

Automated Single Cell Isolation for Proteome Analysis

From Cell to Insight

Laser Microdissection for
Precise Spatial Proteomics

High-Throughput automated Laser Microdissection

Cancer research benefits from spatial proteomics by revealing tumor heterogeneity, identifying biomarkers, and mapping the tumor microenvironment. This approach analyzes protein distribution within tissues while preserving spatial context, providing deeper insights into disease mechanisms. By understanding how proteins interact in different tumor regions, spatial proteomics helps drive the development of more precise diagnostics and targeted therapies.



Gentle, automated laser microdissection of single cells, followed by precise transfer to a 96-well plate using CellRobot.

Prof. Ruijun Tian's team has developed a groundbreaking method combining laser microdissection (LMD) with ultra-sensitive mass spectrometry, which enables contamination-free proteome analysis at the single cell level, allowing precise differentiation between cancerous and healthy cells in the same microenvironment.



Automated Laser Microdissection

Cell shapes of interest can be defined using separate AI-based imaging analysis software, such as StrataQuest, BIAS and CellDetector and then imported and aligned into the Laser Microdissection (LMD) software. All common data formats, including XML, are supported. For high-throughput applications, cells can be directly isolated into 96-well plates.

For accurate alignment, three reference points are selected from recognisable features of the sample on the whole slide image. After importing the shapes, these reference points are identified on the live image of the LMD system for precise alignment of the cell shapes.



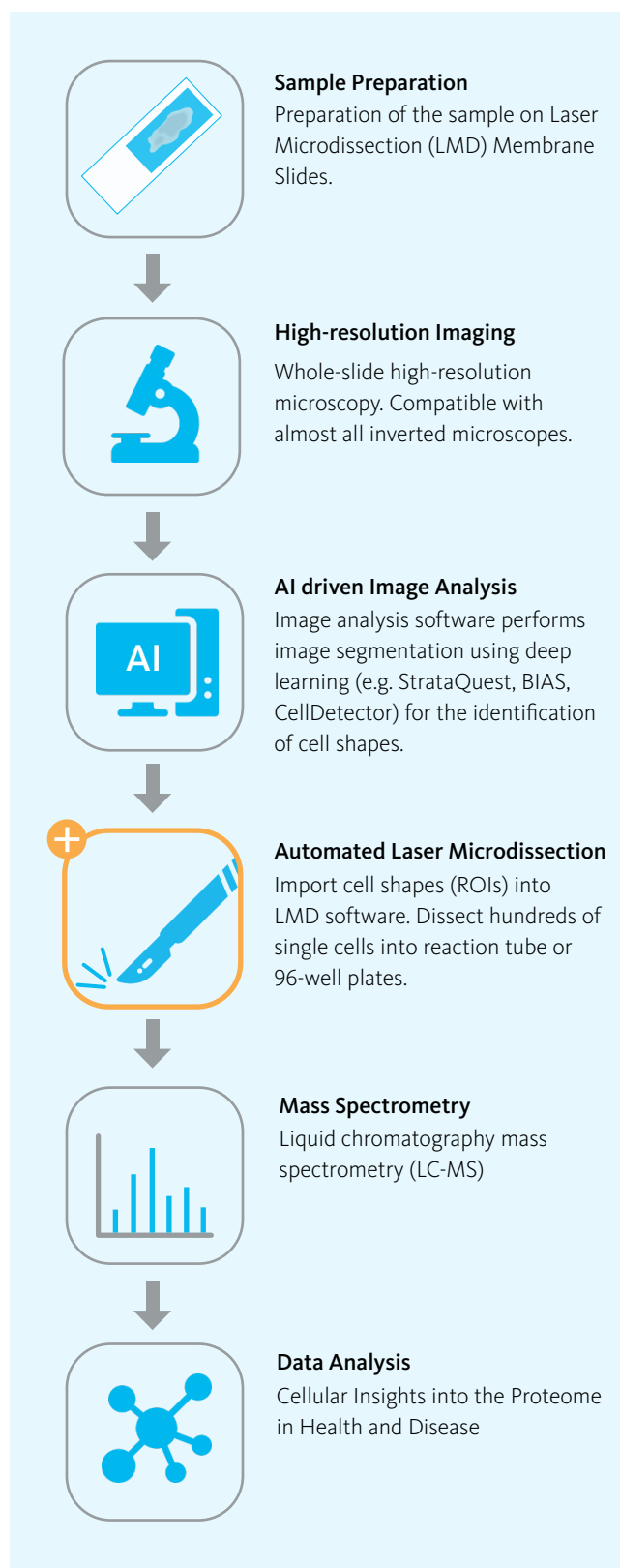
Microscope



Image Alignment



LMD



Demo and
Details