

## 基于液相色谱-质谱联用系统的系统性红斑狼疮患者血浆代谢组学分析

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## Plasma metabonomics study of systemic lupus erythematosus based on liquid chromatography-mass spectrometry

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摘要	参考文献	相关文章
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**摘要** 应用快速分离液相色谱-串联四极杆飞行时间质谱(RRLC-Q-TOF/MS)系统对系统性红斑狼疮(SLE)患者血浆样本进行代谢指纹图谱的分析。分别应用监督模式识别方法正交信号校正结合偏最小二乘法-判别分析(OSC-PLS-DA)对代谢组数据进行处理,结果显示SLE患者与健康人群对照组的代谢指纹存在明显差异;进一步从SLE患者血清代谢图谱中筛选出10个对分类有显著贡献的离子,定性鉴定出7种代谢标志物,发现SLE患者存在异常的氨基酸、磷脂和卟啉的代谢状态。本研究可为SLE的监测和诊断以及SLE发病的分子基础研究提供科学依据。

**关键词:** 快速分离液相色谱-串联四极杆飞行时间质谱 正交变换偏最小二乘-判别分析 系统性红斑狼疮 代谢组学

**Abstract:** A rapid resolution liquid chromatography coupled with quadrupole-time of flight mass spectrometry method (RRLC-Q-TOF/MS) was used to analyze metabolic fingerprint of the plasma samples from systemic lupus erythematosus (SLE) patients. Supervised pattern recognition methods combined with orthogonal signal correction partial least square-discriminate analysis (OSC-PLS-DA) were used to process the metabolic data. A nice distinction between SLE patients and healthy control group was observed. Further, ten ions, which had a significant contribution to classification, had been selected from metabolic profiles of SLE patients. The ten ions were identified and belong to seven metabolic biomarkers. It was shown that there were abnormal metabolisms of amino acids, phospholipids and porphyrin in SLE patients. It provided a scientific basis for the monitoring and diagnosis of SLE. These results will benefit the early intervention and treatment of SLE and the research of the mechanism of pathogenesis.

**Keywords:** rapid resolution liquid chromatography coupled with quadrupole-time of flight mass spectrometry (RRLC-Q-TOF/MS) partial least square-discriminate analysis (PLS-DA) systemic lupus erythematosus metabonomics

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