Innovation and Commercialization

UNIVERSITY OF TEXAS ARLINGTON

Dual MS-Based Cleavable Cross-Linker to Identify and Analyze Protein Interaction Networks

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TECHNOLOGY NEED

Chemical cross-linking and mass spectrometry (MS) is now widely being used for large-scale protein to protein interaction analysis. Knowledge of structures of protein complexes is fundamental for understanding protein functions and regulations. Current chemical cross-linking coupled with MS method has been proven challenging in unambiguous identification of cross-linked peptides and cross-linked sites. Furthermore, current biochemical methods are only applicable for strong and stable interaction and are not very efficient in analyzing system-level or cellular level large-scale protein interaction networks. Additionally, traditional cross-linking strategies generate enormous amount of mass spectrometry data making the data analysis extremely difficult. Therefore, design of the effective chemical cross-linker with innovative features and an easy analysis protocol are required for the analysis of protein interaction networks.

INVENTION DESCRIPTION/SOLUTION

UTA researchers have developed a novel cross-linker called dual mass spectrometry-cleavable cross-linking technology (DUCCT) for easy analysis of cross-linked peptides. This method unambiguously detects the low-abundance cross-linked peptides and protein interaction sites from complex mixtures with high confidence by overcoming the challenges of current MS analysis techniques. These cross-linkers have dual mass spectrometry cleavable sites and produces two signature mass spectra of same cross-linked peptides, providing high confidence in identifying sites of interaction. Further tandem mass spectrometry can also give additional confidence on the individual cross-linked peptide sequence. Thus, DUCCT is an unambiguous, sensitive, reliable, feasible and fast identification method.

APPLICATIONS

- Protein structure and/or function determination
- Protein or other biomolecule immobilization
- General biomolecule-biomolecule conjugations
- Data acquisition and analysis technique for protein interaction networks

KEY BENEFITS

- Identification of large-scale protein interactions
- Identification of protein structures in their native biological conditions
- Analysis of highly efficient cross-linked products
- Allow quick screening of interacting partners and provide the details of interacting proteins for further biochemical or molecular biology validations
- DUCCT cross-linker can be constructed with or without enrichment functionality

STAGE OF DEVELOPMENT

Component Validation

INTELLECTUAL PROPERTY STATUS

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