

研究论文

## 磺化修饰结合离子交换色谱和生物质谱富集鉴定含组氨酸肽段

曹冬1, 2, 周春喜2, 张养军2, 韩春光2, 邓玉林1, 钱小红2\*

1.北京理工大学, 北京 100081; 2.北京蛋白质组研究中心 蛋白质组学国家重点实验室 北京放射与辐射医学研究所, 北京 102206

收稿日期 2008-11-3 修回日期 2009-1-5 网络版发布日期 2009-3-27 接受日期 2009-1-9

**摘要** 通过在肽段的N端引入磺酸基, 从而使含组氨酸的肽段与其他肽段在pH<3.0的条件下产生电荷差异, 建立了一种基于强阳离子交换色谱(SCX)结合生物质谱富集鉴定含组氨酸肽段的方法, 并以含有组氨酸的标准蛋白质为模型, 进行了方法学考察。结果表明, 经N端磺酸化后, 含组氨酸的肽段能有效地被阳离子交换色谱富集, 且在肽的N端引入磺酸基促进了肽的裂解, 使之产生简单而信息丰富的二级质谱图, 从而得到完美的质谱鉴定结果。这说明磺化修饰结合强阳离子交换色谱用于含组氨酸肽段的富集鉴定是可行的, 且具有在蛋白质组研究中的应用的潜力。

**关键词** [强阳离子交换色谱](#) [基质辅助激光解吸电离飞行时间串联质谱](#) [磺化修饰](#) [富集](#) [鉴定](#) [组氨酸标签肽](#)

## Sulfonation modification-assisted enrichment and identification of histidine-containing peptides by strong cation exchange chromatography and mass spectrometry

CAO Dong<sup>1,2</sup>, ZHOU Chunxi<sup>2</sup>, ZHANG Yangjun<sup>2</sup>, HAN Chunguang<sup>2</sup>, DENG Yulin<sup>1</sup>, \*

1.Beijing Institute of Technology, Beijing 100081, China; 2.State Key Laboratory of Proteomics, Beijing Proteome Research Center, Beijing Institute of Radiation Medicine, Beijing 102206, China

### Abstract

By the sulfonation at the N-terminal of peptides, the charge state of histidine-containing peptides is different from that of other peptides in pH<3.0 solution. Based on this difference, a new method was developed to isolate and identify sulfonated histidine-containing peptides from tryptic digest of proteins by strong cation exchange (SCX) chromatography and matrix-assisted laser desorption/ionization tandem time-of-flight mass spectrometry (MALDI-TOF MS/MS). Using the standard proteins containing histidines as the model, the methodology was evaluated. The results show that sulfonated histidine-containing peptides were efficiently enriched by SCX, and the N-terminal sulfonation of the peptides simplifies the interpretation of the acquired mass spectra and facilitates the sequencing of histidine-containing peptides by producing consecutive and predominant ions in positive mode MS<sup>2</sup> spectra, which is thought to be the result of the charge neutralization of b ions by the N-terminal sulfonic acid group. The discrimination of b ions and y ions can greatly enhance the confidence in peptide and subsequent protein identification. It is feasible to isolate and enrich the histidine-containing peptides by using this method which has the potential applications in proteomics.

**Key words** [strong cation exchange chromatography \(SCX\)](#) [matrix-assisted laser desorption/ionization tandem time-of-flight mass spectrometry \(MALDI-TOF MS/MS\)](#) [sulfonation modification](#) [enrichment](#) [identification](#) [histidine-containing peptides](#)

DOI:

通讯作者 钱小红 [qianxh@nic.bmi.ac.cn](mailto:qianxh@nic.bmi.ac.cn)

### 扩展功能

#### 本文信息

▶ [Supporting info](#)

▶ [PDF\(691KB\)](#)

▶ [\[HTML全文\]\(0KB\)](#)

▶ [参考文献](#)

#### 服务与反馈

▶ [把本文推荐给朋友](#)

▶ [加入我的书架](#)

▶ [加入引用管理器](#)

▶ [复制索引](#)

▶ [Email Alert](#)

#### 相关信息

▶ [本刊中 包含“强阳离子交换色谱”的 相关文章](#)

▶ [本文作者相关文章](#)

- [曹冬](#)
- [周春喜](#)
- [张养军](#)
- [韩春光](#)
- [邓玉林](#)
- [钱小红](#)