

2022

Catalog

promise
ADVANCED PROTEOMICS

DIGESTIF CONTROL

TO OPTIMIZE DIGESTION PROCESS AND LC-MS ANALYSES

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

www.promise-proteomics.com | contact@promise-proteomics.com

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 designed by Promise Proteomics.

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

Why use DIGESTIF ?

Digestif is a two-in-one quality control reagent used to check both digestion quality and efficiency and LC-MS performance during bottom-up proteomic experiments.

Protein digestion quality

- Easy solution that controls and optimizes digestion process
- Can be spiked and used in all biological samples

LC-MS performance

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

With DIGESTIF, you can

Optimize digestion process

Standardize sample preparation steps

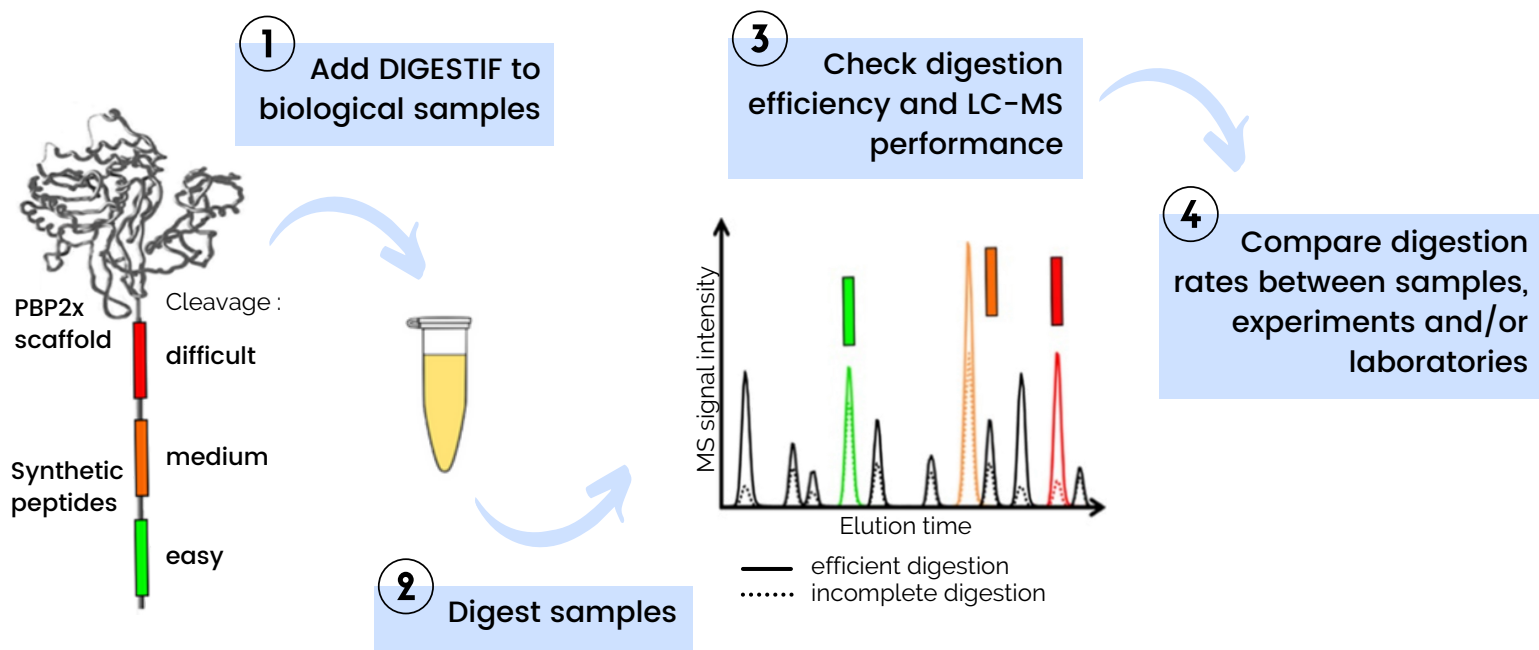
Easily create LC-MS methods

Monitor retention times

For any further information or to request a quote :
orders@promise-proteomics.com



How to use it ?



References

- **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>

Available in labeled ⓘ
and unlabeled ⓘ forms



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