

2024

Catalogue

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ADVANCED PROTEOMICS

# DIGESTIF CONTROL

## TO OPTIMIZE DIGESTION PROCESS AND LC-MS ANALYSIS

Universal quality standard for digestion control  
and optimization of bottom-up proteomics experiments

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# A TWO-IN-ONE SOLUTION

DIGESTIF is a universal protein standard to assess simultaneously the quality of sample workup and the performance of your LC-MS system

## What is DIGESTIF ?

DIGESTIF is a soluble recombinant **protein** scaffold (PBP2x, Penicillin-binding protein 2x from *Streptococcus pneumoniae*) deleted of its N-ter part and **resulting from the collaboration between Biognosys, Promise Proteomics and academic teams**<sup>1</sup>.

DIGESTIF is composed of **11 artificial peptides (iRT)** of various hydrophobicity with good ionization.

## Why use DIGESTIF ?

DIGESTIF is a two-in-one quality control reagent used to check digestion quality & efficiency as well as LC-MS performances during bottom-up proteomic experiments.

### Protein digestion quality

- Easy solution to control and optimize digestion process
- Can be spiked and used in all biological samples

### LC-MS performances

- Allows control of retention times
- Facilitates spectra alignment during shotgun proteomic
- Simplifies the set-up of LC-MS methods

## With DIGESTIF, you can:

- Check and optimize digestion process
- Standardize sample preparation steps
- Easily set-up LC-MS methods
- Monitor retention times

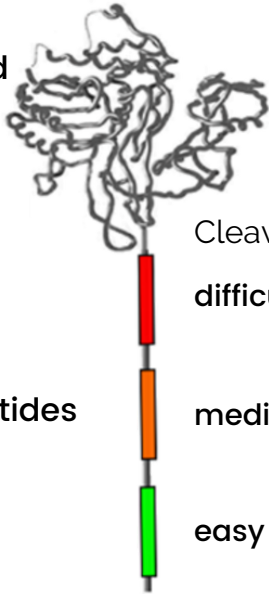
# How to use it ?



Available in [labelled](#) and [unlabelled](#) presentations

## DIGESTIF

PBP2x scaffold



Cleavage :  
difficult

iRT peptides

medium

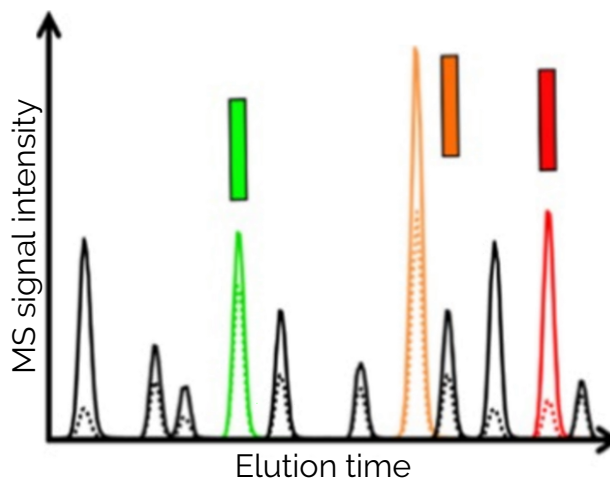
easy

1 Add DIGESTIF to biological samples



2 Digest samples

3 Check digestion efficiency and LC-MS performance



4 Compare digestion rates between samples, experiments and/or laboratories

— efficient digestion  
..... incomplete digestion

# REFERENCES

Peer reviewed publications using our SIL-proteins

- **University Hospital Grenoble-Alpes**

Lebert, D. and al. (2014). DIGESTIF : A Universal Quality Standard for the Control of Bottom-Up Proteomics Experiments. *Journal of Proteome Research*, 14(2), 787-803. <https://doi.org/10.1021/pr500834z>

- **Rapid Novor**

McDonald, Z., Taylor, P., Liyasova, M., Liu, Q., & Ma, B. (2021). Mass Spectrometry Provides a Highly Sensitive Noninvasive Means of Sequencing and Tracking M-Protein in the Blood of Multiple Myeloma Patients. *Journal of Proteome Research*, 20(8), 4176-4185. <https://doi.org/10.1021/acs.jproteome.0c01022>

- **Clinical Cancer Research**

Liyasova, M. and al. (2021). A Personalized Mass Spectrometry–Based Assay to Monitor M-Protein in Patients with Multiple Myeloma (EasyM). *Clinical Cancer Research*, 27(18), 5028-5037. <https://doi.org/10.1158/1078-0432.ccr-21-0649>