FlashNote

SoloCell: One Cell, One Shot — Unlocking Single Cell Multiomic Insights through MALDI Imaging

Why it matters

Current single-cell methods rely heavily on transcriptomics, often missing the functional phenotype driven by the cell surface and metabolic state. SoloCell fills this gap by simultaneously measuring lipids and released N-glycans (and metabolites and glycogen) from thousands of individual cells in minutes, revealing functionally distinct subpopulations that bulk and conventional single-cell analyses miss. Powered by AI automation and MALDI Imaging, SoloCell delivers native glycan structures, free from amplification bias and lectin selection artifacts, alongside lipid phenotypes that predict disease response and cellular function. For translational researchers seeking biomarkers and cell therapists hunting rare functional states, SoloCell turns single-cell profiling from a low-throughput bottleneck into a high-volume screening tool.

How it works

Antibodies or lectins selectively capture cells onto a grid of micro-patterned spots created using poly(dimethylsiloxane) (PDMS) stamps, with each spot typically capturing between one and four cells.

Following cell capture, a convolutional neural network, trained to detect single cells, scans the grid, identifies individual cells, and records their coordinates. Then, with adapted MALDI Imaging protocols, lipid imaging followed by N-glycan imaging is performed. Further methodological details can be found in the referenced literature [1].

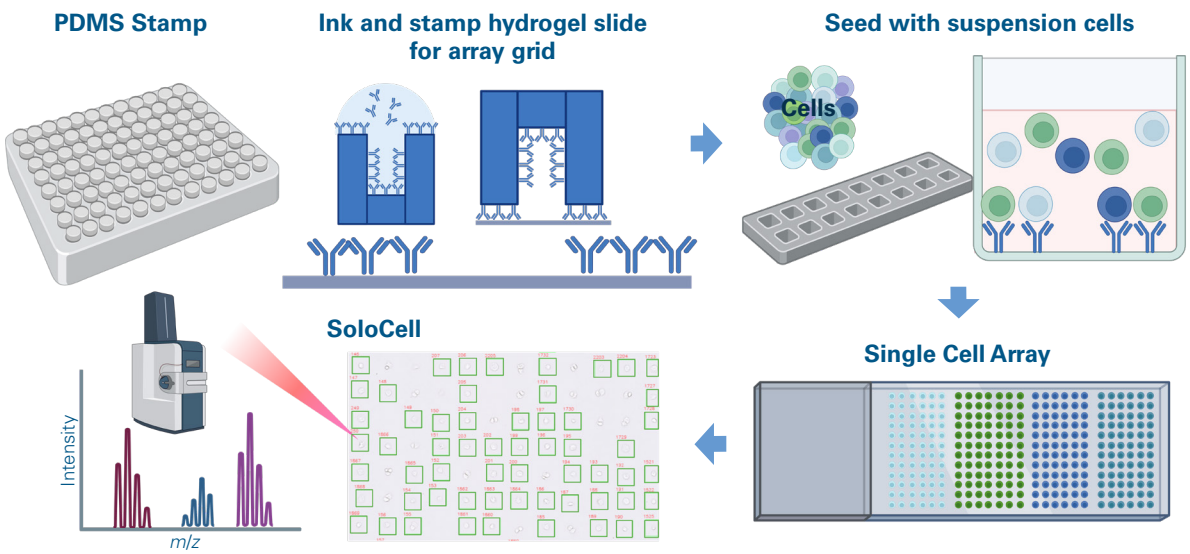

Figure 1. Schematic of the single-cell capture workflow (adapted from Dressmann et. al [1]).

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Outcome

- **Speed and scalability:** A high-throughput method for single-cell analysis using MALDI Imaging with analysis of up to 6 cells per second, or thousands of cells in minutes.
- **Multiomic profiling:** Achieves sequential analysis of lipids and N-glycans from the same cell, linking membrane composition to cell surface identity without the amplification bias of sequencing and the ability to add additional OMIC layers.
- **AI-powered automation:** The custom-developed software uses deep learning to identify and log single-cell coordinates, streamlining data acquisition.
- **Broad applicability:** Compatible with both adherent and nonadherent cells, and adaptable to various capture proteins (e.g., antibodies, lectins).
- **Validated performance:** Demonstrated ability to distinguish between two cell types (Jurkat and 4T1) based on lipid and glycan profiles, with strong correlation to bulk data.

For more information see the original publication "*Single-Cell Multiomic MALDI-MSI Analysis of Lipids and N-Glycans through Affinity Array Capture*" published by Dressman et al. [1].

References

[1] Dressman JW, Bayram MF, Angel PM, Drake RR, Mehta AS (2025). *Single-Cell Multiomic MALDI-MSI Analysis of Lipids and N-Glycans through Affinity Array Capture*. Analytical Chemistry. **97**(24), 12493-12502. https://doi.org/10.1021/acs.analchem.4c06233

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"Our research presents a groundbreaking strategy for single-cell analysis, integrating high-throughput capabilities with multiomic profiling. By overcoming major limitations of current methods, it holds promise for deepening our insights into cellular function and accelerating progress in biomedical research, diagnostics, and therapeutic innovation."

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