

The full assignment of protein spectra can last days up to weeks. Normally 3D and 4D spectra are used. In this practical course the principle procedure should be practiced by the assignment of a stretch of an SH3 domain. The sequence to assign consists of 9 amino acids. The aim of the exercise is to analyze which part of the SH3 sequence it is. The spectra that are used are a ^{15}N -HSQC and 2D projections of 3Ds of this part of SH3, they have no ^{15}N axis and are thus ^1H - ^{13}C correlations.

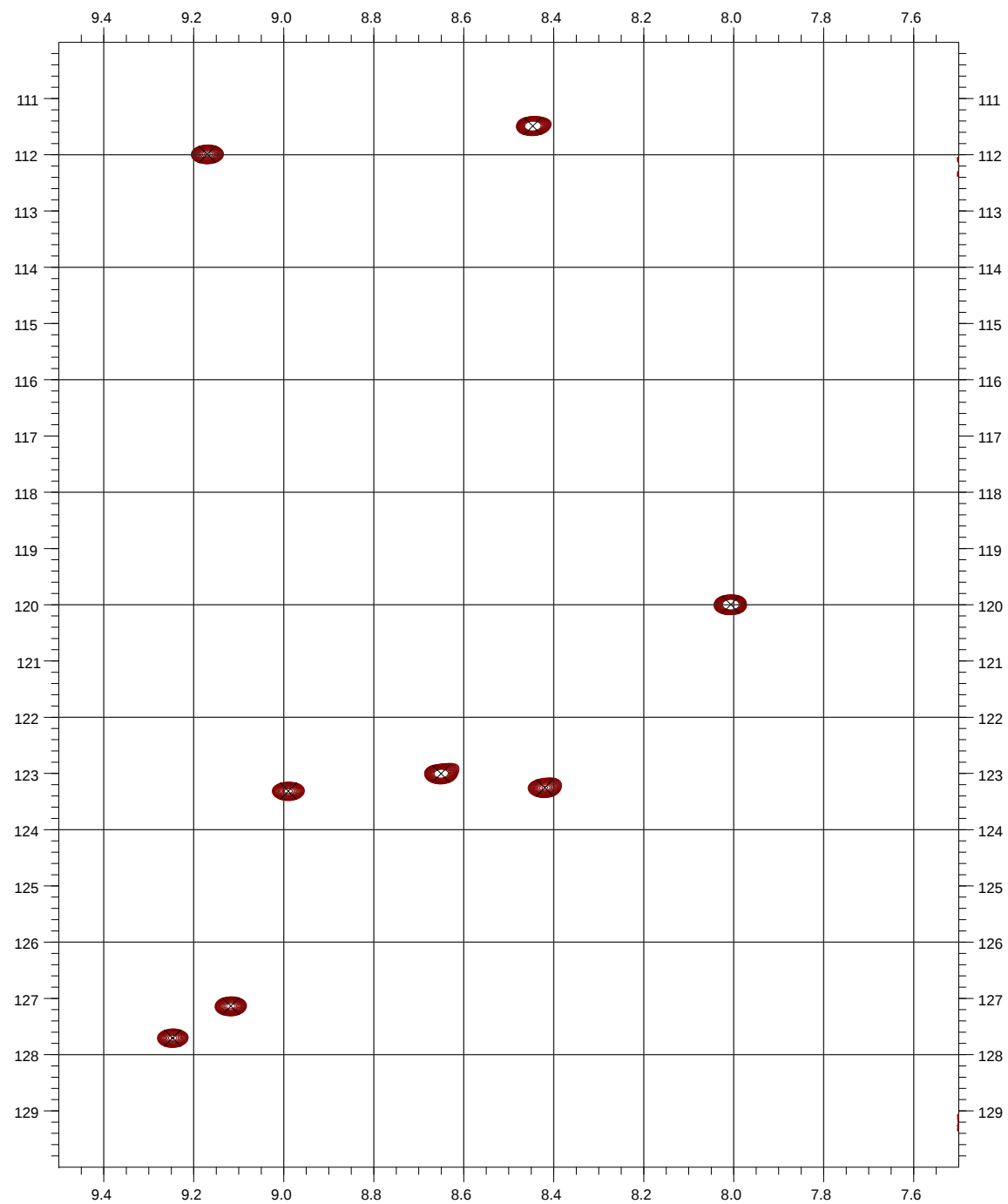
Spectra:

- Procedure:

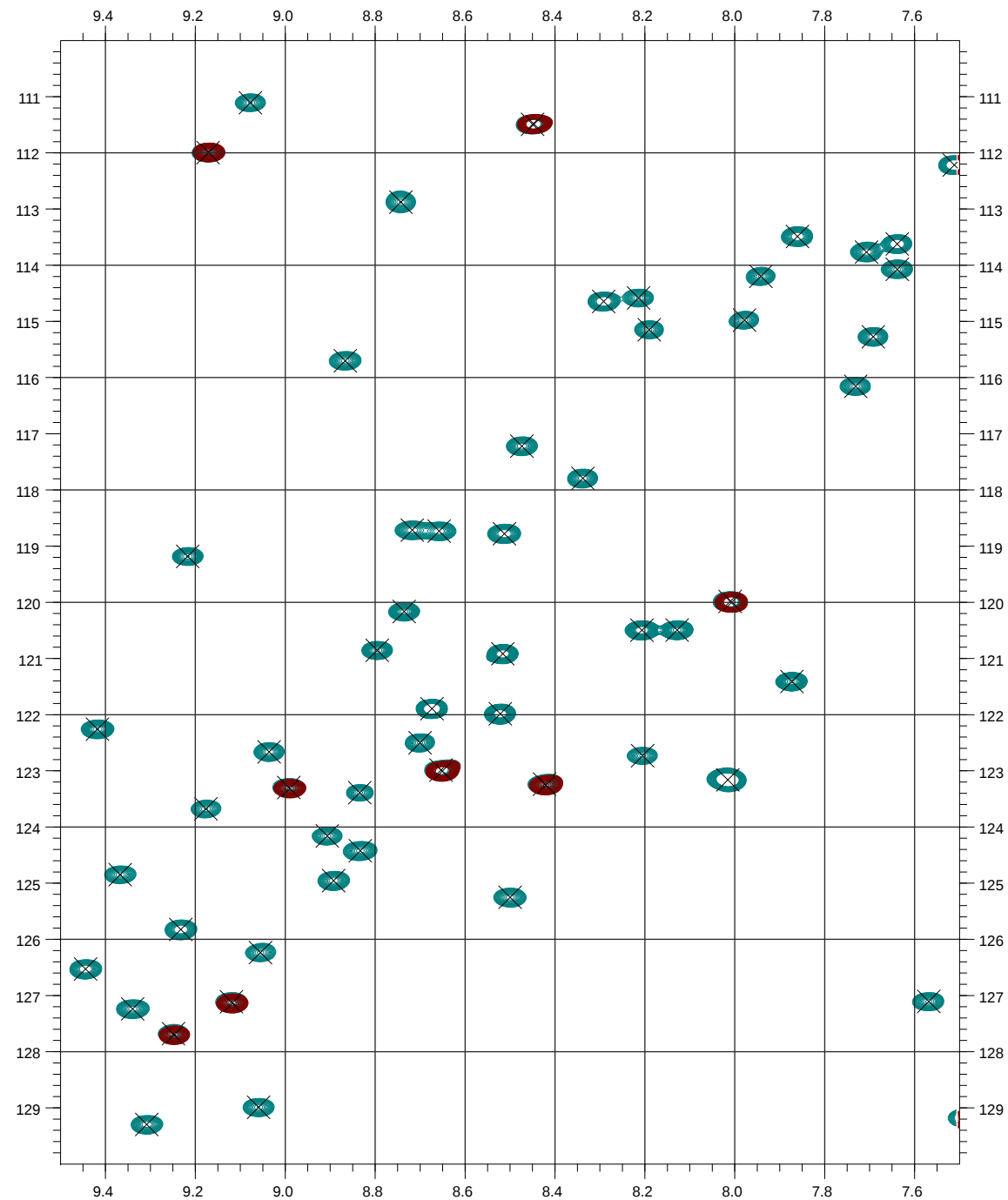
1. group spectra in strips of the eight amino acids
2. arrange strips in sequential order due to their correlation peaks to the previous amino acid
3. derive the amino acid type of the eight amino acids from their $C\alpha$ and $C\beta$ chemical shifts
4. match the amino acids to the sequence
5. fill the shift table and transfer the assignment to the ^{15}N -HSQC

[illegible]

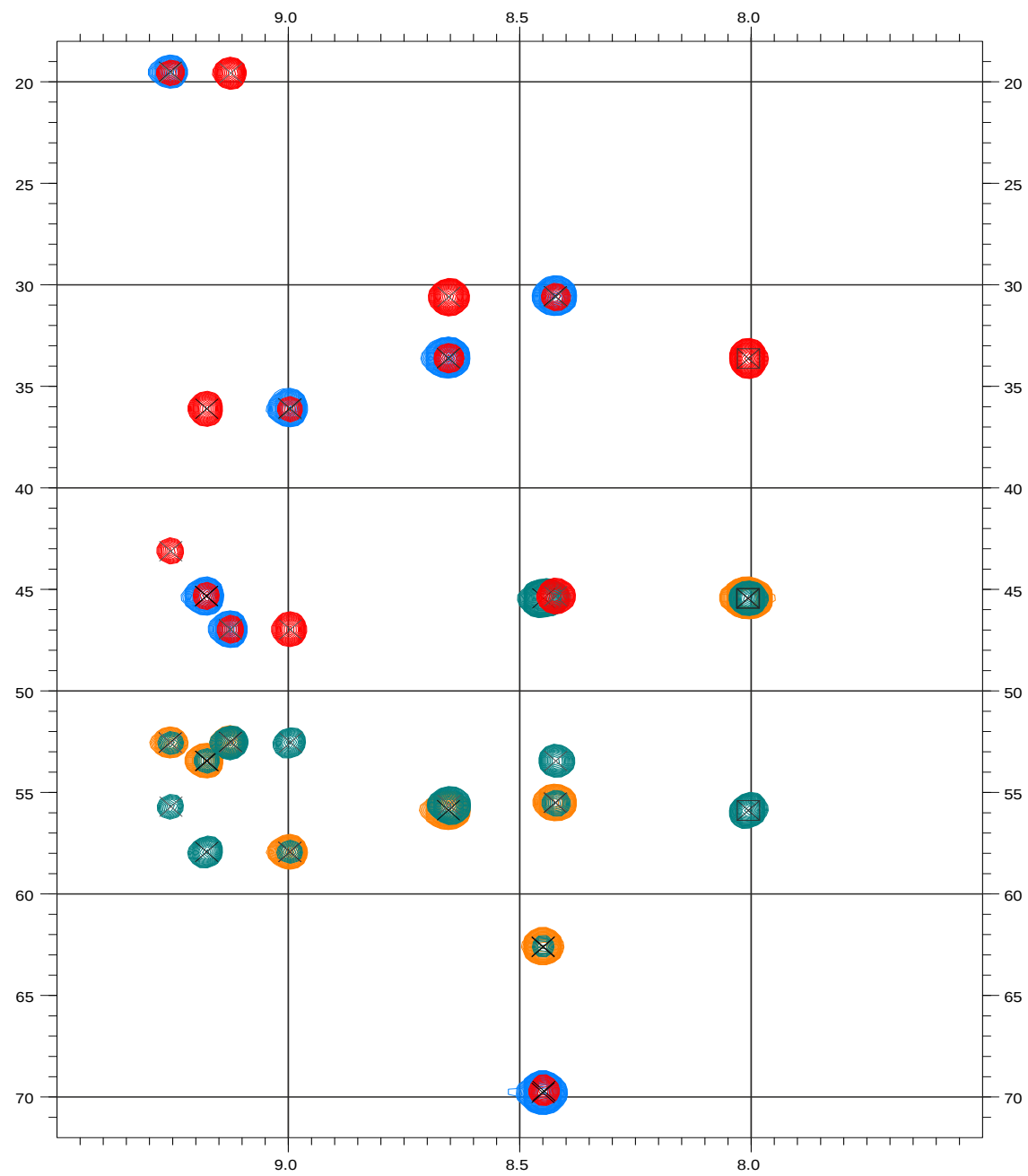
HSQC



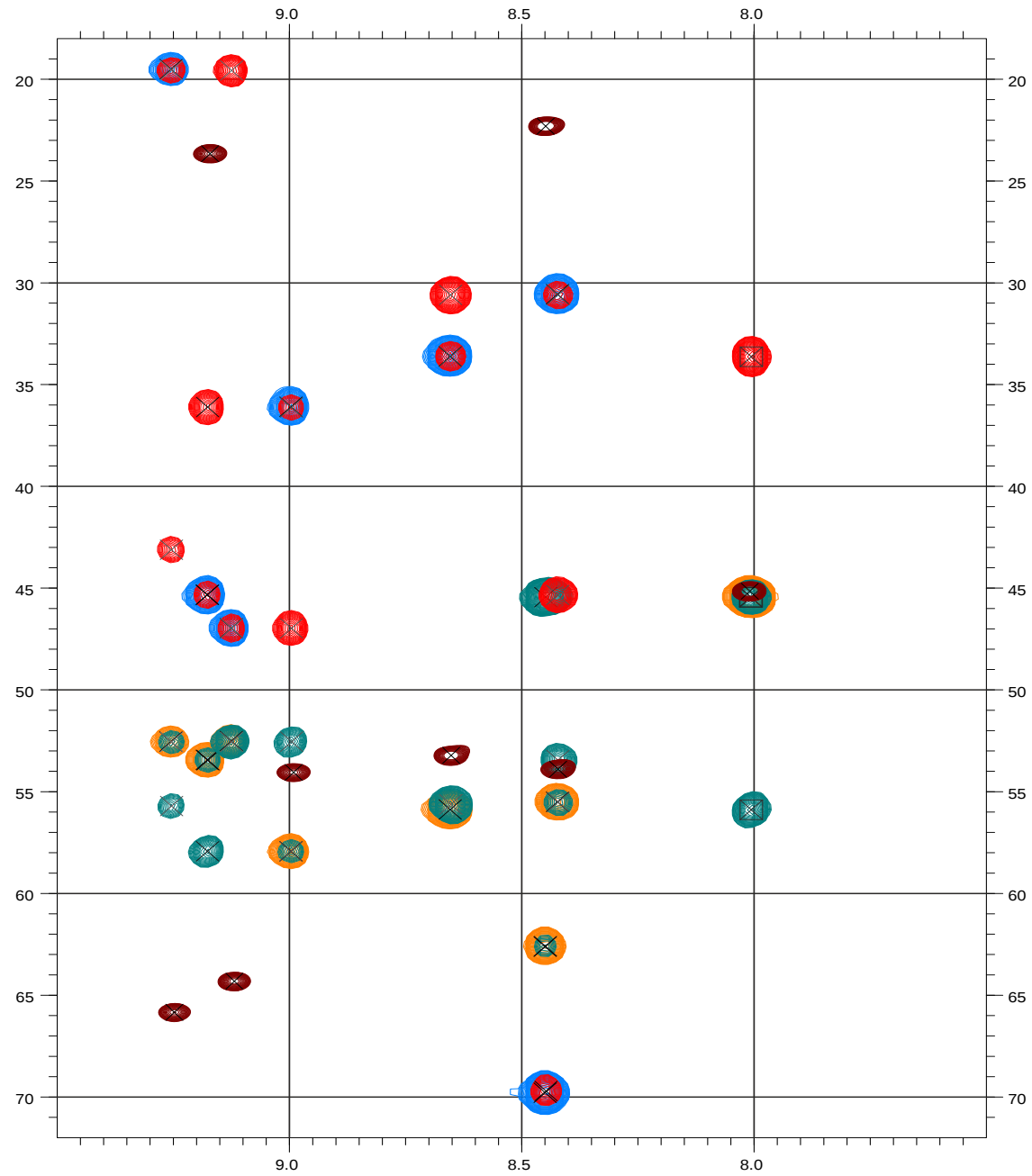
HSQC



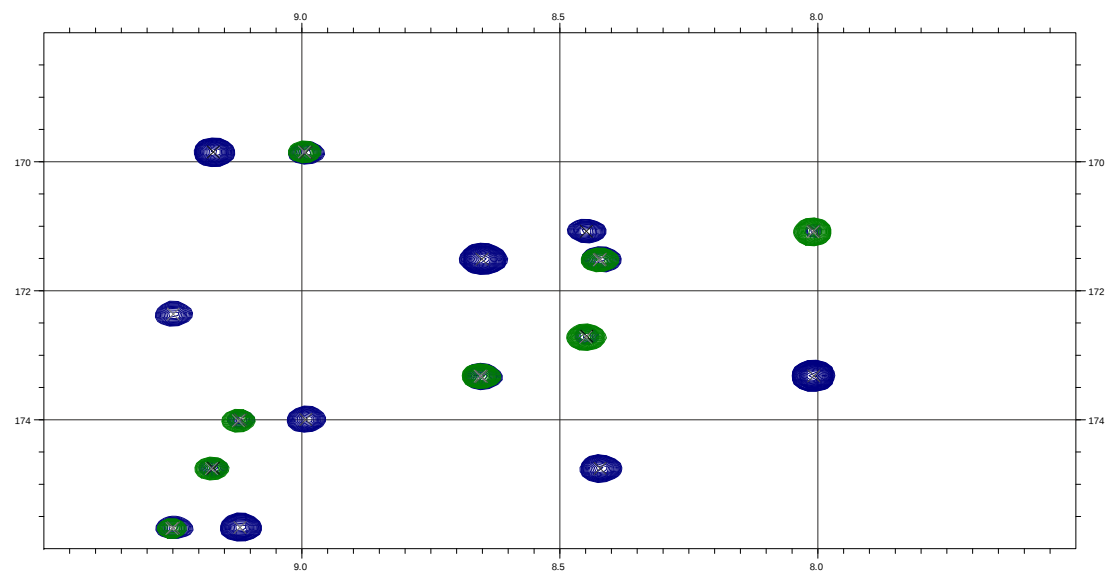
HNCACB/HNCOACB



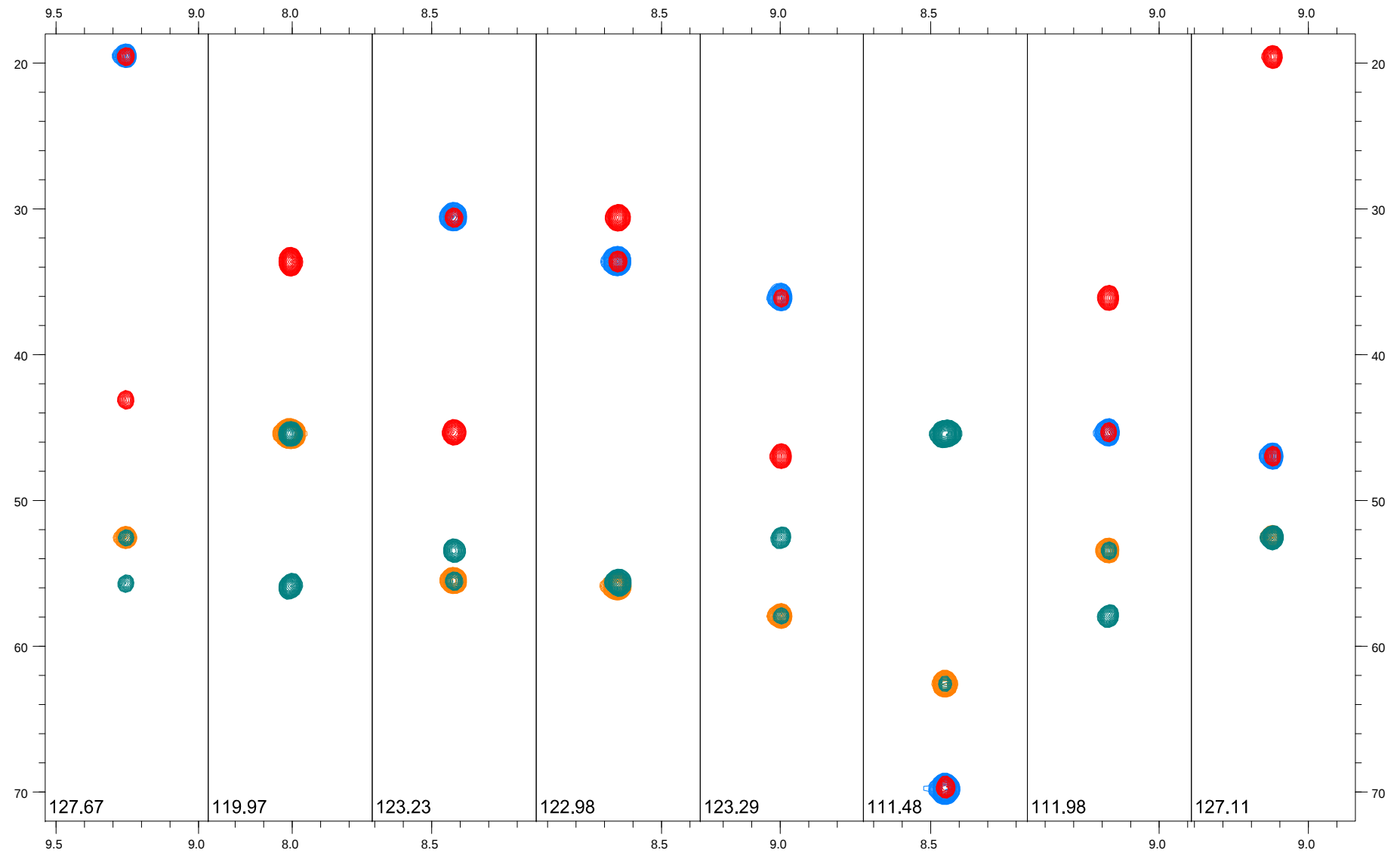
HNCACB/HNCOACB



HNCACO/HNCO



HNCACB/HNCOCACB



HNCACO/HNCO

