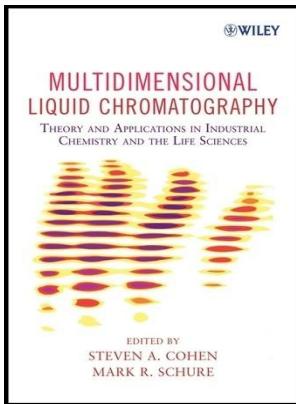


Multidimensional chromatography

Wiley - Multidimensional Chromatography



Description: -

- Education -- Germany -- North Rhine-Westphalia -- Philosophy.

Education -- Germany -- North Rhine-Westphalia -- History -- 19th century.

Holthoff, Fritz, 1915-

Benson, E. F. -- 1867-1940.

Chromatographic analysis Multidimensional chromatography

- Multidimensional chromatography

Notes: Includes bibliographical references and index

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A multidimensional chromatography technology for in

A key objective of global phosphorylation analysis is to obtain an in-depth mapping of low abundance protein phosphorylation in cells; this necessitates the use of suitable separation techniques because of the complexity of the phosphoproteome.

What Is Multidimensional Chromatography? Chromatography Today

Le Bizec, in , 2010 3. Here we developed a multidimensional chromatography technology, combining IMAC, hydrophilic interaction chromatography, and reverse phase LC, for phosphopeptide purification and fractionation.

What Is Multidimensional Chromatography? Chromatography Today

However, by combining two different chromatographic separations stages, which have different selectivities for the desired analytes, these mixtures can be more effectively broken down. Using an off-line configuration combining weak ion-exchange chromatography using a packed column format and a 50 mm × 1 mm i.

Multi

Additionally, the adaptation of the existing algorithms and the development of new data handling tools capable of dealing with such complex data should continue as the existing techniques, for instance the warping approaches, are unable to provide satisfactory, automated results and remain time-consuming. Comparison of the RP-HPLC profile and phosphopeptide identification from three adjacent HILIC fractions. Protein phosphorylation is a post-translational modification widely used to regulate cellular responses.

Multi

Many of these groups are of particular concern because they can cause severe damage to human health e. This led to the identification of 8764 unique phosphopeptides from 2278 proteins.

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