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The Crystal Structure of the Trp Repressor Binding Protein TwqN from *B. subtilis*. Y. Kim, P. Quartey and A. Joachimiak, Midwest Center for Structural Genomics and Structural Biology Center, Biosciences, Argonne National Laboratory, 9700 South Cass Ave., Bldg 202, Argonne, IL 60439, USA.

The Trp repressor binding protein TwqN from *B. subtilis* belongs to the family of flavodoxin-like proteins, also known as the NADPH-dependent FMN reductases, as indicated by sequence analysis. However, its biological function remains to be determined. Since SeMet derivative crystals couldn't be obtained, the heavy atom derivative crystals were prepared by soaking the native crystals in relatively high concentration of PtCl₄ for less than half an hour. The structure was determined to 1.7 Å by SAD phasing and utilizing Pt anomalous scattering. The TwqN is an α/β fold, a five stranded parallel β -sheet is flanked by three α -helices in one side and four in the other, strikingly similar to previously determined flavoproteins such as Ylr011wp, *S. cerevisiae* NADPH-dependent FMN reductase (1TOI), and a monomeric flavoprotein azobenzene reductase from *B. subtilis* (1NNI). The crystal structure of TwqN assembles into a tetramer unique among flavodoxin-like proteins. In the crystal structure none of four protomers binds FMN. Structural analysis is reported.

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