Optimal Isotope Labeling_for Protein Structure Determination by NMR: The SAIL method

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The SAIL (*S*tereo-*A*rray *I*sotope *L*abeling) technology for protein NMR spectroscopy exclusively utilizes chemically or enzymatically synthesized amino acids, designed to have an optimal stereo- and regiospecific pattern of stable isotopes, from which proteins are obtained by cell-free synthesis. As demonstrated for the calcium-bound form of *Xenopus laevis* calmodulin (CaM, 17kDa) and the cyclodextrin bound maltose binding protein (MBP, 41kDa), SAIL offers sharpened lines, spectral simplification without loss of information, and the ability to rapidly collect the structural restraints required to solve a high-quality solution structure. SAIL is expected to largely eliminate the key limiting factors for detailed solution structure determinations of larger proteins.