

Letters to the Editor

^{1}H, ^{15}N and ^{13}C resonance assignments of the putative Bet v 1 family protein At1g24000.1 from *Arabidopsis thaliana*

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On the basis of 23% sequence identity, At1g24000.1 was identified as member of the Bet v 1 family, which includes the major birch pollen allergen and is the main cause of type I allergies observed in early spring (Breiteneder and Ebner 2000). To gain insight into the structural features of At1g24000.1, we initiated an NMR investigation of the recombinant protein. A structure also was solved by X-ray crystallography (PDB 1VJH). Assignments were based on 2D and 3D heteronuclear NMR experiments recorded on ^{13}C,^{15}N-labeled At1g24000.1. Assignment completeness was $\sim$ 94% overall: 90% for $^{13}C'$, 94% for $^{13}C^{\alpha}$ and 95% for $^{1}H^{\alpha}$ atoms. The amides of Ser1, Thr2, Thr28, Lys34, Thr38, His100 and Ser101 were unassigned. About 90% of the total side-chain resonances were assigned. Side chains remaining unassigned were those of Ser1, Asp27, Glu33, Pro99, and His100. In addition, assignments were not determined for the ^{13}C resonances of the aromatic rings or the labile protons of Lys and Arg residues. Supported by the NIH Protein Structure Initiative (GM P50 GM64598). NMR data were collected at the National Magnetic Resonance Facility at Madison. BMRB deposit with accession number 6585.

References: Breiteneder, H., and Ebner, C. (2000) *J. Allergy Clin. Immunol.*, **106**, 27–36

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NMR assignment reveals an α-helical fold for the F-actin binding domain of human Bcr-Abl/c-Abl

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N-terminal fusion of cellular Abelson tyrosine kinase (c-Abl) with sequences from the breakpoint-cluster region (BCR) protein gives rise to a constitutively active kinase, Bcr-Abl, that causes most cases of chronic myelogenous leukemia. While nuclear Abl participates in the regulation of gene expression and apoptosis, cytoplasmic Abl functions in cell adhesion and cytoskeletal dynamics. F-actin interaction is mediated by a 120-residue domain at the very C-terminus of Bcr-Abl/c-Abl that also harbors the only reported nuclear export signal (Taagepera et al., 1998). As a first step towards understanding the structural basis of nuclear export and F-actin binding, we report the nearly complete sequence-specific ^{1}H, ^{15}N, and ^{13}C resonance assignments of the $\sim$120 C-terminal residues of human Bcr-Abl/c-Abl. Analysis of triple resonance spectra resulted in complete assignment of backbone NH resonances, while side-chain resonance assignments are over 95% complete. $^{13}C^{\alpha}$ and $^{13}C^{\beta}$ secondary chemical shifts indicate an α-helical fold for the Bcr-Abl/c-Abl FABD. BMRB deposit has the accession number 6570.

References: Taagepera et al. (1998) *Proc. Natl. Acad. Sci., USA.*, **95**, 7457–7462

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