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**Joint X-ray and NMR Refinement of the L30e-mRNA Complex.** James R. Williamson, Jeffrey A. Chao, Molecular Biology, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037 USA.

L30e is a yeast ribosomal protein that autoregulates its own expression by binding to its own mRNA. We previously solved the structure of the L30e-mRNA complex using NMR, and recently obtained diffracting crystals of the same complex. We were able to solve the structure of the complex at 3.2 Å, but the position of several RNA bases was different in the NMR and X-ray structure. We were able to resolve this discrepancy by identifying a single mis-assigned imino proton in the NMR spectra, resulting in a local distortion of the RNA structure. The X-ray data and the remaining large number of NOE constraints could be included in a joint X-ray and NMR refinement of this complex. The NOE data allowed additional residues on the RNA and the protein to be modeled, resulted in improved local geometry of the RNA, and led to a modest improvement in the structural statistics. Such a joint refinement may have applicability to other systems where there is low NOE density and poor electron density. NOEs contribute to the empirical energy function during refinement in cartesian space, while the structure factors contribute in reciprocal space. Thus, these two types of data can provide complementary structural information that is more powerful than either alone in cases where diffraction resolution and NMR restraint density are limiting.