results suggested that different protein acids in folded proteins resulted in the that NMR could actually be used to determine conditions, for example) could be of native proteins would, later on, the equivalent free amino acids. The spectral peaks in these spectra, but this point remained in question until later in the decade. McDonald and Phillips conducted experiments in 1967 with ribonuclease, lysozyme, and cytochrome c, and their results suggested that different protein conformations (under different denaturing conditions, for example) could be identified by NMR spectroscopy. In the case of ribonuclease, improved resolution of the NMR spectrum was achieved by thermal denaturation, suggesting that the broad peaks in the native protein spectrum did result from interactions between residues in the folded state. Other experiments, performed by Cohen and Jardetzky with lysozyme in 1969, supported the idea that the conformations of proteins can be distinguished by NMR spectroscopy. They identified several different conformations of lysozyme, including native, denatured, and reduced denatured states. In 1969, McDonald and Phillips compiled an extensive set of data showing that experimental spectra of many denatured proteins were closely matched by spectra that were computed by summing the spectra of the equivalent free amino acids. The spectra of native proteins would, later on, require much greater deconvolution, and experiments such as these on denatured proteins set the stage for attempts to resolve these more complex overlapping spectra. Moreover, this work laid the early foundation for investigating protein folding by NMR spectroscopy. Tracy Smith