A Method to Identify Actively Degraded Proteins

BioPlatforms

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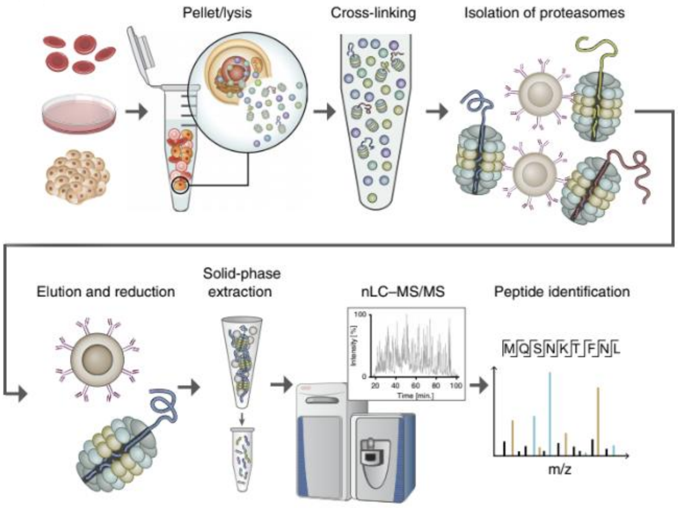
MAPP (Mass Spectrometry Analysis of Proteolytic Peptides) is a groundbreaking technology that isolates and identifies proteins actively degraded by the proteasome, offering an unparalleled and direct view of the "active degradome." This innovative approach provides a sensitive and comprehensive analysis of degradation products, distinguishing it as the only technology capable of examining proteasome-mediated degradation directly. MAPP holds transformative potential in identifying novel therapeutic targets, such as differentially degraded or stabilized proteins under varying conditions or disease states. Its applications span various human diseases, including cancer, autoimmune disorders, infections, and beyond, paving the way for breakthroughs in precision medicine and targeted therapies.



MAPP method workflow

APPLICATIONS

- **Target Discovery**: Identify disease-specific degradation patterns and proteins to uncover therapeutic targets and enhance immune recognition.
- **Biomarker Discovery and precision medicine**: Identify degradation-derived peptides as biomarkers and detect proteasomal "fingerprints" in tissues and fluids to guide personalized treatment in cancer, autoimmunity, neurodegeneration, and infections.
- **Efficacy Studies in PROTAC-Related Research**: stratifying patients, examining downstream effects, and comparing different lead compounds.

DEVELOPMENT STAGE

MAPP demonstrated superior sensitivity over standard mass spectrometry, distinguishing SLE patients from healthy donors via PBMC degradome profiles—an outcome standard methods failed to achieve.

DIFFERENTIATION

- High Sensitivity
- Unbiased Sampling
- Versatile
- Novel Insights

REFERENCES

- Wolf-Levy H et al, Nat Biotech, 2018
- Javitt A et al, Nat Cancer, 2023