 

# Letters to the Editor

## NMR assignment of the apo and peptide-bound SH2 domain from the Rous sarcoma viral protein Src

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Src homology 2 (SH2) domains are important mediators of protein–protein interactions in eukaryotic protein tyrosine kinase (PTK) signaling. SH2 domains recognise ligands containing phosphotyrosine (pY), and the 106-residue Src domain has been shown to preferentially bind the sequence pYEEI (Songyang et al., 1993). Src plays a key role in many cellular signalling pathways, and is a validated target for anti-cancer and anti-osteoporotic agents (Machida and Mayer, 2005). Src is also the prototypical non-receptor PTK and continues to be the focus of academic biophysical study. We have used 2D/3D heteronuclear experiments with $^{15}$N and $^{13}$C labelled *v*-Src SH2 to obtain essentially complete (>99%) backbone and sidechain resonance assignments for the domain in both its apo state and bound to a PQpYEEIPI peptide. BMRB depositions have accession numbers 6503 (apo) and 6604 (peptide-bound).

References: Machida and Mayer, (2005) *Biochim. Biophys. Acta*, **1747**, 1–25; Songyang et al. (1993) *Cell*, **72**, 767–778.

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## $^{1}$H, $^{15}$N, and $^{13}$C chemical shift assignments of the human Sulfiredoxin (hSrx)

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Based on 25% sequence identity, human sulfiredoxin (hSrx) was identified as the yeast (*Saccharomyces cerevisiae*) homologue of the mammalian sulfiredoxin (Srx), which is a protein responsible for the reduction of cysteine-sulfinic acid to cysteine utilizing ATP in eukaryotes (Biteau et al., 2003). To understand the reduction mechanism of Srx, we initiated a NMR structure determination of the recombinant polypeptide hSrx-ΔN16 (17–137), which is the truncated form of full length hSrx. Removing the N terminal 16 residues by thrombin prevented precipitation and yields sharp signals in the 1D spectrum. For the assignments we used 2D and 3D heteronuclear NMR experiments with $^{13}$C,$^{15}$N-labeled hSrx-ΔN16 (17–137). The assignments for a 121 amino acid, well-structured polypeptide with 100% of backbone and 98% of side chain resonances are reported, excluding carbonyls for which no experiments were performed. Deposited with BMRB, accession number 6590.

References: Biteau et al. (2003) *Nature*, **425**, 980–984; Chang et al. (2004) *J. Biol. Chem.*, **279**, 50994–51001.

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