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Structural Studies on *Helicobacter pylori* Apoflavodoxin Contributes to Investigate Conformational Changes in Flavodoxins Induced by FMN Binding. M. Martínez-Júlvez, M. Bueno, N. Cremades, J. Sancho, and J. Hermoso, Dept. de Bioquímica y Biología Molecular y Celular, Facultad de Ciencias y BIFI, Univ. de Zaragoza, España, Grupo de Cristalografía Macromolecular y Biología Estructural, Inst. Química-Física Rocasolano. C.S.I.C - Madrid, España.

In this work, we present the structure of apoflavodoxin from *Helicobacter pylori* solved by X-ray diffraction at 2.1 Å. The active form, holoflavodoxin, contains a non-covalently bound FMN that receives electrons from the pyruvate oxidoreductase complex during the metabolism of the pathogen. The α/β folding of the structure of the apo form shows high similarity to that of holoprotein when both structures are superimposed. Nevertheless, some differences are detected in the FMN binding regions. Some details of this structure in these regions and crystallisation conditions reveal important clues to investigate the mechanism of protein/flavin recognition. Our conclusions are that apoflavodoxins display, regardless of the presence of an aromatic residue in the binding loop, a closed isoalloxazine pocket, together with a native phosphate site that carries whatever available anion is present in solution. The high flexibility of one of the isoalloxazine loops (55-58) might facilitate that FMN binding begins there.