

Publication**Automated resonance assignment of proteins: 6D APSY-NMR****JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)****ID** 755130**Author(s)** Fiorito, Francesco; Hiller, Sebastian; Wider, Gerhard; Wüthrich, Kurt**Author(s) at UniBasel** [Hiller, Sebastian](#) ;**Year** 2006**Title** Automated resonance assignment of proteins: 6D APSY-NMR**Journal** Journal of biomolecular NMR**Volume** 35**Number** 1**Pages / Article-Number** 27-37

The 6-dimensional (6D) APSY-seq-HNCOCANH NMR experiment correlates two sequentially neighboring amide moieties in proteins via the C' and Calpha nuclei, with efficient suppression of the back transfer from Calpha to the originating amide moiety. The automatic analysis of two-dimensional (2D) projections of this 6D experiment with the use of GAPRO (Hiller et al., 2005) provides a high-precision 6D peak list, which permits automated sequential assignments of proteins with the assignment software GARANT (Bartels et al., 1997). The procedure was applied to two proteins, the 63-residue 434-repressor(1-63) and the 115-residue TM1290. For both proteins, complete sequential assignments for all NMR-observable backbone resonances were obtained, and the polypeptide segments thus identified could be unambiguously located in the amino acid sequence. These results demonstrate that APSY-NMR spectroscopy in combination with a suitable assignment algorithm can provide fully automated sequence-specific backbone assignments of small proteins.

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