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New Cross-Linking Mass Spectrometry Platform: SDASO-L, SDASO-M, and SDASO-S

Tech ID: 33453 / UC Case 2021-763-0

BRIEF DESCRIPTION

An innovative mass spectrometry platform that utilizes sulfoxide-containing MS-cleavable heterobifunctional photoactivated cross-linkers to enhance protein structural elucidation.

APPLICATIONS

- Structural elucidation of protein complexes
- Proteomics and protein research
- Development of new MS-cleavable cross-linker derivatives
- Creation of a comprehensive protein-protein interaction map of cellular systems

ADVANTAGES

- Enhances protein structural elucidation
- Improves the detection and identification of photocross-linked peptides
- Overcomes limitations of residue-specific cross-linkers
- Nonspecific nature allows capturing inaccessible regions

Problems Solved:

- » Difficulty in mapping interaction regions lacking targetable residues
- » Complexity and low abundance of cross-linked products complicating MS analysis and database search

FULL DESCRIPTION

This technology introduces three novel sulfoxide-containing cross-linking reagents: SDASO-L, SDASO-M, and SDASO-S. They aid in identifying protein interaction interfaces that are typically resistant to crosslinking due to a lack of targetable residues. The introduced linkers, SDASO-L (long), -M (medium), and -S (short), are created to facilitate the identification of photocross-linked peptides, thereby enabling photocrosslinking of complex samples.

PATENT STATUS

Country	Type	Number	Dated	Case
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CONTACT

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INVENTORS

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OTHER INFORMATION

CATEGORIZED AS

- » **Biotechnology**
 - » Bioinformatics
 - » Health
 - » Other
 - » Proteomics
- » **Medical**
 - » Diagnostics
 - » Other
 - » Research Tools
 - » Screening
- » **Research Tools**
 - » Bioinformatics

RELATED CASES

2021-763-0

ADDITIONAL TECHNOLOGIES BY THESE INVENTORS

- ▶ [New Collision-Induced Dissociation Cross Linker and Related Software Package for Fast and Accurate Mass Spectrometry Analysis of Proteins](#)
- ▶ [New Sulfoxide-Containing MS-Cleavable Cross-Linker for Proteomics](#)

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