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Letters to the Editor

^{1}H, ^{13}C and ^{15}N resonance assignments of a Bcl-x_L/Bad peptide complex

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The Bcl-2 family of proteins has been shown to be an important modulator of mitochondrial membrane integrity and is thus a key regulator of the apoptotic process. Peptides derived from the BH3 domains of pro-apoptotic Bcl-2 family members can bind to anti-apoptotic family members such as Bcl-x_L and modulate Bcl-2 regulated apoptotic pathways in living cells. The structures of Bcl-x_L/peptide complexes (Sattler et al., 1997; Petros et al., 2000) have led to a better understanding of apoptosis on the molecular level. These data are currently being used to aid in the discovery of small molecule inhibitors. Three-dimensional heteronuclear NMR experiments using uniformly ^{15}N-labeled, ^{15}N,^{13}C-labeled, or uniformly ^{15}N,^{13}C-labeled, 75% ^{2}H samples were used to obtain ^{1}H, ^{13}C, and ^{15}N assignments of Bcl-x_L complexed to a 25 residue BH3 Bad peptide. Assignments for ~95% of the backbone and sidechain resonances of Bcl-x_L were obtained and have been deposited in the BioMagResBank (accession number: 6578).

References: Petros et al. (2000) *Protein Sci.*, **9**, 2528–2534; Sattler et al. (1997) *Science*, **275**, 983–986.

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NMR assignment of the holo-ACP from malaria parasite *Plasmodium falciparum*

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Acyl carrier proteins play a key role in fatty acid biosynthesis. The acyl carrier protein of *Plasmodium falciparum* (*Pf*ACP) is a potential target for design of antimalarials. Our aim is to determine the solution structure of *Pf*ACP and to study its interaction with other proteins in this pathway. *Pf*ACP exhibits a 51.9, 48.8 and 22.6% sequence identity to *E. coli*, *B. subtilis* and *M. tuberculosis* ACP's, respectively. $^{13}C/^{15}N$ and ^{15}N-labeled proteins were prepared using modifications that enabled the purification of isotopically enriched holo-*Pf*ACP, i.e., the biosynthetically derived 4′-phosphopantetheine group (4′-PP) was also isotopically enriched. Here we report the backbone and side-chain assignments for ^{1}H, ^{13}C and ^{15}N nuclei (except C′) of the polypeptide and 4′-PP that were obtained using 2D and 3D heteronuclear NMR experiments (Sattler et al., 1999). CSI and NOE data has shown that the protein is predominantly α-helical in secondary structure. Chemical shift and *J*-coupling data have been deposited (BMRB # 6516).

Reference: Sattler et al. (1999) *Prog. NMR Spectrosc.*, **34**, 93–158.

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