

Stabilization and activity improvement of a Baeyer-Villiger monooxygenase by mutagenesis of the susceptible to oxidation residues around flavin



Angeli C., Mertika T., Pavlidis I.V.*



Department of Chemistry, University of Crete, Heraklion, Greece. E-mail: ipavlidis@uoc.gr URL: <http://www.chemistry.uoc.gr/pavlidis>

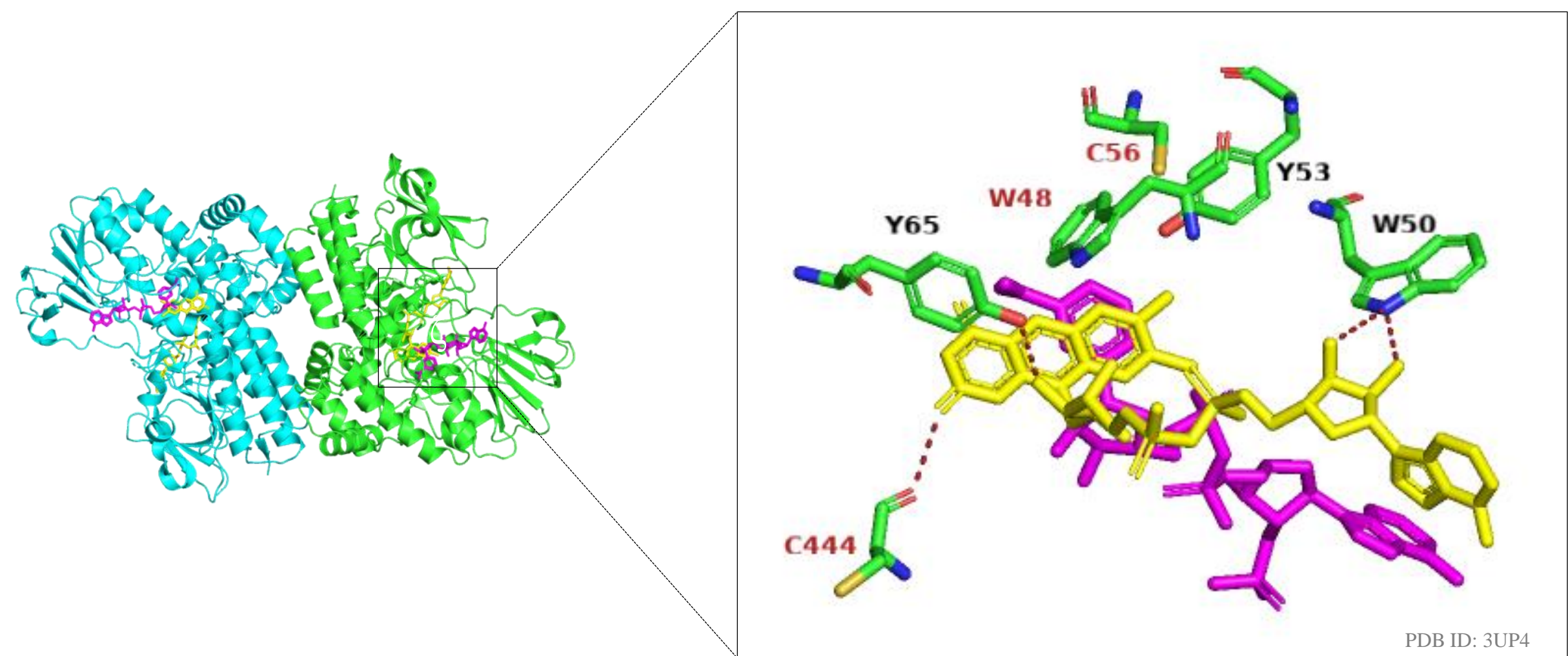
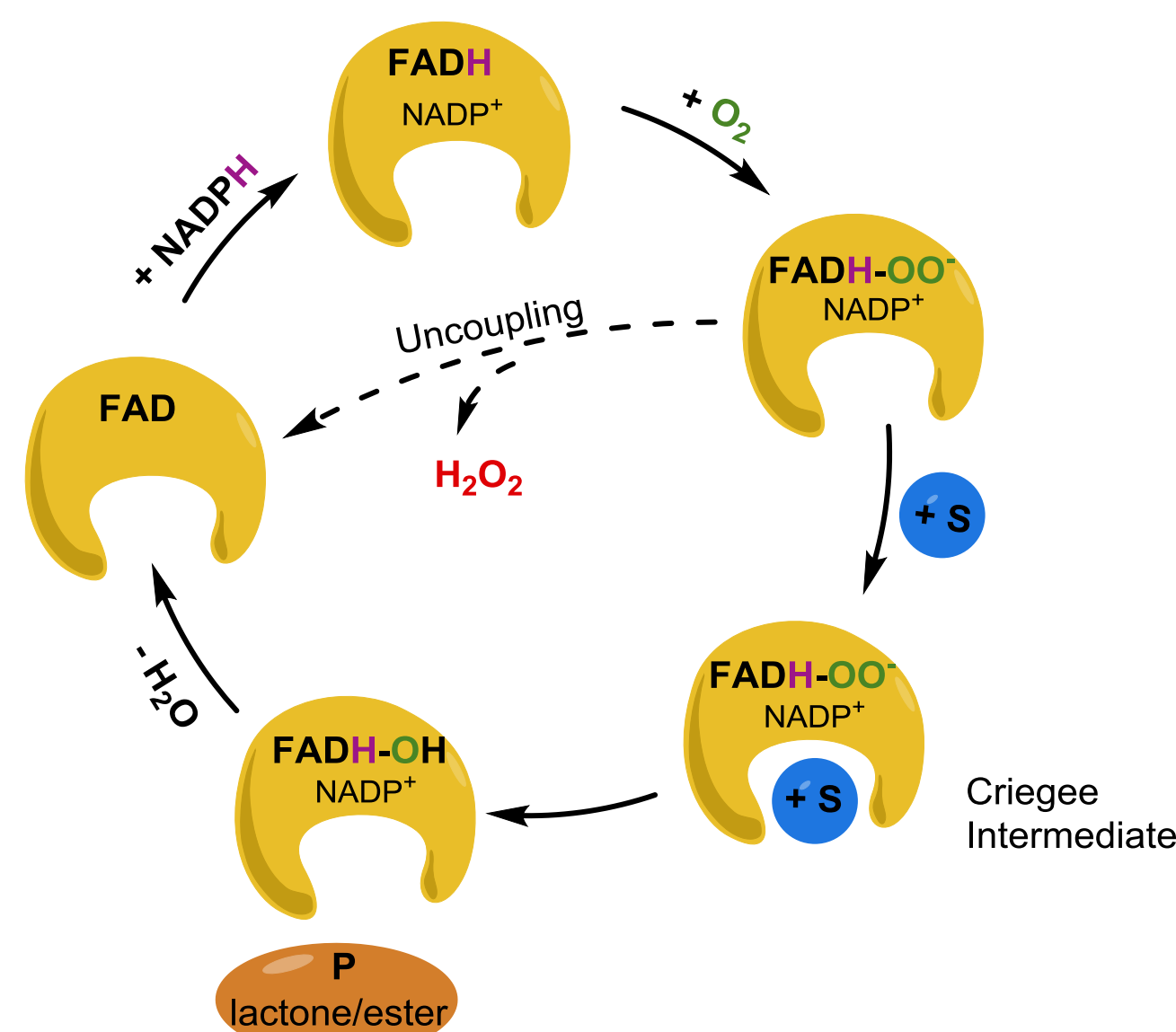


Introduction

Baeyer-Villiger-Monooxygenases (BVMOs) belong to the large family of Flavoprotein-Monooxygenases (FPMOs), and can catalyze the Baeyer-Villiger oxidation reaction under mild conditions, leading to a sustainable chemical process.^[1] BVMOs type I, have FAD as a prosthetic group in their active site, and use NADPH as a coenzyme. They utilize molecular oxygen from air to perform the insertion of an oxygen atom next to a carbonyl group, leading to the formation of an ester or a lactone, often with high enantio- and regioselectivity. Despite that, there are many limitations in the application of BVMOs on an industrial scale, due to their low thermo-, pH-, solvent- and oxidative stability.^[2] In this study, 2-oxo-D3-4,5,5-trimethylcyclopentenylacetyl-CoA monooxygenase from *Pseudomonas putida* (OTEMO), was biochemically characterized and its oxidative stability was studied using rational design mutagenesis, in order to expand the reaction portfolio of the enzyme.

Rational design for the optimization of oxidative stability

Because of the uncoupling reaction that occurs in the active site of BVMOs, H_2O_2 is formed very close to the isoalloxazine ring of FAD, and can lead to loss of activity due to oxidation of the enzyme.^[2] Trp, Tyr, His, Met and Cys residues are susceptible to oxidation.^[3] We identified the respective residues, 5 Å from FAD, and we designed three variants (C56A, C444S, W48L). The wild type, and the mutants were overexpressed in *E. coli* BL21[DE3] strain, and were purified through affinity chromatography using a Ni-NTA column, as the proteins carry a N-terminal 6-His-Tag sequence.

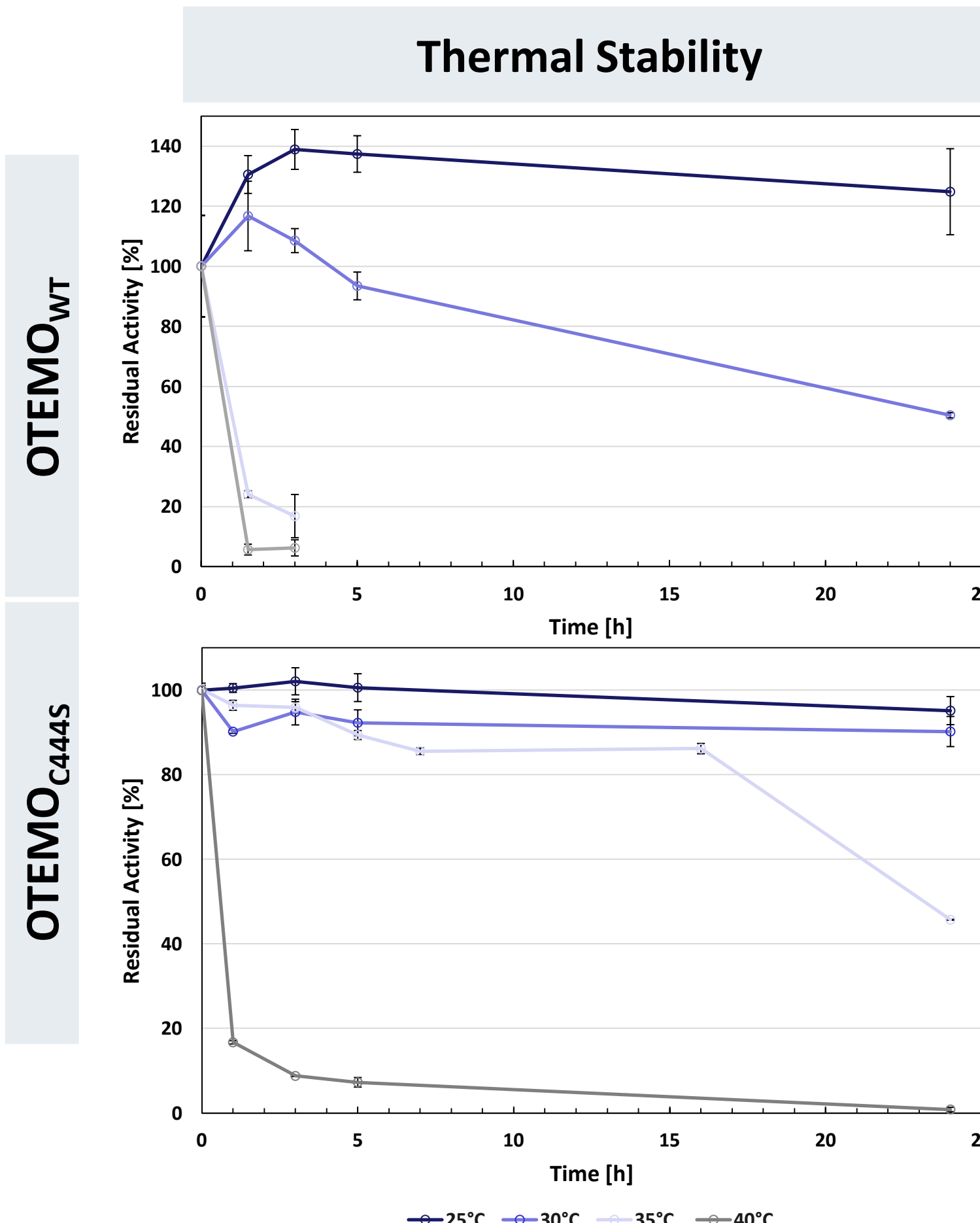


OTEMO_{C444S} maintains good expression levels in *E. coli* and FAD coordination in the active site. W48L affects negatively the expression, while it seems to lead to mostly apoprotein. Proteins expressed as holoenzymes exhibit activity, with the OTEMO_{C444S} having 4-fold increased, compare to the wild type.

- The activity measurements for the oxidation of bicyclo[3.2.0]hept-2-en-6-one were performed spectrophotometrically by monitoring the NADPH consumption at $\lambda=340$ nm.
- To determine the concentration of FAD, standard curve was made in the range of 0,014 to 0,140 mg mL⁻¹ FAD, and absorbance was taken at $\lambda=448$ nm^[4].

Biochemical characterization of OTEMO_{WT} and OTEMO_{C444S}

Thermal Stability

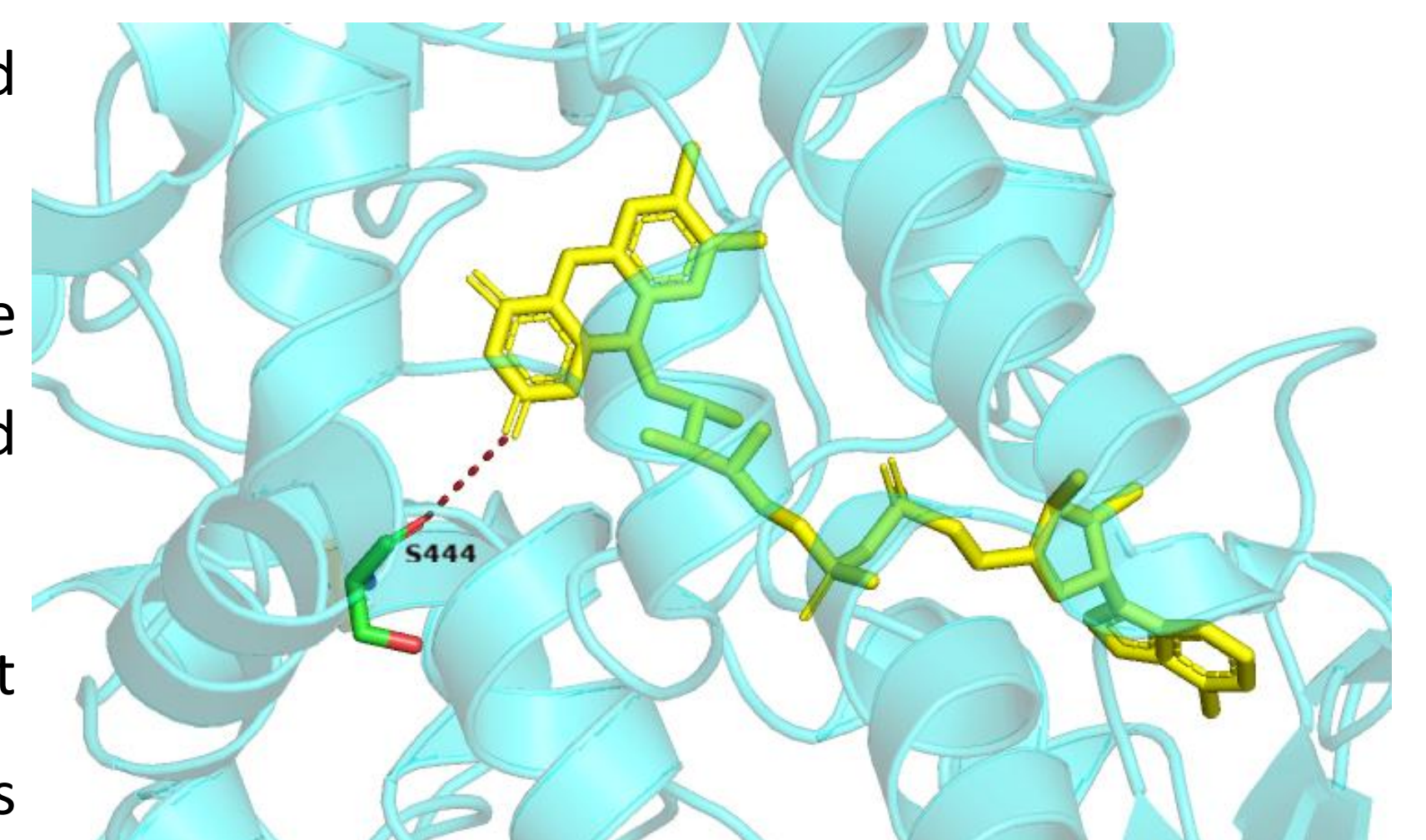


From the determination of pH profile, temperature profile, pH, temperature and cosolvent stability, OTEMO_{C444S} shows an improvement compared to the WT.

The mutant and the wild type are more stable in phosphate buffers and in presence of 5% DMSO. Optimum pH was found to be 9,0 in Tris-HCl 50 mM buffer, and optimum temperature 40°C.

The OTEMO_{C444S} variant appeared to be stable for 24h at 30°C, a temperature at which OTEMO_{wt} loses 50% of its catalytic activity. Also, an improved stability was observed at 35°C.

- For the biochemical characterization of the OTEMO_{WT} and OTEMO_{C444S}, the NADPH-dependent activity towards bicyclo[3.2.0]hept-2-en-6-one, was measured spectrophotometrically, by monitoring NADPH consumption at 340 nm.



Phenylacetone monooxygenase (PAMO) from *Thermobifida fusca* is the only protein showing remarkable stability.^[5] [PDB ID: 1W4X]

Conclusions

- OTEMO_{C444S}, shows good expression in *E. coli* and keeps FAD coordination in the active site
- The specific activity of OTEMO_{C444S} towards bicyclo[3.2.0]hept-2-en-6-one, is 4-fold increased compared to OTEMO_{WT}
- The mutation C444S, increased the thermostability of the OTEMO_{WT}, which comes to correlation with the tertiary structure of PAMO

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