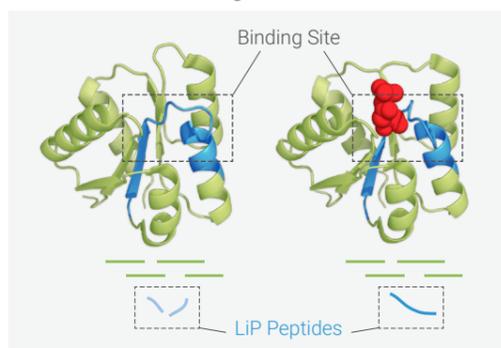


GREATER PRECISION FOR TRANSFORMATIVE DRUG DISCOVERY

Target identification and validation are key challenges in drug discovery.

Limited Proteolysis Mass Spectrometry (LiP-MS) is a robust, reliable way to identify on- and off-target binding effects throughout the proteome, elucidate mechanisms of action and reveal potential toxicities.

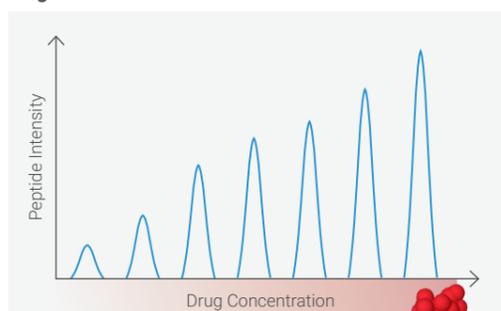
LiP-MS Differentiates the Structural Fingerprints of Bound versus Free Targets



How does LiP-MS work?

Drug-treated and control cell extracts are digested with proteases, creating distinctive peptide fingerprints depending on where and how the drug is bound. Peptides are identified and quantified with high-precision mass spectrometry and comparison of treated and control extracts reveals on- and off-target binding effects throughout the whole proteome.^(1,2)

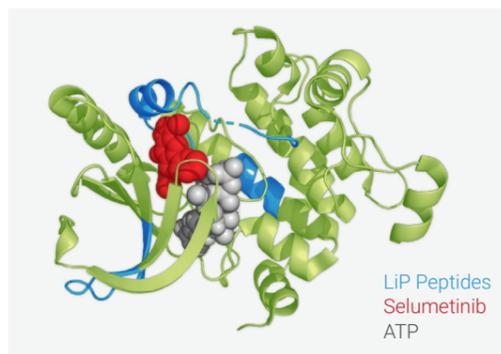
A Streamlined Workflow for Small Molecule Target Identification



A robust pipeline for target identification

Label-free mass spectrometry enables proteome-wide coverage to support target-based and phenotypic drug discovery. LiP-MS offers a unique workflow for target scoring based on dose response curves and machine learning algorithms, resulting in an efficient and robust target deconvolution approach.⁽³⁾

LiP-MS Resolves the Binding Site of a Kinase Inhibitor to its Target



High resolution insights for drug discovery

LiP-MS supports robust target identification through peptide-level resolution of binding across the whole proteome, along with allosteric effects caused by drug-induced structural changes.⁽³⁾ It also highlights potential off-target effects early in the discovery journey, and reveals novel binding sites and mechanisms of action.

1) Feng et al., Nat Biotech 32, 1036 (2014)

2) Piazza et al., Cell 172,358 (2018)

3) Piazza et al., Nat Comms 11, 4200 (2020)



«The LiP technology is a very valuable tool to identify target and off-target of novel compounds, whatever the organism, and to support the process of target deconvolution in research.»

Thomas Knobloch, PhD
Laboratory Manager, Bayer

BENEFITS

Unique

Exclusively licensed to Biognosys, LiP-MS is the only tool to probe structural alterations in proteins with peptide-level resolution.

Insightful

Unbiased whole proteome approach reveals novel mechanisms of action and unanticipated off-target effects.

Versatile

Applicable to complex biological matrices, including a wide variety of cell lines and organisms.

Label-free

Identifies on and off-target drug binding sites without requiring compound labelling.

Efficient

Established robust pipeline provides ranked protein target candidates for rapid target deconvolution and streamlined target validation.

Our LiP-MS Target Deconvolution Service can help you optimize and de-risk your drug discovery journey. Get in touch to find out more.

biognosys.com/limited-proteolysis-services@biognosys.com

