

### N°1633 / PC TOPIC(s) : Enzyme production, immobilization / Artifical intelligence / computational methods

# Bioinformatic analysis of immobilized enzymes

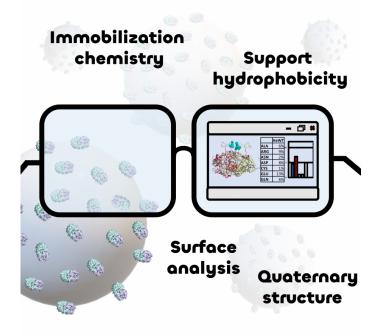
#### **AUTHORS**

David ROURA PADROSA / UNIVERSITY OF BERN, FREIESTRASSE 3, BERN Francesca PARADISI / UNIVERSITY OF BERN, FREIESTRASSE 3, BERN

#### PURPOSE OF THE ABSTRACT

Protein bioinformatics has been applied to a myriad of opportunities in biocatalysis, from enzyme engineering to enzyme discovery, but its application in enzyme immobilization is still very limited. Enzyme immobilization brings clear advantages from the sustainability and cost-efficiency terms but is nowadays still limited in its implementation as it remains tied to a quasi-blind protocol of trial and error. Here, we present the use of a set of bioinformatic tools to rationalize results of protein immobilization that have been previously described. The study of these proteins through new bioinformatic tools, allows the discovery of key driving forces in the process of immobilization that explain the obtained results, moving us a step forward to the final goal: predictable enzyme immobilization protocols.

### FIGURES



## FIGURE 1

FIGURE 2

Graphical abstract Application of different analysis and bioinformatic tools to rationalize the process of enzyme immobilization.

#### **KEYWORDS**

Enzyme immobilization | Bioinformatics | Protein modelling | Biocatalysis

#### **BIBLIOGRAPHY**

- [1] D. Roura Padrosa, V. Marchini, F. Paradisi, Bioinformatics 2021, 37, 2761-2762.
- [2] R. A. Sheldon, D. Brady, ChemSusChem 2022, 15, DOI 10.1002/cssc.202102628.
- [3] M. E. Hassan, Q. Yang, Z. Xiao, L. Liu, N. Wang, X. Cui, L. Yang, 3 Biotech 2019, 9, 1-16.