Nov 25, 2020

A New Method for Quantitative Tandem Mass Spectrometry of Protein Ubiquitination Based on Peptide Isobaric Labeling

181830691 [1], G G[2], te[3]

[1]gdf; [2]sfr; [3]fsfs

Other This protocol is published without a DOI.

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ABSTRACT

Protein ubiquitination is a common post-translational modification in organisms, and it participates in many important cellular physiological processes such as the regulation of cell cycle progress, protein degradation and DNA repair. Abnormal protein ubiquitination is closely related to the occurrence and development of many diseases. Qualitative and quantitative analysis of ubiquitination at the proteomic level helps to further understand the process of protein ubiquitination in organisms, and is important for understanding and treating various diseases caused by disorders of the ubiquitination system, especially malignant tumors. significance.

EXTERNAL LINK

https://www.creative-proteomics.com/services/ubiquitination.htm

ATTACHMENTS

A New Method for Quantitative Tandem Mass Spectrometry of Protein Ubiquitination Based on Peptide Isobaric Labeling.docx

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PROTOCOL CITATION

181830691 , G G, te 2020. A New Method for Quantitative Tandem Mass Spectrometry of Protein Ubiquitination Based on Peptide Isobaric Labeling. **protocols.io** https://protocols.io/view/a-new-method-for-quantitative-tandem-mass-spectrom-bp37mqrn

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CREATED

Nov 25, 2020

LAST MODIFIED

Nov 25, 2020

PROTOCOL INTEGER ID

44895

ATTACHMENTS

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