

Applications of the residue-selective SAIL approach for structural studies of proteins

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The salient features of the SAIL–NMR approach are ascribed to the design of various stereo- and region-specifically [2H, 13C, 15N]-triple labeled amino acids (SAIL amino acids), which are optimized to afford necessary structural information for the targeted proteins¹. We have proven that proteins exclusively composed of SAIL amino acids are extremely useful for determining the solution structures of relatively large proteins^{2,3}. By virtue of the dramatically improved spectral qualities of SAIL proteins, most of the time-consuming spectral analysis and structural calculation steps can be fully automated for relatively small proteins. SAIL amino acid residues are also useful to refine local structures and to characterize their conformational dynamics in detail. For such purposes, the isotope-labeling patterns of standard SAIL amino acids can be further improved. We have recently developed various new types of SAIL aromatic amino acids, aiming to study the large-amplitude, slow breathing motions involving the hydrophobic cores of proteins. Applications of various types of SAIL amino acids will generate new possibilities to obtain information to fill the gap between the structure and the biological function of a protein, which could only be addressed by solution NMR spectroscopy

