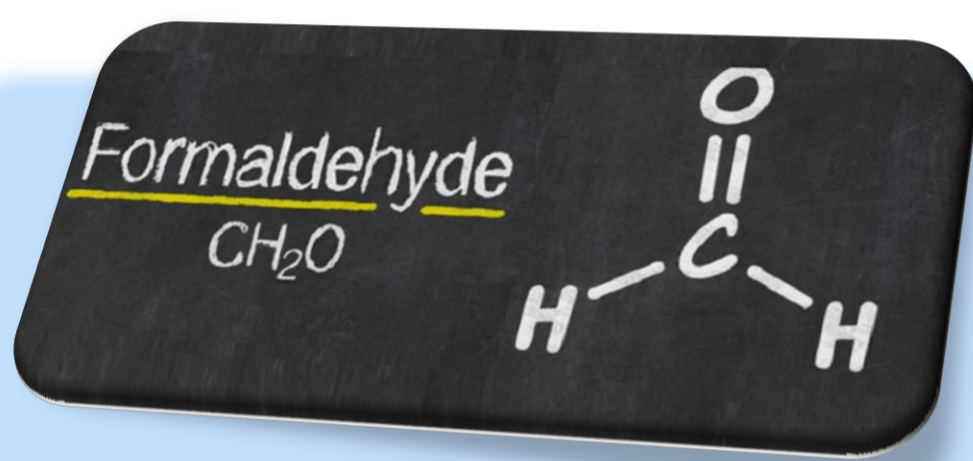


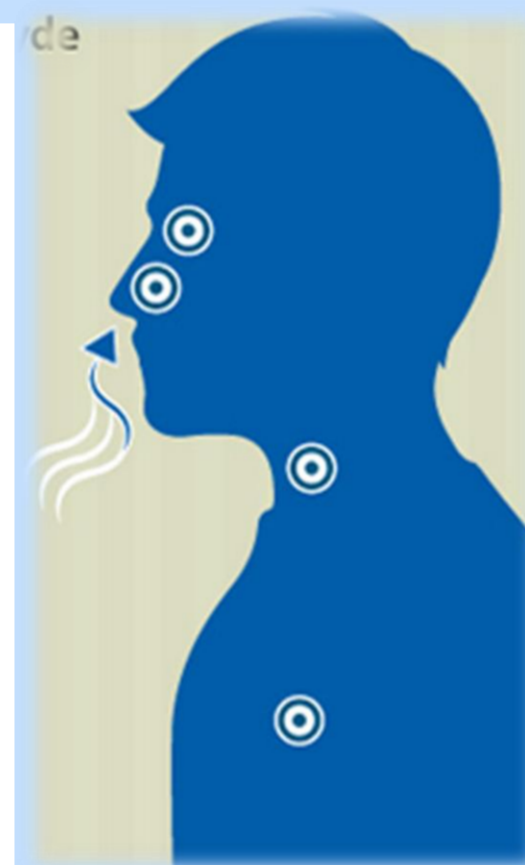
## INTRODUCTION

Indoor pollution in buildings and structures is creating some health and comfort concerns. Volatile organic compounds (VOCs) released by consume household products, adhesives and building materials, or combustion processes, are some of pollutants usually present in residential units and workplaces indoor air. Formaldehyde (FA) is one of the most representative oxygenated-VOCs, and a widespread chemical pollutant of water, air and soil [1]. It is known by its mutagenic, immunogenic, allergenic and carcinogenic effects [2]. Understanding and controlling this pollutant can help reducing the illness risks associated. Biological degradation strategies of FA through biomolecules transformation is being more and more explored. Formaldehyde dehydrogenase (FDH) is an enzyme known to degrade FA. In the present work, the ability of a wild *Pseudomonas putida* strain to produce FDH under distinct carbon and energy sources is evaluated. Selecting the fermentation conditions able to induce FDH overproduction by *P. putida*, cells will be incorporated into a coating to be further used as an innovative solution for indoor FA-depollution.



### FA exposure symptoms:

- Irritation of eyes, nose and throat
- Breathing difficulties
- Serious injuries at the respiratory level and chronic pulmonary obstruction
- Pulmonary cancer



Used in different industries and consumer products, widely used in construction materials, wood processing, furniture, textiles, carpeting, and chemical industries

Time Exposure & Concentration  
+

## FA degradation methods

### Physical

- Adsorption to a carrier
- Photocatalysis

### Chemical

- Oxidation
- Combustion

### Biological

- Biofilter
- Trickling biofilter
- Bioscrubber

- Development of a selective, highly sensitive, reliable and simple method for fast and inexpensive detection and degradation of FA from the indoor air
- **Biological degradation:** flexible, low-cost and efficient strategy, respecting health and environmental procedure

## Formaldehyde dehydrogenase (FDH)

- ✓ Enzyme able to transform FA into less toxic compounds, as formic acid, naturally oxidized to CO<sub>2</sub> and H<sub>2</sub>O
- ✓ Synthesized by different bacteria, cyanobacteria, fungi or yeasts
- ✓ *Pseudomonas putida* is a FDH-producing bacteria, commonly used for the biodegradation of FA [3,4]
- ✓ The ability to synthesize the FDH can be improved in the presence of co-substrates, used as carbon and energy sources

### Enzymatic degradation of FA:



## MATERIALS AND METHODS

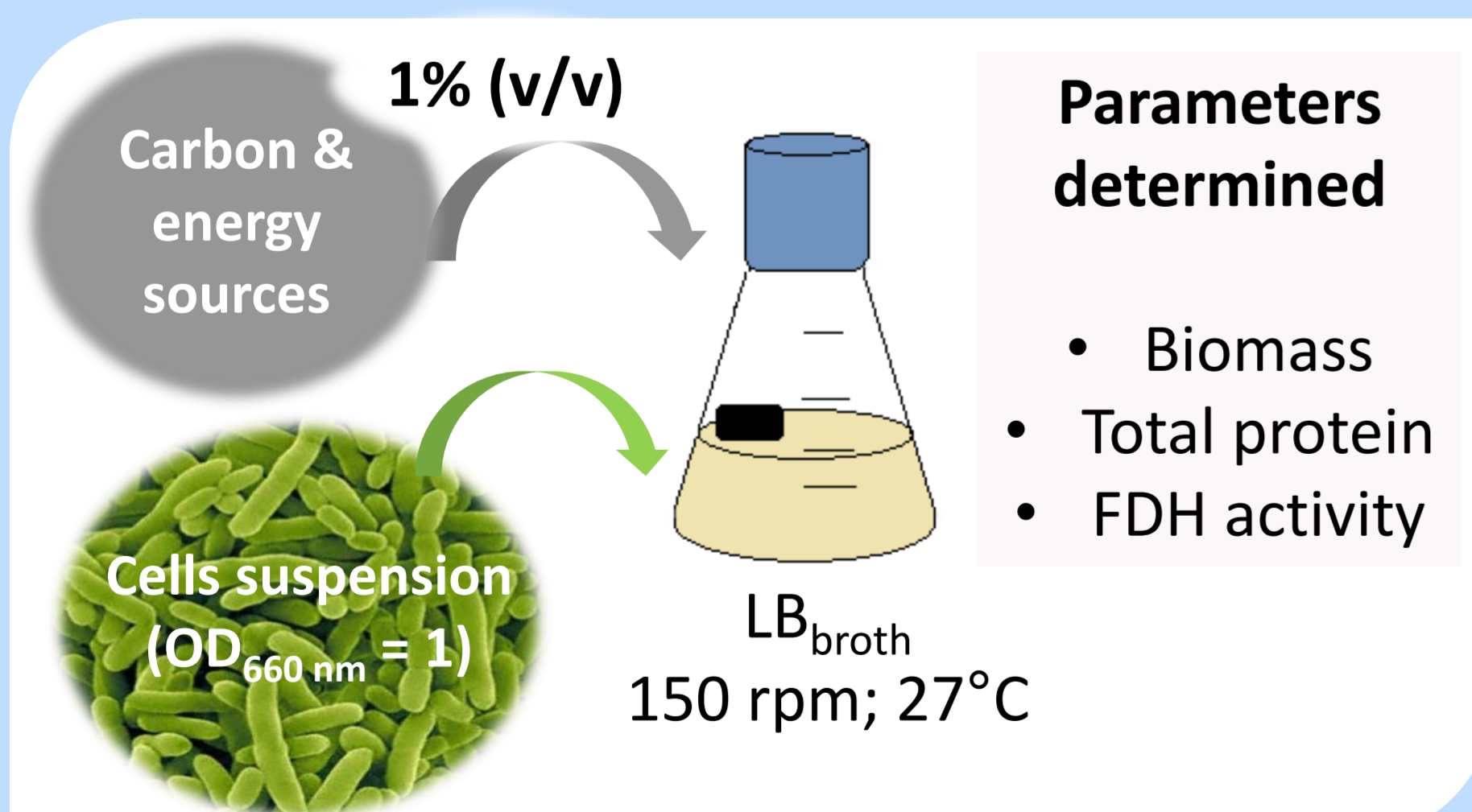
### Carbon / energy sources

- |              |              |
|--------------|--------------|
| 1 - Glucose  | 6 - Methanol |
| 2 - Mannitol | 7 - Alanine  |
| 3 - Sorbitol | 8 - Ribose   |
| 4 - Glycerol | 9 - Lactose  |
| 5 - Ethanol  | 10 - Control |



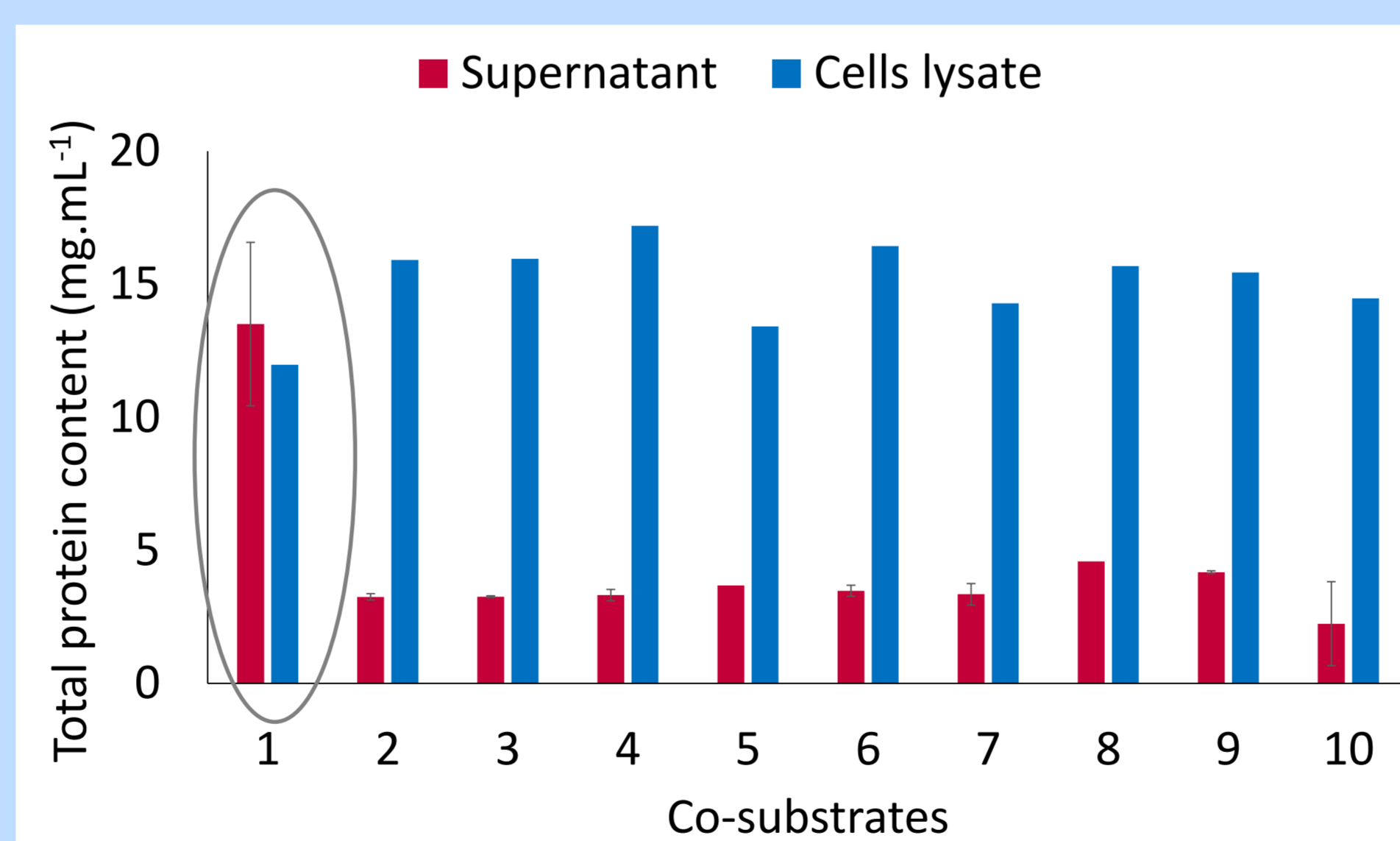
*Pseudomonas putida*  
LMG 24210 (BCCM)

### FDH Overproduction strategy



## RESULTS AND DISCUSSION

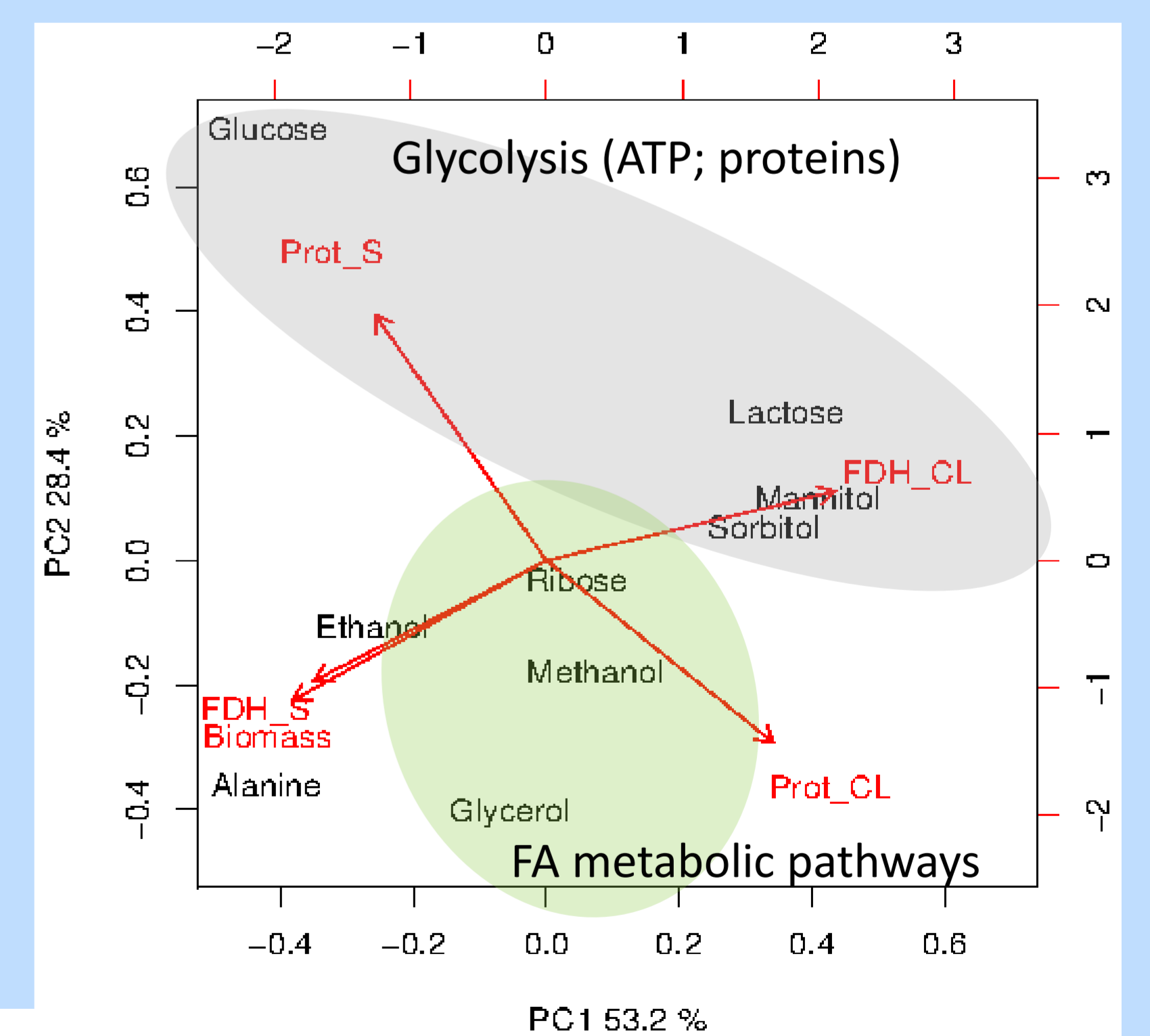
### Total protein content



➤ Protein content in cells lysate is higher than in supernatant, **except** in the presence of glucose

- **Glucose** induces protein secretion to the supernatant
- Co-substrates (**Ethanol**, **Alanine**) which promote biomass growth, improve FDH release to the supernatant
- **Lactose**, **Mannitol** and **Sorbitol** induced higher enzymatic activity of FDH in cells lysate

### Multivariate analysis



## CONCLUSIONS

- ❑ Depending on the substrate used in the fermentation medium, distinct metabolic pathways, associated either to cells growth or FDH production, could be activated.
- ❑ Sequential fermentations where, in a first fermentation, cells growth is induced, followed by a second fermentation where, FDH production is promoted, can increase FDH activity.
- ❑ In future work, the incorporation of these biomolecules coated on solid surfaces, can be presented as an innovative solution for FA degradation from indoor air.

## References

- [1] Guieysse B. et al. (2008), *Biotechnol. Adv.*, 26, 398–410.
- [2] Salthammer T. et al. (2010), *Chem. Rev.*, 110.
- [3] Roca A. et al. (2008), *Microb. Biotechnol.*, 1,158–169.
- [4] Fujii T. et al. (1975), *Agric. Biol. Chem.* 39, 2325–2330.