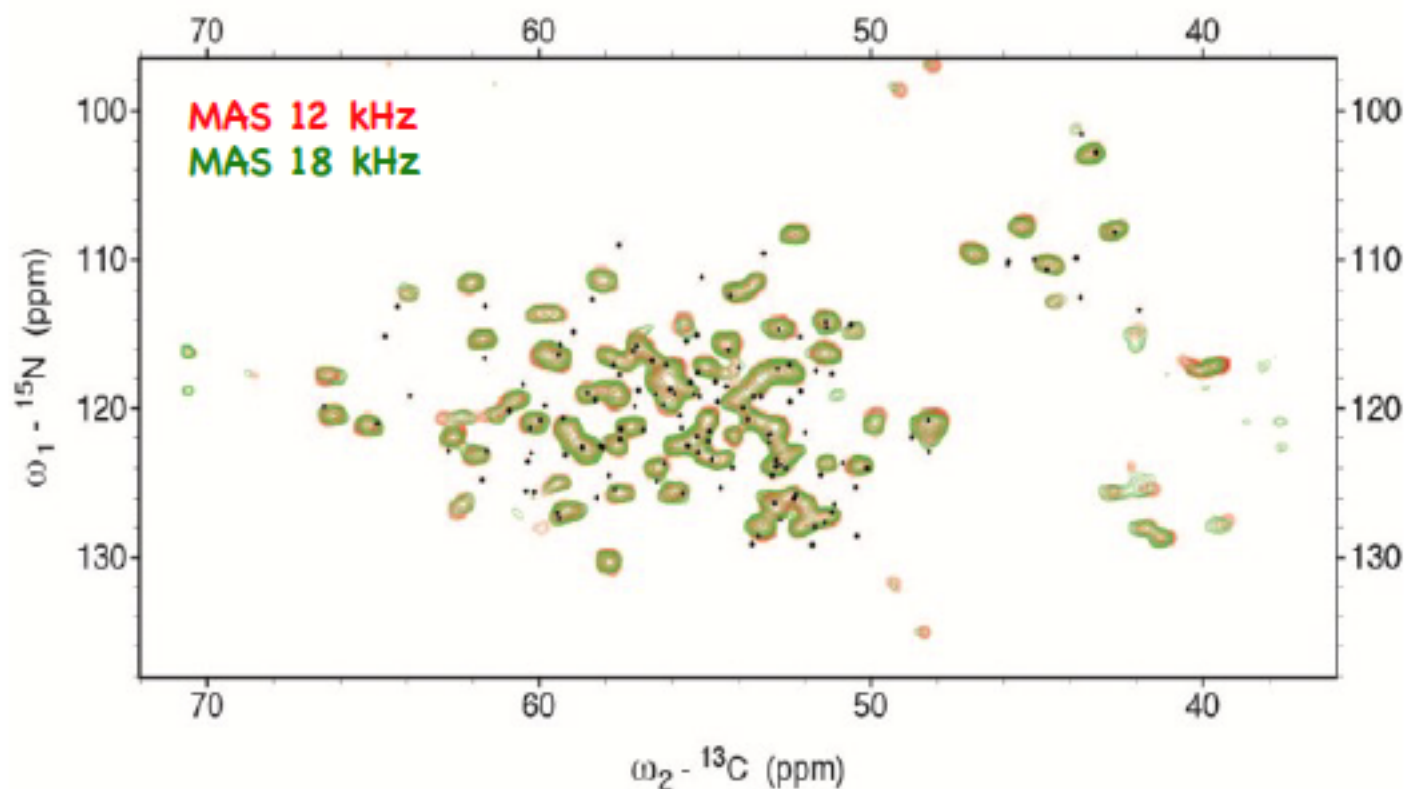
2D PDSD (mix=50 ms)



2D DARR (mix=50 ms)

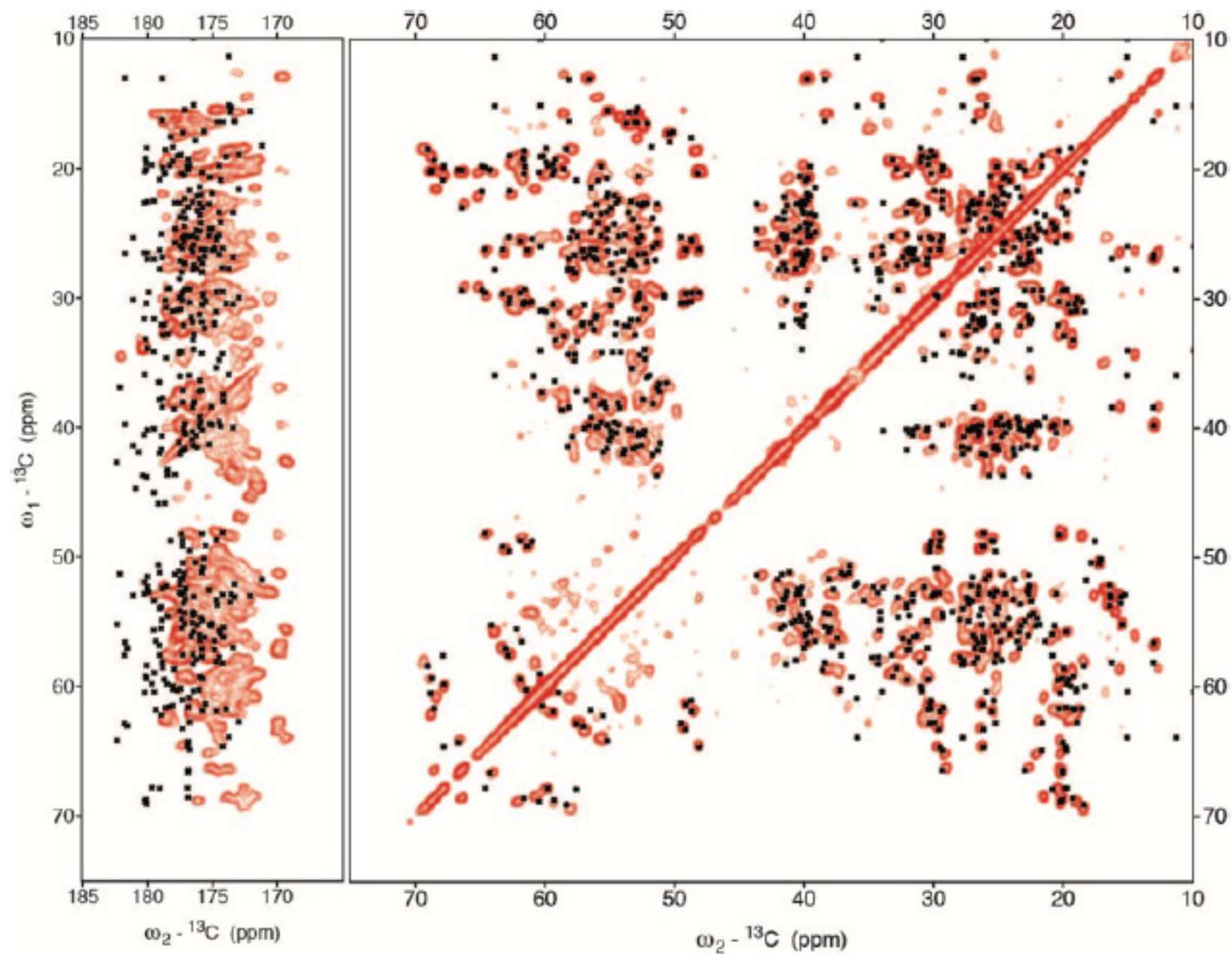


Is higher MAS frequency really beneficial ?



	^{13}C linewidth	^{15}N linewidth
MAS 12 kHz	100 Hz (≈ 0.6 ppm)	80 Hz (≈ 1.1 ppm)
MAS 18 kHz	100 Hz (≈ 0.6 ppm)	70 Hz (≈ 1.0 ppm)

Comparison with solution NMR data



Comparison with solution NMR data

