2022

Catalog

promise

ADVANCED PROTEOMICS

SIL-PROTEINS

FOR TARGETED LC-MS QUANTIFICATION

The gold standard for robust and reliable quantitative LC-MS workflow

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

SIL-PROTEINS

Promise Proteomics is a pioneer and expert in mass spectrometry-based quantification methods development and in bioproduction of Stable Isotope Labelled (SIL) proteins

Why using our SIL-Protein ?

Our SIL-proteins are the gold standard for quantitative LC-MS.

SIL-Proteins correct bias occuring during the preparation and analytical workflow and due to losses, incomplete digestion, adsorption, proteolysis... With SIL-Proteins, the accuracy and reproducibility of your quantification data is improved.

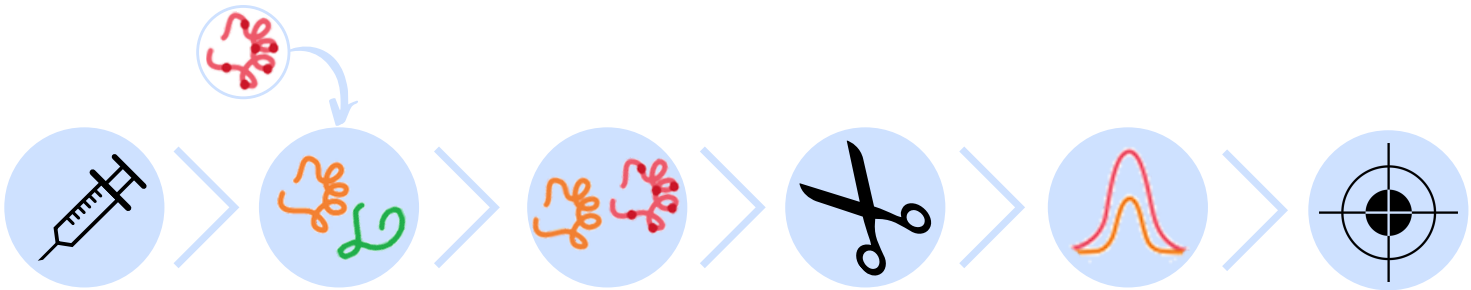
This product is useful for :

- Bioanalysis pharmacokinetics studies (clinical & nonclinical),
- Research and Discovery/pre-clinical/clinical drug development
- Biomarker's quantification

Characteristics

- **Full length recombinant proteins**
- **Identical to the protein of interest,** same sequence as native protein
- **High isotopic incorporation, stability and purity**
- **Uniform or specific labelling,** 13C,15N isotope
- **Unlabelled option**

How to use it ?



Unlike the use of SIL-peptides, Promise's SIL-proteins are processed along with the target analytes throughout the pre-analytical and LC-MS workflow.

OFF-THE-SHELF PRODUCTS

SIL-Proteins* are available to support your innovative and ambitious studies

28 proteins

Human Proteins	Unlabelled	Labelled
Neuroscience/Psychiatric diseases biomarkers		
Apolipoprotein E3	ℹ	U15N ℹ
Neurofilament	ℹ	(Arg,Lys) 13C15N ℹ
Synuclein alpha	ℹ	(Arg,Lys) 13C15N ℹ
Synuclein beta		U15N ℹ
Synuclein gamma		U15N ℹ
Tau 441	ℹ	(Arg,Lys) 13C15N ℹ
Tau 352		U15N ℹ
Cardiovascular disease biomarkers		
Apolipoprotein A1	ℹ	U15N ℹ
Carboxypeptidase B2		(Arg,Lys) 13C15N ℹ
Clusterin protein		(Arg,Lys) 13C15N ℹ
NT-proBNP	ℹ	U15N ℹ
Troponin I		U15N ℹ
Metabolic biomarkers		
Albumin		U15N ℹ
Cystatin C	ℹ	U15N ℹ
Erythropoietin		(Arg,Lys) 13C15N ℹ
Growth hormone 22	ℹ	U15N ℹ
Vitamin D binding Protein		(Arg,Lys) 13C15N ℹ
Cancer biomarkers		
Alpha Feto Protein		(Arg,Lys) 13C15N ℹ
Choriogonadotropin		(Arg,Lys) 13C15N ℹ
KRAS 2A	ℹ	U15N ℹ
KRAS 2B G12C mutant	ℹ	(Arg,Lys) 13C15N ℹ
KRAS 2B G12C/C118A mutant	ℹ	
KRAS 2B 12C/C51S/C80L/C118S	ℹ	
KRAS 2B G12D mutant		(Arg,Lys) 13C15N ℹ
KRAS 2B G13C mutant		(Arg,Lys) 13C15N ℹ
KRAS 2B G13D mutant		(Arg,Lys) 13C15N ℹ
NRAS	ℹ	U15N ℹ
Sepsis biomarker		
Procalcitonin	ℹ	U15N ℹ

**for Research Use Only*

Your protein of interest is not listed ?

For 10 years with more than 150 proteins produced, Promise Proteomics offers custom bioproduction options. Contact us for further information.

bsi ISO 9001 Quality Management CERTIFIED

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

REFERENCES

Publications citing our Stable Isotope Labelled Proteins and endorsing their quality and suitability for quantitative LC-MS work

References using our proteins

- **Clinical Cancer Research**
  Wheeler, J. and al. (2022). Quantitation of thrombin-activatable fibrinolysis inhibitor in human plasma by isotope dilution mass spectrometry. Analytical Biochemistry. https://doi.org/10.1016/j.ab.2021.114413
- **National Institute for Biological Standards and Control**
  Liyasova, M. and al. (2021). A Personalized Mass Spectrometry–Based Assay to Monitor M-Protein in Patients with Multiple Myeloma (EasyM). https://doi.org/10.1158/1078-0432.ccr-21-0649
- **Janssen Pharmaceutica**
  Bijttebier, S. and al. (2021). Development of immunoprecipitation – two-dimensional liquid chromatography – mass spectrometry methodology as biomarker read-out to quantify phosphorylated tau in cerebrospinal fluid from Alzheimer disease patients. https://doi.org/10.1016/j.chroma.2021.462299
- **Rapid Novor**
  McDonald, Z. and al. (2021). Mass Spectrometry Provides a Highly Sensitive Noninvasive Means of Sequencing and Tracking M-Protein in the Blood of Multiple Myeloma Patients. https://doi.org/10.1021/acs.jproteome.0c01022
- **Merck**
  Lassman, M. E. and al. (2021). Experimental Medicine Study to Measure Immune Checkpoint Receptors PD-1 and GITR Turnover Rates In Vivo in Humans. https://doi.org/10.1002/cpt.2129
- **Merck**
  Vasicek, L. A. and al. (2019). Direct quantitation of therapeutic antibodies for pharmacokinetic studies using immuno-purification and intact mass analysis. Bioanalysis, 11(3), 203-213. https://doi.org/10.4155/bio-2018-0240
- **University Medical Center Utrecht**
  el Amrani, M. and al (2019). Quantification of neutralizing anti-drug antibodies and their neutralizing capacity using competitive displacement and tandem mass spectrometry : Infliximab as proof of principle. Journal of Translational Autoimmunity, 1, 100004. https://doi.org/10.1016/j.jtauto.2019.100004
- **National Institute of Standards and Technology**
  Schneck, N. A., and al. (2018). Quantification of cardiac troponin I in human plasma by immunoaffinity enrichment and targeted mass spectrometry. Analytical and Bioanalytical Chemistry, 410(11), 2805-2813. https://doi.org/10.1007/s00216-018-0960-7
- **Hospices Civils de Lyon**
  Millet, A. and al. (2019). Determination of Cetuximab in Plasma by Liquid Chromatography–High-Resolution Mass Spectrometry Orbitrap With a Stable Labeled 13C,15N-Cetuximab Internal Standard. Therapeutic Drug Monitoring, 41(4), 467-475. https://doi.org/10.1097/ftd.0000000000000613
- **University Hospital Grenoble-Alpes**
  Jourdil, J. F. and al. (2018). Simultaneous Quantification of Adalimumab and Infliximab in Human Plasma by Liquid Chromatography–Tandem Mass Spectrometry. Therapeutic Drug Monitoring, 40(4), 417-424. https://doi.org/10.1097/ftd.0000000000000514
- **Wellspring Biosciences**
  Hansen, R. and al. (2018). An Internally Controlled Quantitative Target Occupancy Assay for Covalent Inhibitors. Scientific Reports, 8(1). https://doi.org/10.1038/s41598-018-32683-w
- **Wellspring Biosciences**
  Janes, M. R. and al. (2018). Targeting KRAS Mutant Cancers with a Covalent G12C-Specific Inhibitor. Cell, 172(3), 578–589.e17. https://doi.org/10.1016/j.cell.2018.01.006

- **Merck**
  Vasicek, L. A. and al. (2017). Quantitation of a Therapeutic Antibody in Serum Using Intact Sequential Affinity Capture, Trypsin Digestion, and LC-MS/MS. Analytical Chemistry, 90(1), 866-871. https://doi.org/10.1021/acs.analchem.7b03716
- **University Hospital Grenoble-Alpes**
  Maes, P. and al. (2017). Introducing plasma/serum glycodepletion for the targeted proteomics analysis of cytolysis biomarkers. Talanta, 170, 473-480. https://doi.org/10.1016/j.talanta.2017.04.042
- **University Hospital Grenoble-Alpes**
  Gilquin, B. and al. (2017). Multiplex and accurate quantification of acute kidney injury biomarker candidates in urine using Protein Standard Absolute Quantification (PSAQ) and targeted proteomics. Talanta, 164, 77-84. https://doi.org/10.1016/j.talanta.2016.11.023
- **University Hospital Grenoble-Alpes**
  Jourdil, J. F. and al. (2016). Infliximab quantitation in human plasma by liquid chromatography-tandem mass spectrometry : towards a standardization of the methods ? Analytical and Bioanalytical Chemistry, 409(5), 1195-1205. https://doi.org/10.1007/s00216-016-0045-4
- **University Medical Center Utrecht**
  el Amrani, M. and al. (2016). Quantification of active infliximab in human serum with liquid chromatography–tandem mass spectrometry using a tumor necrosis factor alpha -based pre-analytical sample purification and a stable isotopic labeled infliximab bio-similar as internal standard : A target-based, sensitive and cost-effective method. Journal of Chromatography A, 1454, 42-48. https://doi.org/10.1016/j.chroma.2016.05.070
- **Centre d'Immunologie Pierre Fabre (CIPF)**
  Lebert, D. and al. (2015). Absolute and multiplex quantification of antibodies in serum using PSAQTM standards and LC-MS/MS. Bioanalysis, 7(10), 1237-1251. https://doi.org/10.4155/bio.15.56
- **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
- **Merck**
  McAvoy, T. and al. (2014). Quantification of Tau in Cerebrospinal Fluid by Immunoaffinity Enrichment and Tandem Mass Spectrometry. Clinical Chemistry, 60(4), 683-689. https://doi.org/10.1373/clinchem.2013.216515
- **LGC Group**
  Pritchard, C. and al. (2014). Quantification of Human Growth Hormone in Serum with a Labeled Protein as an Internal Standard : Essential Considerations. Analytical Chemistry, 86(13), 6525-6532. https://doi.org/10.1021/ac501032q
- **LGC Group**
  Pritchard, C. and al. (2013). The Role of Ion Mobility Spectrometry–Mass Spectrometry in the Analysis of Protein Reference Standards. Analytical Chemistry, 85(15), 7205-7212. https://doi.org/10.1021/ac400927s
- **INSERM**
  Picard, G. and al. (2012). PSAQTM standards for accurate MS-based quantification of proteins : from the concept to biomedical applications. Journal of Mass Spectrometry, 47(10), 1353-1363. https://doi.org/10.1002/jms.3106
- **INSERM**
  Adrait, A. and al. (2012). Development of a Protein Standard Absolute Quantification (PSAQTM) assay for the quantification of Staphylococcus aureus enterotoxin A in serum. Journal of Proteomics, 75(10), 3041-3049. https://doi.org/10.1016/j.jprot.2011.11.031
- **INSERM**
  Huillet, C. and al. (2012). Accurate Quantification of Cardiovascular Biomarkers in Serum Using Protein Standard Absolute Quantification (PSAQTM) and Selected Reaction Monitoring. Molecular & Cellular Proteomics, 11(2), M111.008235. https://doi.org/10.1074/mcp.m111.008235
- **INSERM**
  Lebert, D., Dupuis, A., Garin, J., Bruley, C., & Brun, V. (2011). Production and Use of Stable Isotope-Labeled Proteins for Absolute Quantitative Proteomics. Methods in Molecular Biology, 93-115. https://doi.org/10.1007/978-1-61779-148-2_7