

New Sulfoxide-Containing MS-Cleavable Cross-Linker for Proteomics

Tech ID: 33456 / UC Case 2023-735-0

CONTACT

Richard Y. Tun  
tunr@uci.edu  
tel: 949-824-3586.

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INVENTORS

- » Huang, Lan

» Rychnovsky, Scott D.

OTHER INFORMATION

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## BRIEF DESCRIPTION

An innovative sulfoxide-containing MS-cleavable cross-linker, DBrASO, specifically designed for cysteine residues and aimed at enhancing protein-protein interactions studies and protein complexes architecture analysis.

## APPLICATIONS

- Studies of protein-protein interactions
- Protein complex architecture elucidation
- Complementing existing lysine-reactive cross-linkers in proteomics studies
- Potential utility in quantitative XL-MS studies

## ADVANTAGES

- Specific target on cysteine residues
- Improved specificity at physiological pH
- Non-hydrolyzable bromoacetamide groups
- Production of homogeneous cross-linked products
- Effective for global XL-MS analysis

### Problems Solved:

- » Fills the existing gap in XL-MS analysis
- » Enables unambiguous identification of cross-linking by carrying the same MS-cleavable
- » characteristics as other sulfoxide-containing MS-cleavable cross-linkers
- » Overcomes the issue of hydrolyzability associated with other cross-linkers

## DESCRIPTION

This technology involves the development of DBrASO, a new sulfoxide-containing, MS-cleavable, cysteinereactive cross-linker. It features bromoacetamide groups providing improved specificity, non-hydrolyzability and homogeneous cross-linked products. The product is designed for unambiguous cross-link identification and has been seen to effectively work on simple and complex samples. DBrASO represents a breakthrough product in proteomics studies, offering a comprehensive solution for protein interaction mapping on a systems-level basis.

## PATENT STATUS

Country	Type	Number	Dated	Case
United States Of America	Published Application	20240353418	10/24/2024	2023-735

### ADDITIONAL TECHNOLOGIES BY THESE INVENTORS

- ▶ New Cross-Linking Mass Spectrometry Platform: SDASO-L, SDASO-M, and SDASO-S
- ▶ New Collision-Induced Dissociation Cross Linker and Related Software Package for Fast and Accurate Mass Spectrometry Analysis of Proteins

