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 standard[1] for absolute quantification of proteins using LC-MS.

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

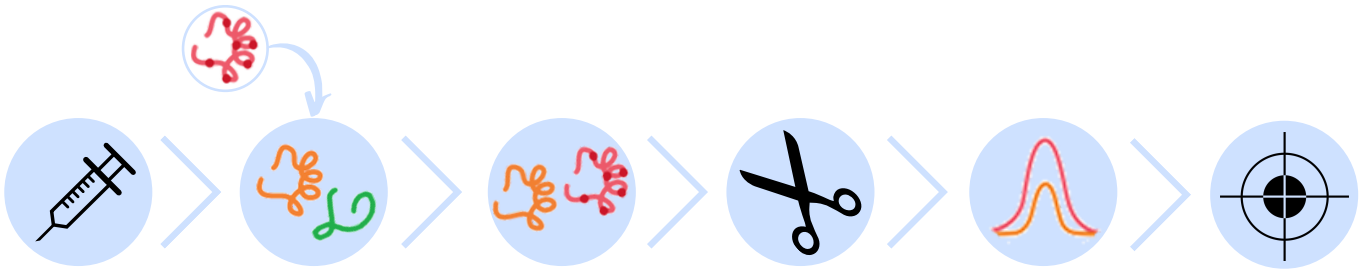
This product is useful for :

- 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** ($U^{15}N$) or **specific labelling on Arg, Lys residues** ($^{13}C^{15}N$ isotope)
- **Unlabelled option available**

How to use it ?



Unlike the use of SIL-peptides, Promise's SIL-mAbs 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 hormons			
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.

bsi ISO 9001 Quality Management CERTIFIED

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