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Letter to the Editor

^{1}H, ^{13}C and ^{15}N resonance assignments of the C-terminal domain of RP2

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The RP2 protein was identified from its link to the disease known as Retinitis Pigmentosa (RP) (Schwahn et al., 1998), which is a hereditary disease characterized by progressive degeneration of the retina that leads to blindness. The disorder is genetically heterogeneous and mutations in the RP2 gene occur in 15–20% of the RP patients. The function of the RP2 protein is currently unknown. The C-terminal domain (residues 230–350) of RP2, where many RP related mutations occur (Miano et al., 2001), has sequence similarity to nucleoside diphosphate kinase (NDK). However, RP2 does not have NDK activity since the conserved catalytic histidine residue in NDKs is replaced by a phenylalanine in RP2, and part of the substrate-binding segments for the NDK activity is deleted in the sequence of RP2. In order to help elucidate its function, we have carried out solution NMR studies to investigate the three-dimensional structure of the C-terminal domain of RP2. As the first step in a structural study using NMR methods, we report the complete chemical shift assignments of the C-terminal domain of RP2. All backbone resonances and more than 98% side chain resonances are assigned. The assignments have been deposited in the BioMagResBank (http://www.bmrb.wisc.edu) under Accession Number 6744.

References: Miano et al. (2001) *Hum. Mutat.*, **18**, 109–119; Schwahn et al. (1998) *Nat. Genet.*, **19**, 327–332

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