

Editorial

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We note with pleasure the appearance in this month's issue of a paper, which we have also highlighted as the cover illustration: *Solution structure of Arabidopsis thaliana protein At5g39720.1, a member of the AIG2-like protein family* by B. L. Lytle, F. C. Peterson, E. M. Tyler, C. L. Newman, D. A. Vinarov, J. L. Markley & B. F. Volkman [(2006), *Acta Cryst.* **F62**, 490–493]. Our publication of this paper is a significant step toward fulfillment of one of our original goals: to ease and speed the publication of structure communications generated by the structural genomics effort. It is also a first for *Acta Crystallographica* in that it reports a solution structure solely determined by NMR methods. We expect that it will be the first of many to follow.

The *Acta Crystallographica* family of journals has always prized its adherence to the highest standards of technical excellence and its requirement of full disclosure of data and coordinates. For publication of NMR structures, we have initially adopted the standards that were generated under the auspices of IUPAC some years ago and published widely [J. L. Markley, A. Bax, Y. Arata, C. W. Hilbers, R. Kaptein, B. D. Sykes, P. E. Wright & K. Wüthrich (1998), *Recommendations for the presentation of NMR structures of proteins and nucleic acids*, *J. Mol. Biol.* **280**, 933–952]. As with X-ray crystallography, these standards must evolve over time to reflect improvements in technology and practice. We rely on our editors, readers and authors to help us maintain the highest standards for NMR publications. We look forward to a lively exchange of suggestions and recommendations from our NMR colleagues.