

## Letter to the Editor

### <sup>1</sup>H, <sup>13</sup>C and <sup>15</sup>N resonance assignment of the N-terminal domain of PilB from *Neisseria meningitidis*

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*Neisseria meningitidis* bacteria possess several antioxidant defence mechanisms that protect them against their host environment among which the PilB protein is postulated to be involved. PilB is composed of three domains including the N-terminal part that was recently shown to reduce the oxidized forms of methionine sulfoxide reductase and belongs to the thioredoxin-fold family (Wu et al., 2005). We report the nearly complete <sup>1</sup>H, <sup>13</sup>C and <sup>15</sup>N resonance assignments of the N-terminal domain of PilB from *N. meningitidis* (143 amino acids). 2D and 3D NMR experiments were performed with uniformly <sup>15</sup>N-, <sup>13</sup>C-labelled protein. More than 95% of backbone H<sup>N</sup>, N, C<sup>α</sup>, C' and side chain C<sup>β</sup> nuclei have been assigned. Secondary structure determination using CSI method and TALOS lead to the prediction of 5α-helical and 5β-sheet segments. BMRB deposit with accession number 6709.

Reference: Wu et al. (2005) *J. Biol. Chem.*, **280**, 12344–12350.

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