

## High Resolution Structures of Formate Dehydrogenase Mutants from *Candida boidinii*

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Formate dehydrogenase from *Candida Boidinii* (*Cbfdh*) is an intensively studied cofactor regenerating biocatalyst. To improve its thermal stability and minimize the oxidative deactivation occurring under the conditions of the industrial process, modifications were designed based on the available X-ray structure from *Pseudomonas sp.* [1]. Structural information on *Cbfdh* is required for engineering coenzyme specificity changes in order to generate regeneration systems for additional applications [2]. Since *Cbfdh* remained reluctant to crystallisation we applied rational site-directed mutagenesis of surface patches based on the results obtained by Derewenda and coworkers [3] and using the FoldIndex prediction software. Dramatic improvement resulting in crystals diffracting to 1.6 Å resolution could be achieved. Structural analysis is ongoing and the results will be presented on the poster. Rational site-directed mutagenesis of selected surface amino acids could become a routine application to decrease the entropy on the protein surface and therefore improve the crystallisation process.

[1] Slusarczyk H. *et al.*, *Eur. J. Biochem.*, 2000 **267**, 1280-1289. [2] Tishkov V.I., *FEBS Letters*, 1996, **390**, 104-108. [3] Derewenda Z.S., *Structure*, 2004, **12**,529-535. **Keywords:** x-ray protein protein, engineering mutagenesis crystallography, protein disorder