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# Letter to the Editor

## $^{1}H$, $^{13}C$ and $^{15}N$ resonance assignment of an oxidized form ($Cys_{51}$–$Cys_{198}$) of Methionine Sulfoxide Reductase A from *Escherichia coli*

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Methionine Sulfoxide Reductase A (MsrA) is involved in the reduction of methionine-(*S*)-sulfoxides generated during an oxidative stress. The catalytic mechanism of *E. coli* MsrA involves the formation of two successive disulfide bonds ($Cys_{51}$–$Cys_{198}$ and $Cys_{198}$–$Cys_{206}$), both are reducible by thioredoxin. We report the nearly complete $^{1}H$, $^{13}C$ and $^{15}N$ resonance assignments of the oxidized form ($Cys_{51}$–$Cys_{198}$). 2D and 3D NMR experiments were performed with uniformly $^{15}N$-, $^{13}C$-labeled protein. 88% of backbone $H^{N}$, N, $C^{\alpha}$, C′ and the large majority of side chain nuclei have been assigned. Almost of the unassigned residues are located in the 122–132 segment, which may be poorly structured, undergoing a conformational exchange, as revealed by linewidth increase for residues up- and down-stream of this segment (certainly due to exchange contribution to transverse relaxation). BMRB deposits with accession number 6786.
Reference: Boschi-Muller et al. (2005) *Biochim. Biophys. Acta*, **1703**, 231–238.

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