

2023

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 an expert in the development of mass spectrometry-based quantification methods and in bioproduction of Stable Isotope Labelled (SIL) proteins

Why use our SIL-proteins ?

A stable isotope labelled (SIL) form of an analyte protein is widely regarded as the optimal internal standard¹ for absolute quantification of proteins using LC-MS.

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

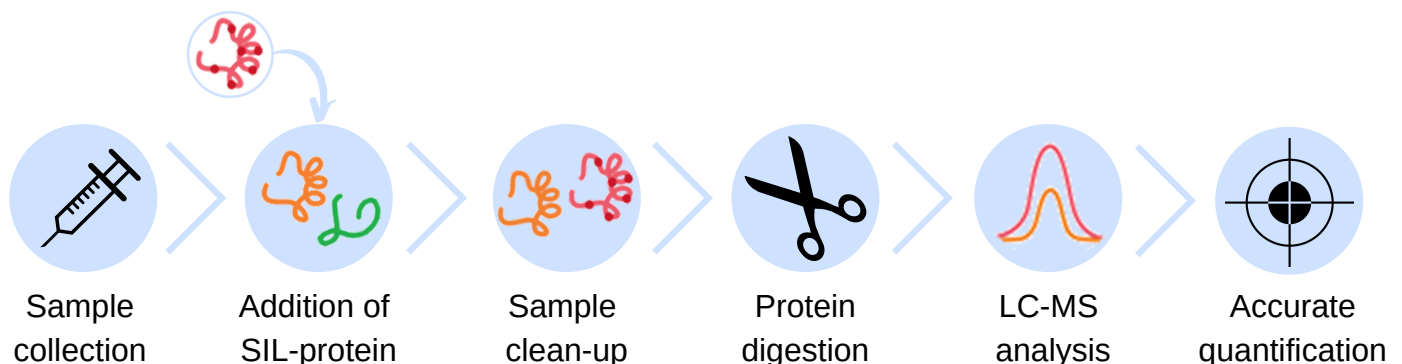
This product is useful for :

- 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 (U¹⁵N) or specific labelling on Arg, Lys residues (¹³C¹⁵N isotope)**
- **Unlabelled option available**

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 thus improving robustness and quality of the quantitative data.

1. Todoroki, K. *et al.* (2020, février). Bioanalytical methods for therapeutic monoclonal antibodies and antibody–drug conjugates : A review of recent advances and future perspectives. *Journal of Pharmaceutical and Biomedical Analysis*, 179, 112991. <https://doi.org/10.1016/j.jpba.2019.112991>

OFF-THE-SHELF PRODUCTS

SIL-proteins* are available to support your studies and clinical trials

HUMAN PROTEINS	LABELLED		UNLABELLED
	LABELLING	REFERENCES	REFERENCES
Neurodegenerative diseases biomarkers			
Apolipoprotein E3	U ¹⁵ N	AP237306	AP237300
Neurofilament	(Arg,Lys) ¹³ C ¹⁵ N	NF169531	NF169530
Synuclein alpha	(Arg,Lys) ¹³ C ¹⁵ N	SY865402	SY865400
Synuclein beta	U ¹⁵ N	SY875286	
Synuclein gamma	U ¹⁵ N	SY925246	
Tau 441	(Arg,Lys) ¹³ C ¹⁵ N	TA928521	TA928520
Tau 352	U ¹⁵ N	TA247576	
Cardiovascular diseases biomarkers			
Apolipoprotein A1	U ¹⁵ N	AP176846	AP176840
Carboxypeptidase B2	(Arg,Lys) ¹³ C ¹⁵ N	CP618731	
Clusterin protein	(Arg,Lys) ¹³ C ¹⁵ N	CL118321	
NT-proBNP	U ¹⁵ N	BN045556	BN045550
Troponin I	U ¹⁵ N	TN946116	
Metabolic biomarkers			
Albumin	U ¹⁵ N	AL170196	
Cystatin C	U ¹⁵ N	CY725606	CY725600
Vitamin D binding Protein	(Arg,Lys) ¹³ C ¹⁵ N	DB128581	
Cancer biomarkers			
Alpha Feto Protein	(Arg,Lys) ¹³ C ¹⁵ N	AF099901	
KRAS 2A	U ¹⁵ N	RA105856	RA105850
KRAS 2B			RA115550
KRAS 2B G12C mutant	(Arg,Lys) ¹³ C ¹⁵ N	RA117051	RA117050
KRAS 2B G12C/C118A mutant			RA119550
KRAS 2B G12C/C51S/C80L/C118S mutant			RA113970
KRAS 2B G12D mutant	(Arg,Lys) ¹³ C ¹⁵ N	RA117061	
KRAS 2B G13C mutant	(Arg,Lys) ¹³ C ¹⁵ N	RA117381	
KRAS 2B G13D mutant	(Arg,Lys) ¹³ C ¹⁵ N	RA117391	
NRAS	U ¹⁵ N	RA985806	RA985806
PD1	(Arg,Lys) ¹³ C ¹⁵ N	Upon request	
PDL1	(Arg,Lys) ¹³ C ¹⁵ N	Upon request	
Peptidic hormones			
Choriogonadotropin	(Arg,Lys) ¹³ C ¹⁵ N	CG115931	
Erythropoietin	(Arg,Lys) ¹³ C ¹⁵ N	EP085791	
Growth hormone 22	U ¹⁵ N	GH596296	GH596290
Sepsis biomarkers			
Procalcitonin	U ¹⁵ N	PC675516	PC675620

*for Research Use Only

Your protein of interest is not listed ?

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



✉ contact@promise-proteomics.com

REFERENCES

Peer reviewed publications using our SIL-proteins

- **Genentech**

Meng, M. *et al.* (2022). Assessment of KRAS G12C Target Engagement by a Covalent Inhibitor in Tumor Biopsies Using an Ultra-Sensitive Immunoaffinity 2D-LC-MS/MS Approach. *Analytical Chemistry*, 94(37), 12927-12933. <https://doi.org/10.1021/acs.analchem.2c03146>

- **Washington University School of Medicine**

Budelier, M. M. *et al.* (2022). A map of neurofilament light chain species in brain and cerebrospinal fluid and alterations in Alzheimer's disease. *Brain Communications*, 4(2). <https://doi.org/10.1093/braincomms/fcac045>

- **AstraZeneca**

Kantae, V. *et al.* (2022). Accelerating the Validation of Endogenous On-Target Engagement and In-cellulo Kinetic Assessment for Covalent Inhibitors of KRASG12C in Early Drug Discovery. *bioRxiv*. <https://doi.org/10.1101/2022.02.17.480880>

- **Janssen**

Bijttebier, S. *et 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>

- **National Institute of Standards and Technology**

Schneck, N. A., *et 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>

- **Wellspring Biosciences**

Hansen, R. *et 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. *et 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>

- **University Hospital Grenoble-Alpes**

Maes, P. *et 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. *et 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>

- **Merck**

McAvoy, T. *et 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>

- **INSERM**

Lebert, D. *et al.* (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