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SANS with contrast variation study of the cooperative assembly of the methionine repressor MetJ-DNA complex

William T. Heller¹, Anne Marie Augustus², Patrick N. Reardon², Leonard D. Spicer²

¹ *Oak Ridge National Laboratory, Oak Ridge, TN 37831*

² *Duke University, Durham, NC 27710*

The methionine repressor MetJ from *E. coli* is responsible for the regulation of several genes involved in the synthesis of methionine. In solution, MetJ exists as a 24 kDa homodimer whose structure was solved by crystallography (Rafferty, J. B., Somers, W. S., Saint-Girons, I. and Phillips, S. E. V. (1989) *Nature* 341: 705-710). Upon activation by its co-repressor S-adenosylmethionine (SAM), MetJ dimers bind to DNA recognition sites (dAGACGTCT), called metbox DNA sites, thereby modulating transcription. There are between two and five contiguous metbox DNA sites in the DNA regulatory sequence to which MetJ binds cooperatively. The structure of a MetJ tetramer on DNA containing two recognition sites was determined by crystallography (Somers, W. S. and Phillips, S. E. V. (1992), *Nature* 359: 387-393), but the higher-order assemblies have proven resistant to crystallization and are generally too large for high-resolution structure determination by NMR. To extend our understanding of the structural basis for this important regulatory mechanism, SANS with contrast variation was used to investigate the solution structure of the previously intractable higher-order MetJ-DNA complexes in the presence of SAM. We report here the results of studies on the three metbox DNA-MetJ complex and on the five metbox DNA-MetJ complex that will prove valuable for understanding the sequential assembly mechanism of this essential repressor complex on the *met* regulon.

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invited

William T. Heller
Chemical Sciences Division and
Center for Structural Molecular Biology
Oak Ridge National Laboratory
Oak Ridge, TN 37831

Email: hellerwt@ornl.gov
Tel: 865-241-5694
Fax: 865-574-6268