

## Resonance assignment of the RGS domain of human RGS10

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RGS10 is a member of the D/R12 subfamily of Regulators of G-protein Signalling (RGS) proteins and acts as a GTPase-activating protein (GAP) via modulation of  $G_{\alpha i}$  and  $G_{\alpha z}$  signalling but does not interact with the structurally distinct  $G_{\alpha s}$  subunit (Hunt et al. 1996). Unlike other subfamilies of RGS proteins, RGS10 lacks the N-terminal amphipathic helix that localizes these proteins to the membrane. Instead, membrane localization is regulated by palmitoylation of a conserved cysteine within the GTPase-activating RGS domain (Tu et al. 1999).  $^1\text{H}$ ,  $^{15}\text{N}$  and  $^{13}\text{C}$  resonance assignments of a construct containing the RGS domain from human RGS10 were obtained from 2D and 3D heteronuclear NMR spectra. The

backbone assignment was completed with the exception of the first and last two residues and a highly overlapped stretch of five Glu residues (132–136 of our construct). Sidechain assignment was 89% complete including 92% of observable aromatics. The assignments were deposited with accession code BMRB-7272.

### References

- Hunt TW et al (1996) Nature 383:175–177  
Tu YP et al (1999) J Biol Chem 274:38260–38267

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**Electronic Supplementary Material** Supplementary material is available in the online version of this article at <http://dx.doi.org/10.1007/s10858-006-9111-0> and is accessible for authorized users.

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