



**Model-Based Construction and Optimisation
of Versatile Chassis Yeast Strains
for Production of Valuable Lipid and Aromatic Compounds**

OFFERING

The EU-funded project CHASSY offers proteomics datasets of three industrially relevant yeast strains, as well as the know-how to generate semi-absolute proteomics data suitable to be implemented into metabolic models. In addition, differential abundance analysis can be carried out under multiple conditions.

EXPERTS

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PARTNERING OPPORTUNITIES

- Research collaboration
- Technical knowledge
- Industrial project development

DEVELOPMENT STATUS

TRL – 3

KEYWORDS

- Mass Spectrometry
- Proteomics
- Semi-absolute quantification
- Microorganism modeling

Method for semi-absolute quantification of proteins for integration in metabolic models

Summary

In the framework of the EU-funded project CHASSY, the PAPPSO proteomic facility has developed an improved method of protein quantification in absolute terms. This approach relies on the use of cutting-edge mass spectrometers and computational algorithms to generate datasets in semi-absolute abundances of proteins from three industrially relevant yeast strains (*S. cerevisiae*, *K. marxianus*, *Y. lipolytica*) cultivated under different stress conditions. This novel methodology enables:

1. Global view of complex biological samples containing thousands of proteins
2. Ability to compare proteins abundances inter-samples
3. Generation of data for large cohorts (up to 80 samples per experimental design)
4. Ability to feed metabolic models requiring absolute quantification

The science

As part of the CHASSY project, we have developed an improved method to determine protein abundances in absolute values for integration into metabolic models allowing inter-protein comparison. The analysis depends on the external protein standard UPS2 (Sigma), a mix of 48 human proteins distributed in 6 molar concentrations, spiked in the protein lysate to generate a calibration curve useful to estimate proteins abundances in fmol. The methodology was developed using open-source and freely available bioinformatic tools created at the PAPPSO proteomics

facility.

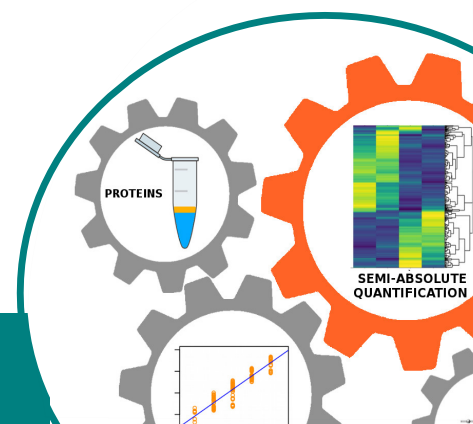
Development stage

The Technology Readiness Level (TRL) of the methodology is 3. The proteomics facility at INRAE who developed this method as part of the CHASSY project are seeking academic and industry partnerships for further application in large cohorts of analysis.

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