

Molecular determinants for FMN-binding in *Desulfovibrio gigas* flavoredoxin



Author(s): [Broco M](#) (Broco, Manuela), [Soares CM](#) (Soares, Claudio M.), [Oliveira S](#) (Oliveira, Solange), [Mayhew SG](#) (Mayhew, Stephen G.), [Rodrigues-Pousada C](#) (Rodrigues-Pousada, Claudina)

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Abstract: Flavoredoxin participates in *Desulfovibrio gigas* thiosulfate reduction pathway. Its 3-dimensional model was generated allowing the oxidized riboflavin-5'-phosphate (FMN) site to be predicted. Residues likely to be involved in FMN-binding were identified (N29, W35, T56, K92, H131 and F164) and mutated to alanine. Fluorescence titration with apoprotein showed that FMN is strongly bound in the wild-type protein. Comparison of K-d values for mutants suggests that interactions with the phosphate group of FMN, contribute more to binding than the interactions with the isoalloxazine ring. The redox potential of bound FMN determined for wild-type and mutants revealed shifts to less negative values. These findings were correlated with the protein structure in order to contribute to a better understanding of the structure-function relationships in flavoredoxin. (c) 2007 Federation of European Biochemical Societies. Published by Elsevier B.V. All rights reserved.