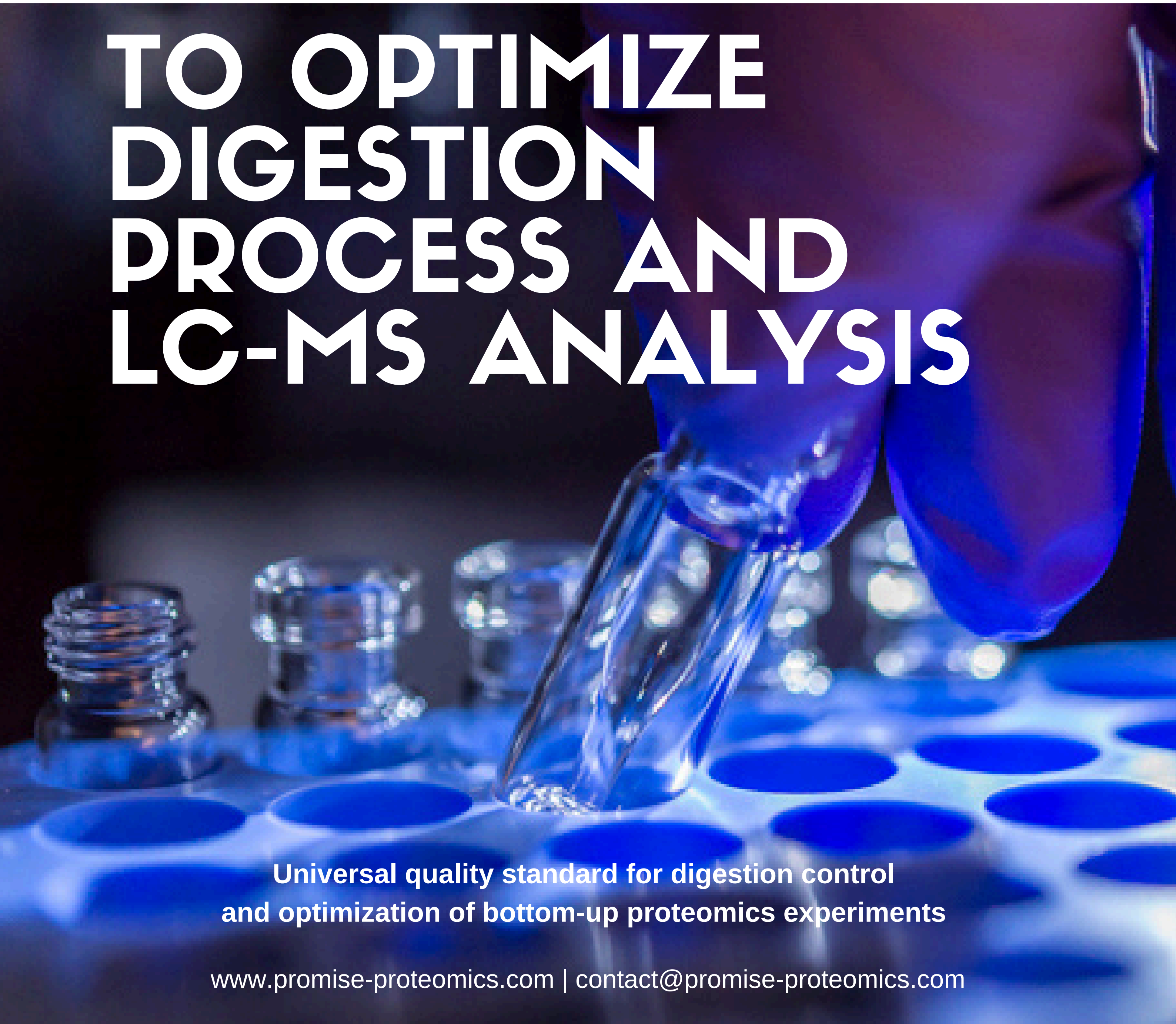
2026

Catalog

promise
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

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 and **resulting from the collaboration between Biognosys, Promise Proteomics and academic teams**[1]**.**

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 perfomances 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:

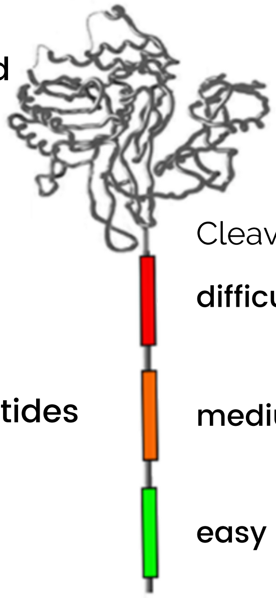
- Check and optimize digestion process
- Standardize sample preparation steps
- Easily set-up LC-MS methods
- Monitor retention times

1. 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

How to use it ?

Available in **labelled**
and **unlabelled** presentations

DIGESTIF



PBP2x scaffold

iRT peptides

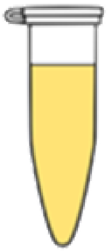
Cleavage :

difficult

medium

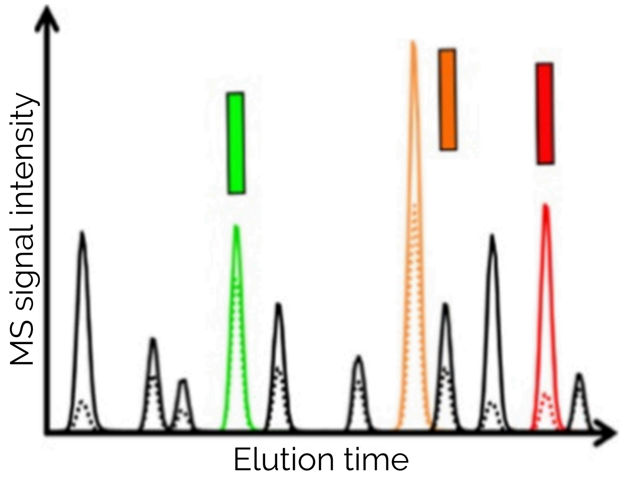
easy

① Add DIGESTIF to biological samples



② Digest samples

③ Check digestion efficiency and LC-MS performance



— efficient digestion
······ incomplete digestion

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

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