The NMR side of lentil:
protein extraction and hydrolyzation, and a bit of data fusion

Francesco Savorani[1]*, Nicola Cavallini[1], Mattia Sozzi[1], Elena Cazzaniga[1], Francesco Geobaldo[1]

[1]Department of Applied Science and Technology, Politecnico di Torino, Corso Duca degli Abruzzi, 24, Torino, TO 10129, Italy

INTRODUCTION

The **lentil flour** belongs to the group of "**functional food**" in the world of food supplements.

In this field, the use of enzymes is becoming more and more important for the improvement of food safety and food treatment processes.

Our study, was primarily focused on the evaluation of different treatment conditions and on the optimization of enzymatic process parameters.
The technique mainly used was **liquid ¹H-NMR spectroscopy**, but we also tested **NIR (SCiO)** and **UV-Vis spectroscopies** to evaluate how a **low-level data fusion** approach (merging experimental data from different techniques) might affects and eventually improve our findings.

Multivariate data analysis methods were used to inspect spectroscopic data: Principal Components Analysis (PCA) was used to explore both NMR data alone and fused spectroscopic data; Partial Least Square (PLS) classification analysis was used to create an enzyme-based classification model.

EXPERIMENTAL CONDITIONS

- *Protease enzyme*: added to half of the solution after extraction process(1).
- *Stirring rate*: two different speed, 60 and 120 RPM(2).
- *Sampling times*: different time of enzyme activity, from 0 to 300 minutes(3).
- *Instruments*: NMR Spectrometer, SCiO Spectrometer and UV-vis Spectrophotometer.

32 samples
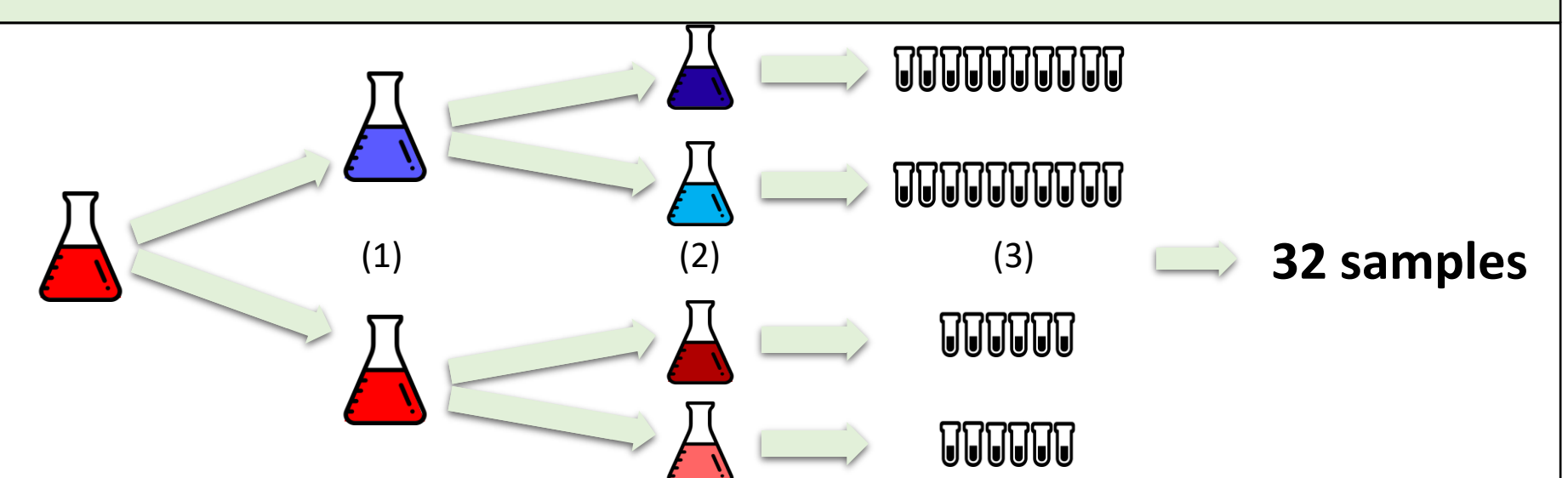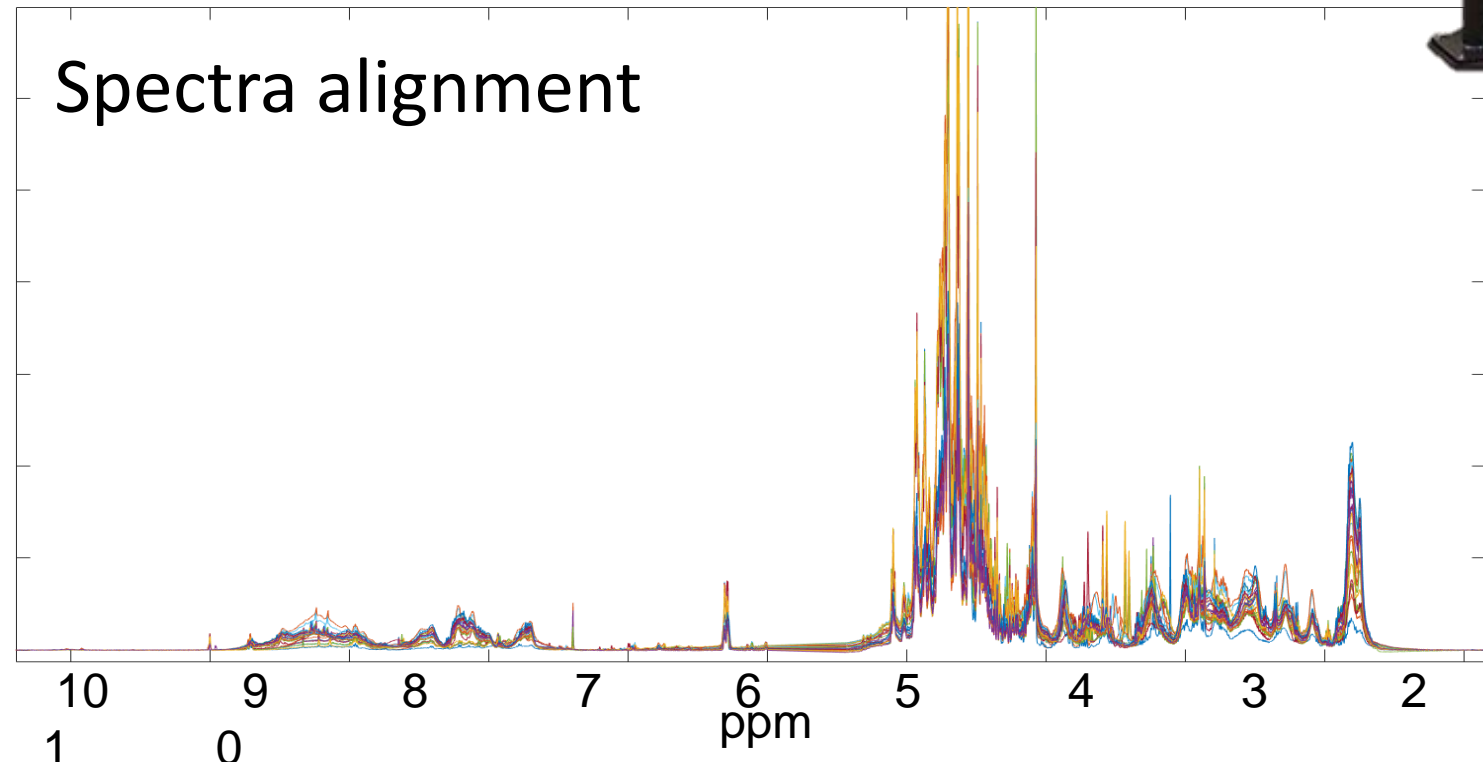
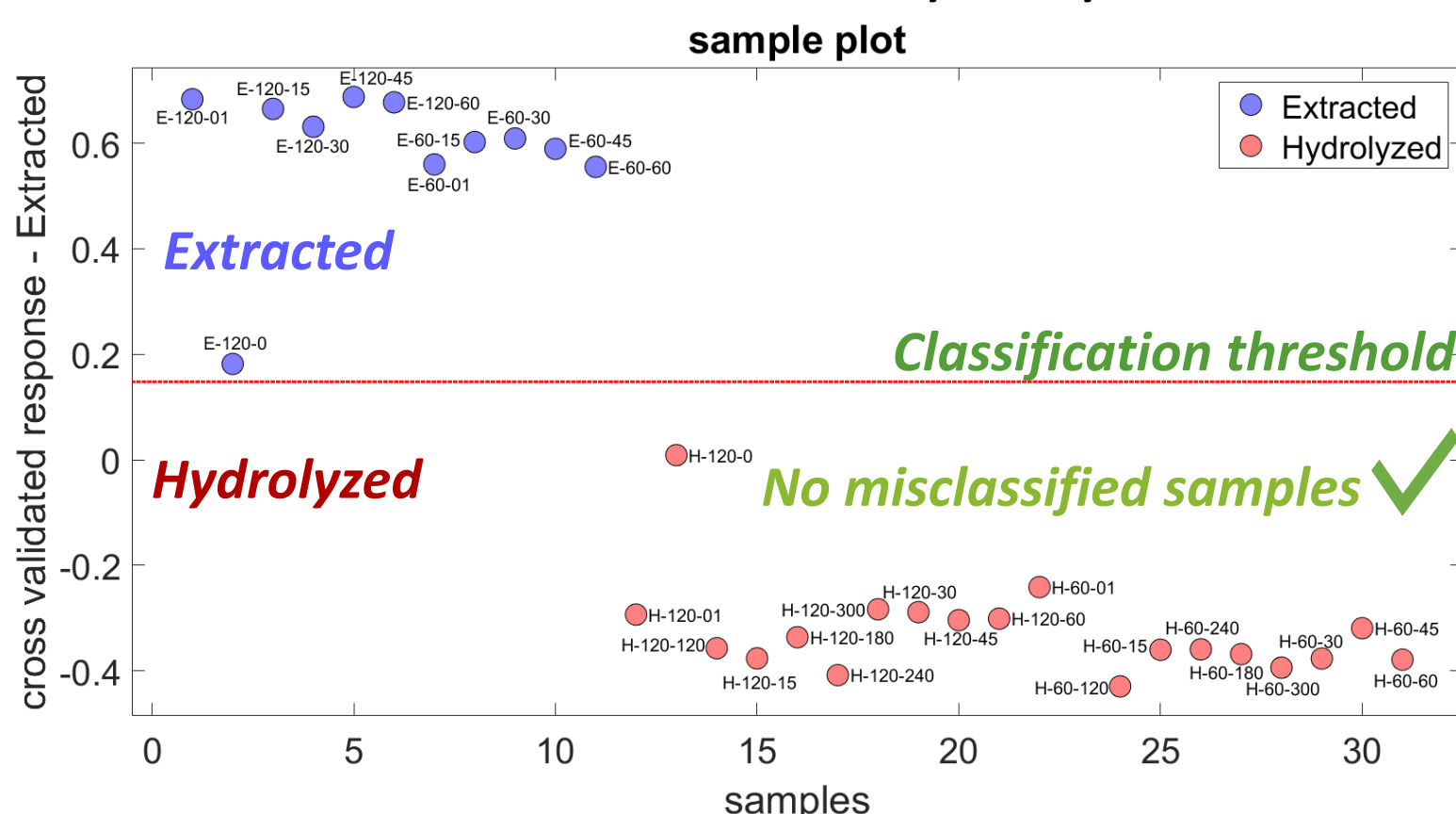# NMR DATA

Focus on PARAMETERS

DATA FUSION
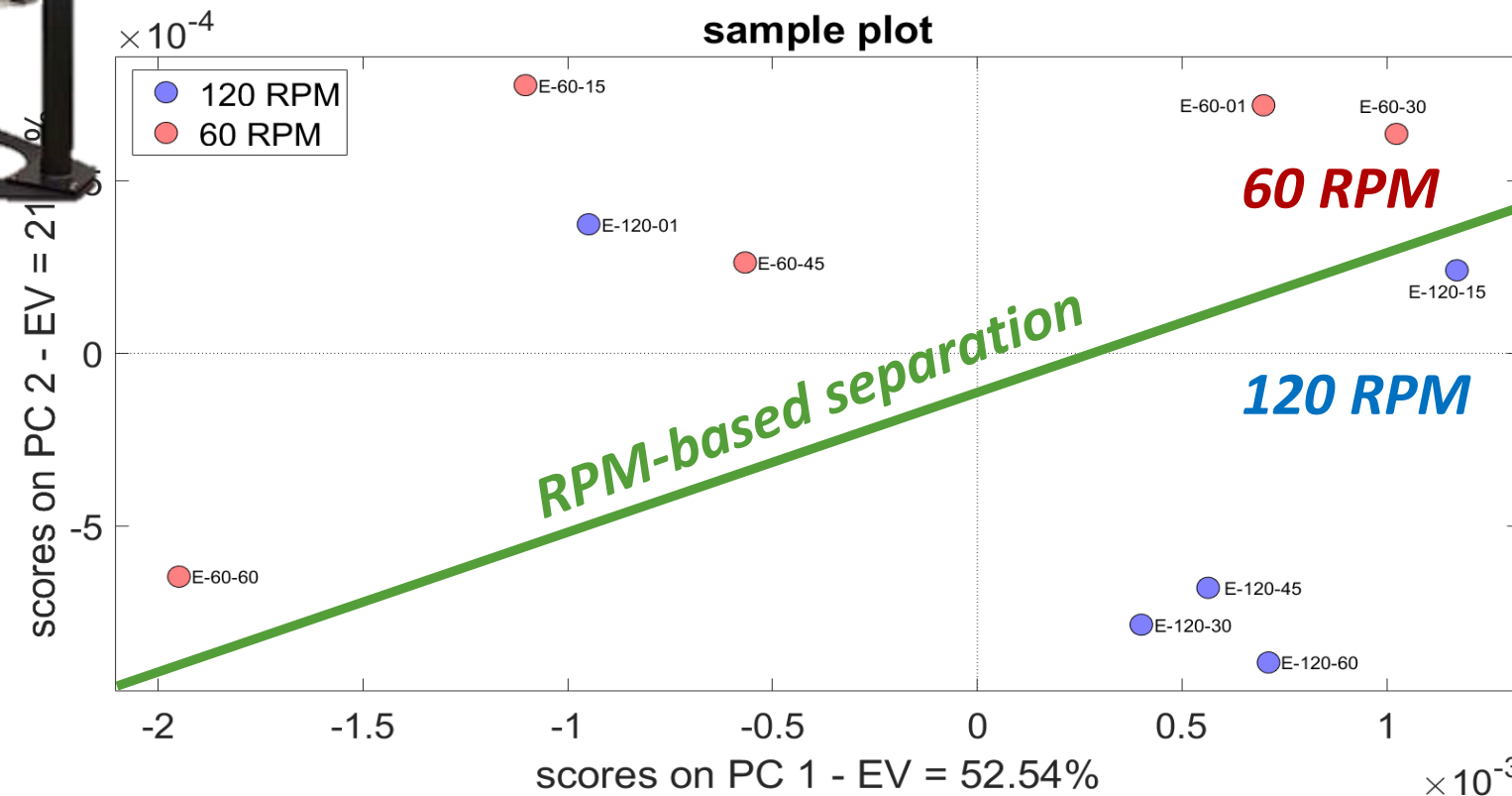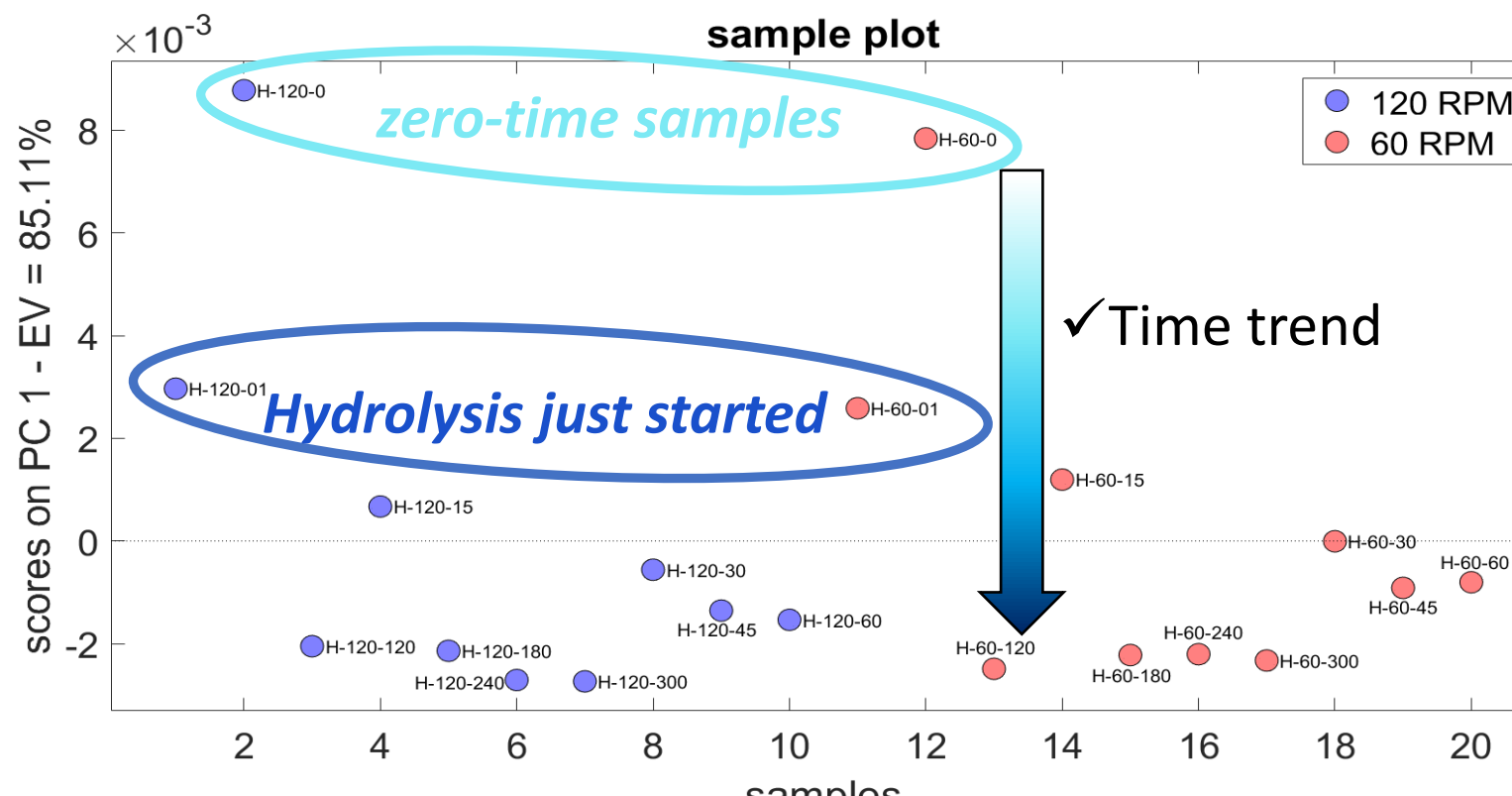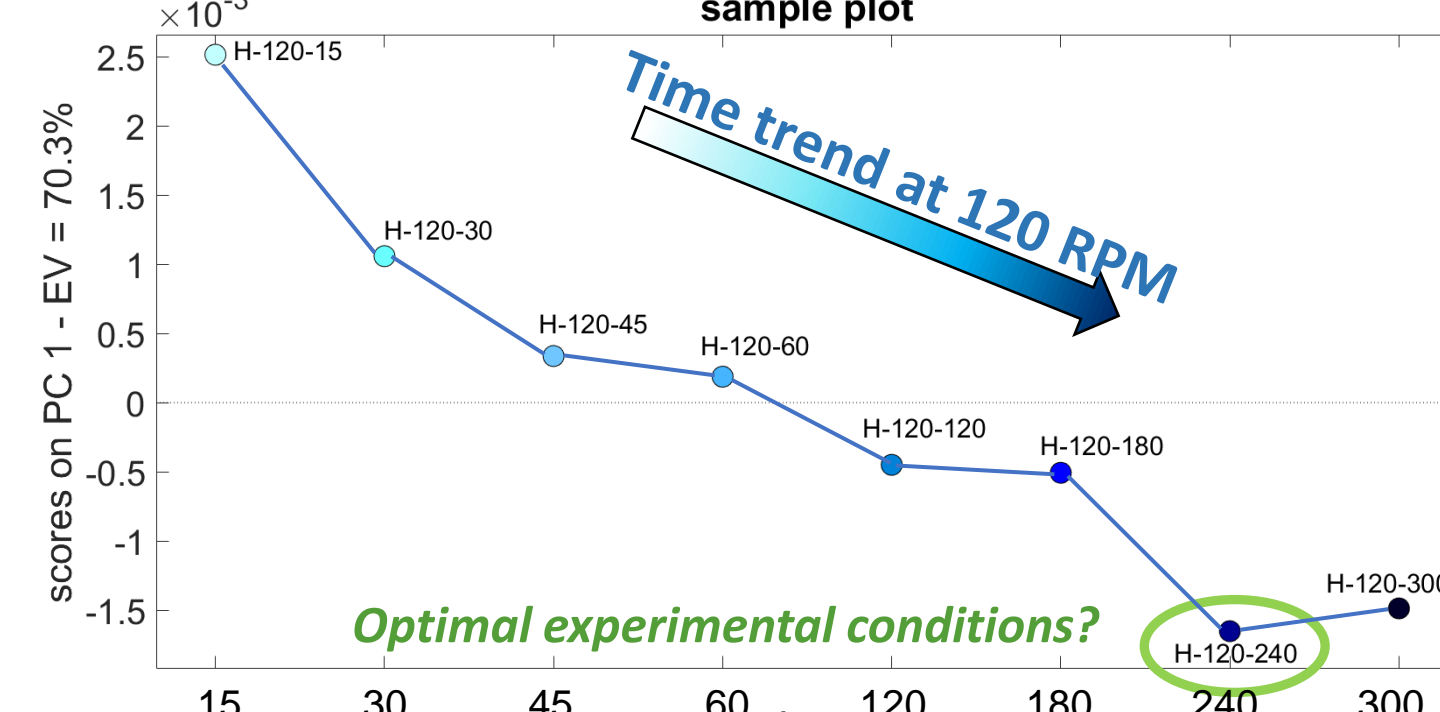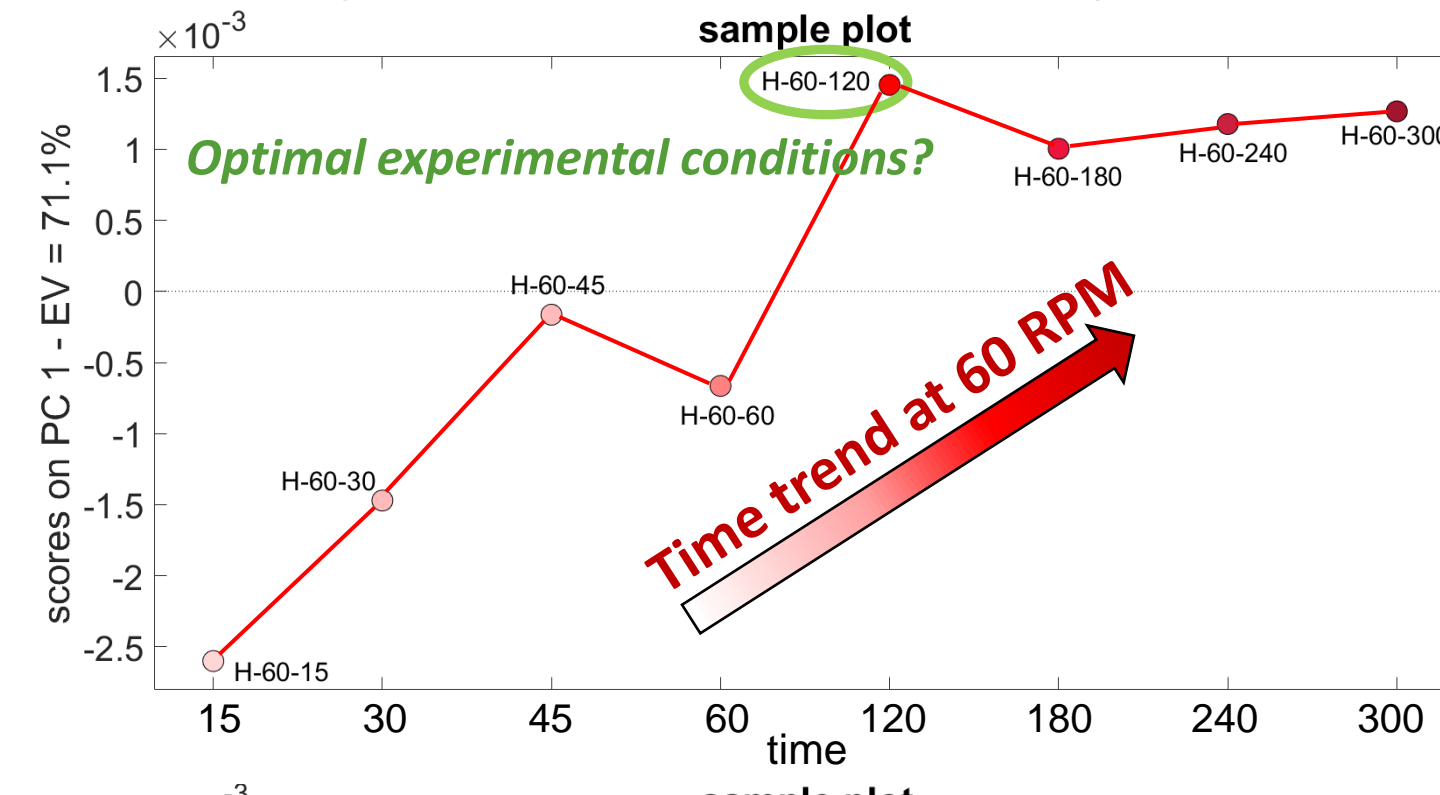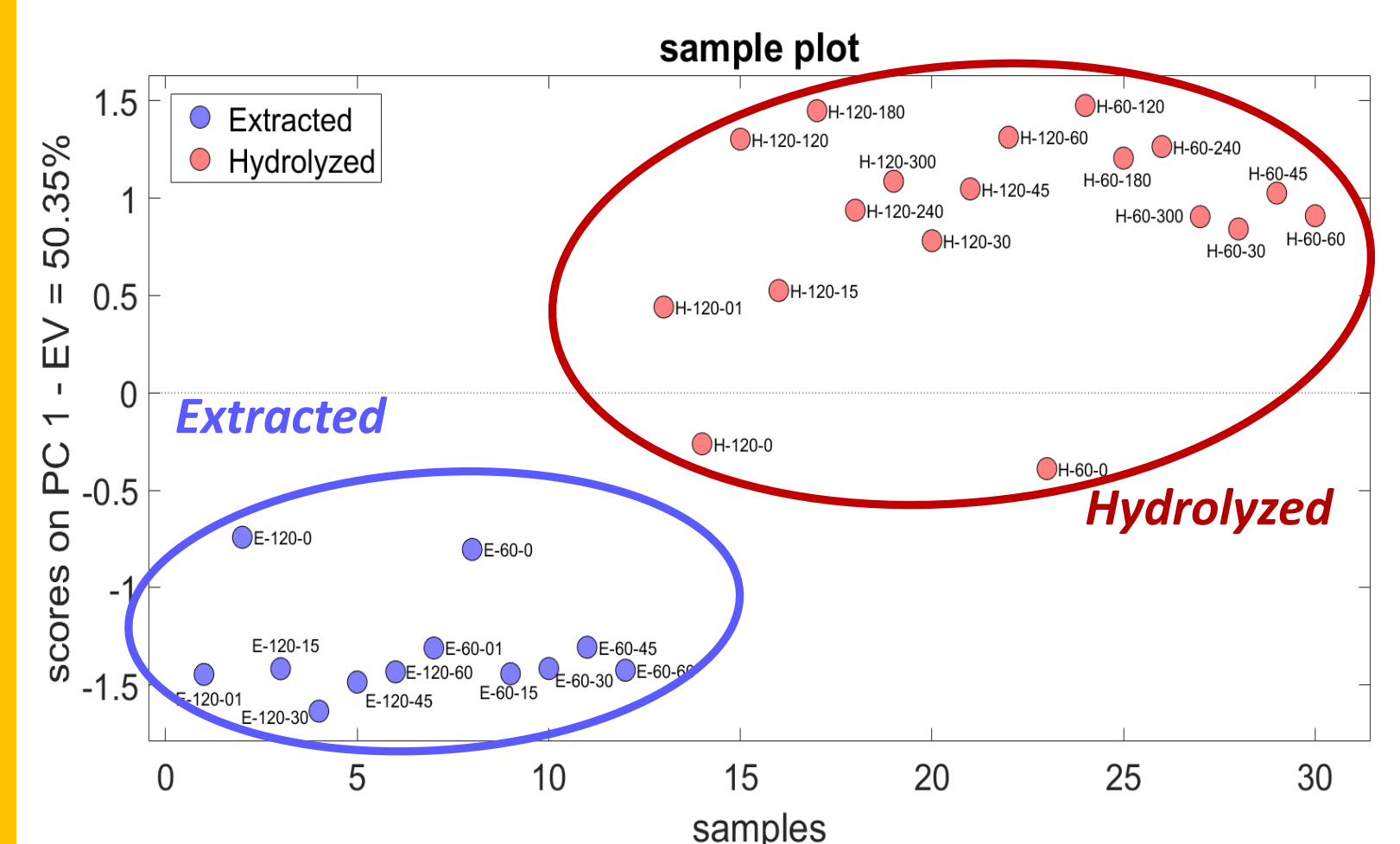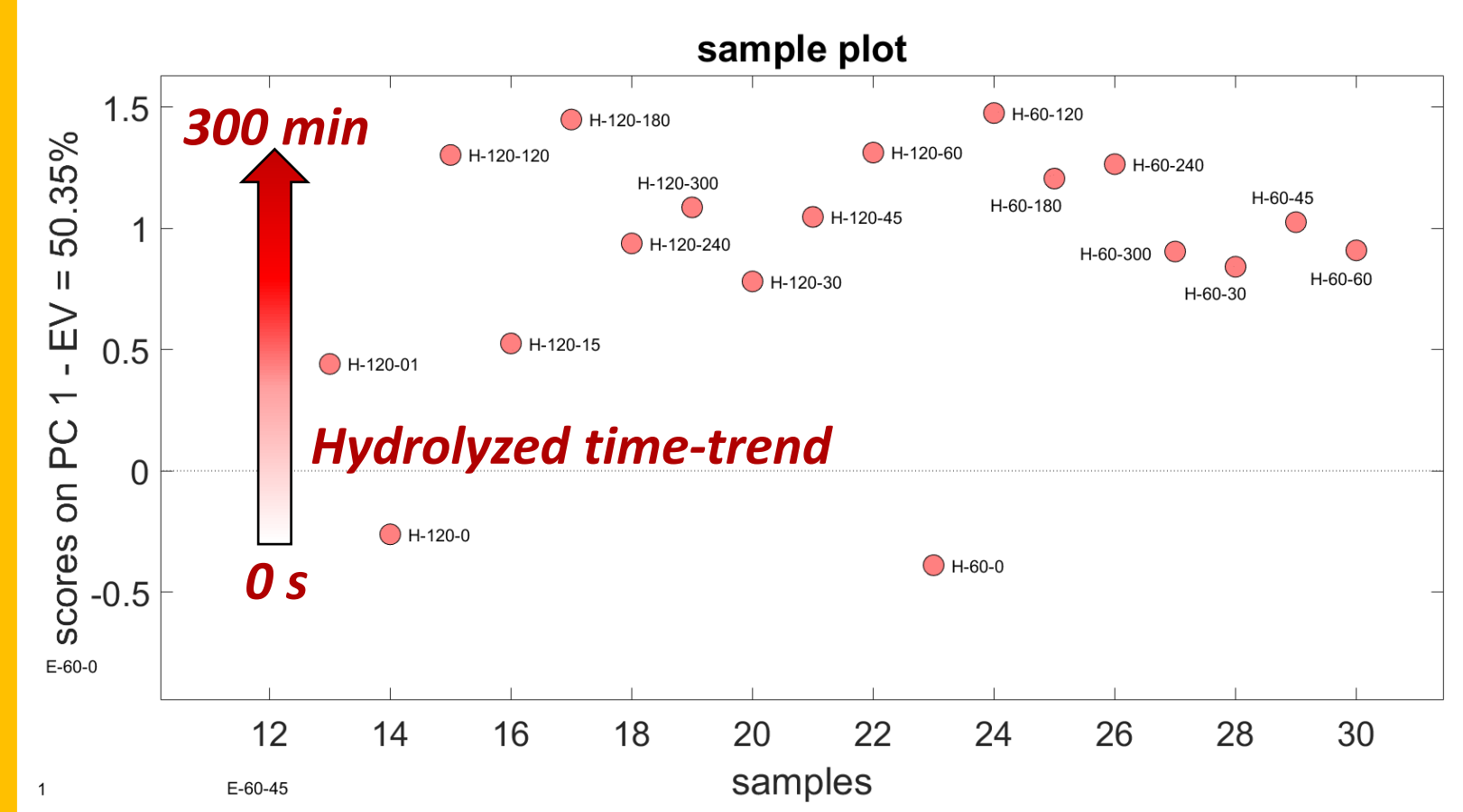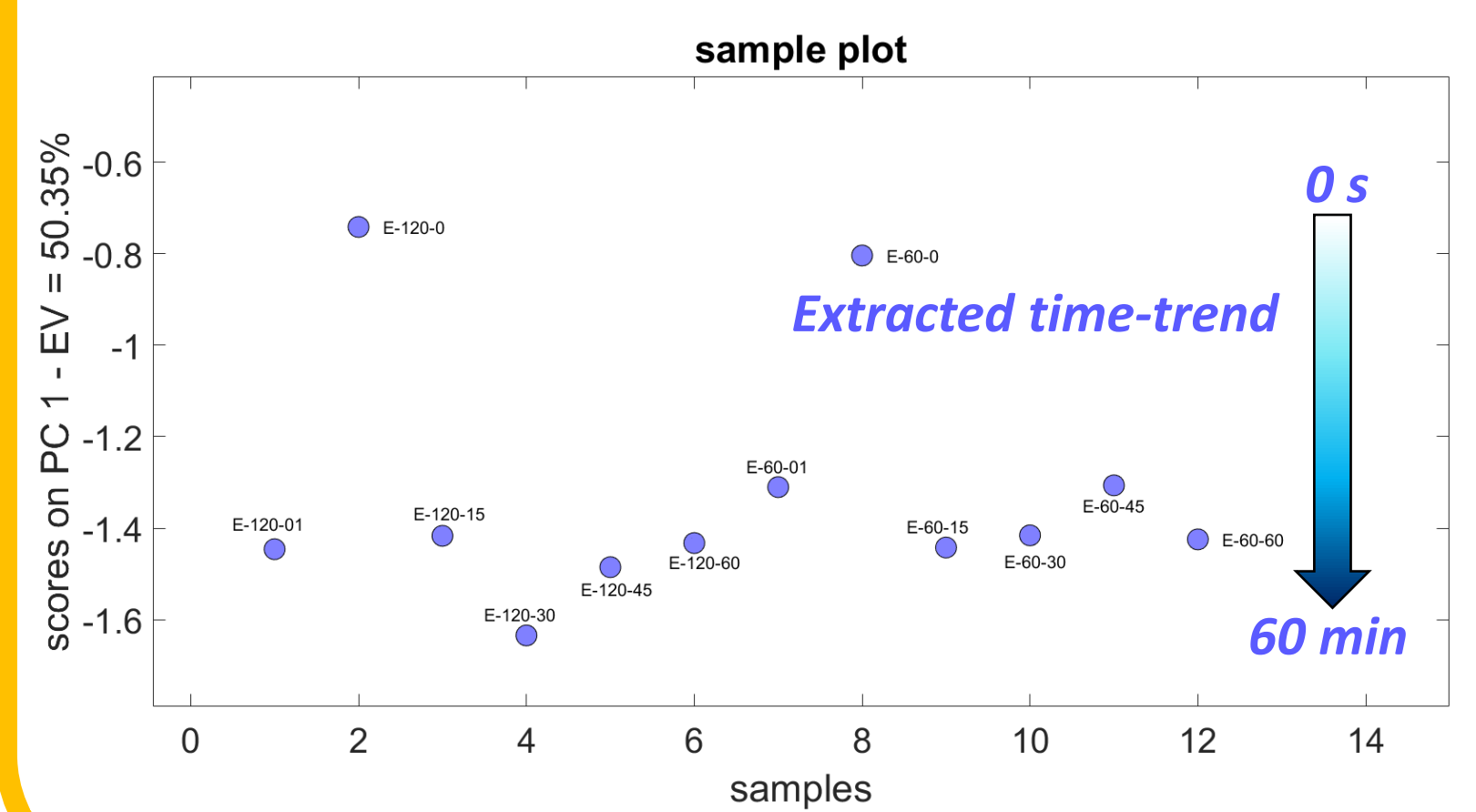
CONCLUSIONS

The results of our investigation demonstrated the possibility of using **NMR spectroscopy** coupled with **multivariate data analysis** to explore and evaluate different parameters for the lentil flour industrial treatment in order to find the best operating conditions. Furthermore, this combined approach proved successful for distinguishing samples with added enzyme from those without.
Eventually, the **low-level data fusion** approach confirmed and improved the findings from exploratory analysis for all data and, in addition, highlighted the presence of a time-dependent trend for both groups of samples with and without the enzyme.