2026

Catalog

promise

ADVANCED PROTEOMICS

SIL-PROTEINS

FOR TARGETED LC-MS QUANTIFICATION

Improve accuracy across your Mass Spectrometry workflows

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

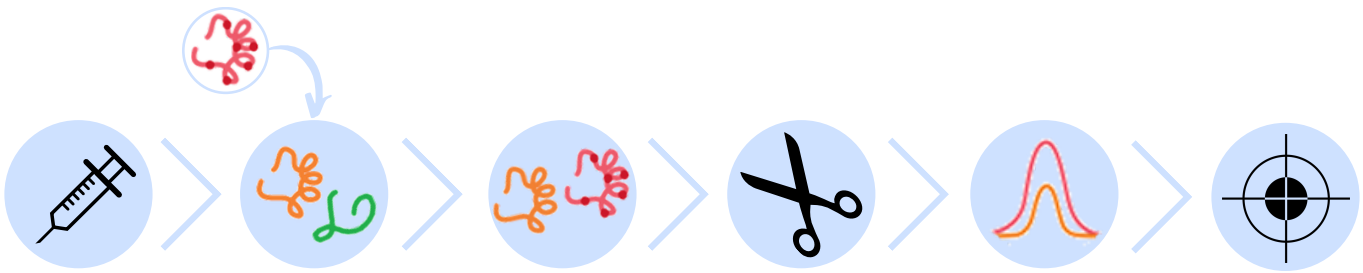
This product is useful for:

- Bioanalysis pharmacokinetics studies (clinical & non-clinical),
- Research & Discovery as well as pre-clinical & clinical Drug Development
- Biomarker's quantification

Characteristics

- **Full length recombinant proteins**
- **Identical to the protein of interest,** same sequence as the 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 our solutions?



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. Faria, M., & Halquist, M. S. (2018). Internal standards for absolute quantification of large molecules (Proteins) from biological matrices by LC-MS/MS. In InTech eBooks. https://doi.org/10.5772/intechopen.75569

OFF-THE-SHELF PRODUCTS

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

Your protein of interest is not listed? Please contact our experts for custom bioproduction.

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
Neurofilament	U^{15}N	NF169536	NF169530
Synuclein alpha	(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	
GFAP	U^{15}N	GF128226	GF128220
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	
HRAS	(Arg,Lys)^{13}C^{15}N	RA125711	*upon request*
KRAS 2A	U^{15}N	RA105856	RA105850
KRAS 2B	(Arg,Lys)^{13}C^{15}N	RA145561	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 G12R mutant	(Arg,Lys)^{13}C^{15}N	RA147211	*upon request*
KRAS 2B G12V mutant	(Arg,Lys)^{13}C^{15}N	RA147251	*upon request*
KRAS 2B G13C mutant	(Arg,Lys)^{13}C^{15}N	RA117381	
KRAS 2B G13D mutant	(Arg,Lys)^{13}C^{15}N	RA117391	
KRAS 2B Q61H mutant	(Arg,Lys)^{13}C^{15}N	RA147701	*upon request*
NRAS	U^{15}N	RA985806	RA985800
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
Growth hormone 22	(Arg,Lys)^{13}C^{15}N	GH596291	GH596290
Sepsis biomarker			
Procalcitonin	U^{15}N	PC675516	PC675620

bsi ISO 9001 Quality Management CERTIFIED

**for Research Use Only*

contact@promise-proteomics.com

REFERENCES

Peer reviewed publications using our SIL-proteins

- **Plateforme de Protéomique Clinique (PPC)**

Hirtz, C. *et al*. (2026). Development of a Novel Liquid Chromatography Coupled to Multiple Reaction Monitoring (LC-MRM) Assay for the Quantification of Neurofilament Light Chain in Cerebrospinal Fluid and Comparison with Ultra-Sensitive Immunoassay: A Step toward Standardization. *Clinical Chemistry,* hvaf180. https://doi.org/10.1515/cclm-2022-1250

- **National Measurement Laboratory**

Goenaga-Infante, H. *et al*. (2025). Neurofilament Light Chain under the Lens of Structural Mass Spectrometry. *ACS Chemical Neuroscience*, 16, 141-151. https://doi.org/10.1021/acschemneuro.4c00526

- **Dementia Research Centre**

Leckey, C. A. *et al*. (2024). CSF Neurofilament Light Chain profiling and quantitation in Neurological Diseases. *Brain Communications*, fcae132. https://doi.org/10.1093/braincomms/fcae132

- **LGC Group**

Zhang, L. *et al*. (2024). A Candidate Reference Measurement Procedure for the Quantification of α-synuclein in Cerebrospinal Fluid Using an SI Traceable Primary Calibrator and Multiple Reaction Monitoring. *Analyst*, 149, 4842-4850. https://doi.org/10.1039/d4an00634h

- **Laboratoire National de Métrologie et d'Essais (LNE)**

Giangrande, C. *et al*. (2023). Development of a candidate reference measurement procedure by ID-LC-MS/MS for total TAU protein measurement in cerebrospinal fluid (CSF). *Clinical Chemistry and Laboratory Medicine*, 61(7), 1235-1244. https://doi.org/10.1515/cclm-2022-1250

- **Janssen**

Bijttebier, S. *et al*. (2023). IP-LC-MSMS enables identification of three TAU O-GLCNAcylation sites as O-GLCNAcase inhibition pharmacodynamic readout in transgenic mice overexpressing human TAU. *Journal of Proteome Research*, 22(4), 1309-1321. https://doi.org/10.1021/acs.jproteome.2c00822

- **Washington University School of Medicine**

Lawler, P. E., *et al*. (2023). Apolipoprotein E o-glycosylation is associated with amyloid plaques and APOE genotype. *Analytical Biochemistry*, 672, 115156. https://doi.org/10.1016/j.ab.2023.115156

- **INSERM**

Pons, M. *et al*. (2023). Absolute quantification of synuclein proteoforms in plasma in patients with synucleinopathies by LC-MRM mass spectrometry. *medRxiv* (Cold Spring Harbor Laboratory). https://doi.org/10.1101/2023.07.17.23292753

- **Merck**

Johns, D. G. *et al*. (2023). Orally bioavailable macrocyclic peptide that inhibits binding of PCSK9 to the low density lipoprotein receptor. *Circulation*, 148(2), 144-158. https://doi.org/10.1161/circulationaha.122.063372

- **University Medical Center Utrecht**

Smeijsters, E. H. E. *et al*. (2023). Optimization of a quantitative Anti-Drug Antibodies against Infliximab assay with the liquid Chromatography-Tandem Mass Spectrometry : A Method Validation Study and Future Perspectives. *Pharmaceutics*, 15(5), 1477. https://doi.org/10.3390/pharmaceutics15051477

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