

# Integrated sample preparation for automated and sensitive proteomic profiling

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## Gold statement

- Fully automated proteomics sample preparation platform
- Integrated sample preparation technologies for spatial proteomics
- Applications for understanding cell-type proteome in tumor microenvironment

## Introduction

Mass spectrometry-based proteomics is the method of choice for high-throughput identification and quantification of proteins on a global level. Generally, relatively large amounts of biological materials are needed for the proteomics analysis. Unfortunately, in many instances for biomedical research, the amount of starting material is limited, which make the proteomics analysis much more challenging. Furthermore, current proteomic analysis based on bulk tissue sample often loss spatial resolution, especially for tumor samples with cell heterogeneity.

## Body

Recently, we developed a Simple and Integrated Spintip-based PROteomics Technology (termed SISPROT), for identifying and quantifying trace amount of proteins from various biological samples. All requisite steps for proteomic sample preparation, including reduction, alkylation, digestion, desalting and 1D or 2D fractionation, are fully integrated in a simple spintip device. The sample loss is significantly reduced, and label-free quantification performance is greatly improved. In this talk, I will firstly present our latest development of the SISPROT technology with fully automated operation on a standard capillary electrophoresis instrument. In the second part of my talk, I will present our recent optimization of the SISPROT protocol for studying cell type proteome in tumor microenvironment directly from clinical tissue samples with spatial resolution.

## Conclusion

These new development of the SISPROT technology provided us new tools for studying various biomedical systems with improved sensitivity and throughput.

## References

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