

Letter to the Editor

Backbone NMR assignment of the 29.6 kDa Rhodanese protein from *Azotobacter vinelandii*

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Rhodanese domains are widely present in all phyla displaying sulfurtransferase activities *in vitro*. The observed abundance of potentially functional rhodanese-like proteins suggests that they may play distinct biological roles. Rhodanese from *Azotobacter vinelandii* (RhdA) (Pagani et al., 1991) is a protein of 29.6 kDa displaying sulfurtransferase activity *in vitro*, transferring the sulfane sulfur atom from thiosulfate to cyanide, producing thiocyanate by a double displacement mechanism. During the transfer of the sulfane sulfur this enzyme cycles between two stable intermediates, a sulfur-loaded (ES) and a sulfur free form (E). The crystal structure of the ES form was solved (Bordo et al., 2000). To gain further insights into RhdA function and physiologically important interactions, 3D heteronuclear NMR experiments with uniformly ^2H , ^{13}C , ^{15}N -labelled sulfur-loaded RhdA were recorded to assign the backbone and C_β atoms. Chemical shift assignments were accomplished for 94% of the backbone amides, 96% of $^{13}\text{C}_\alpha$, 85% of $^{13}\text{C}_\beta$, and 96% of ^{13}CO . Amide groups of M1, L9-V10, R45-V47, L69, R79, V86, W100-V104, L113, and Q231 remained unassigned. BMRB accession Nr.7130.

References: Pagani et al. (1991) *FEBS Lett.*, **278**, 151–154; Bordo et al. (2000) *J. Mol. Biol.* **298**, 691–704.

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