Proteomics

Evolution of modern single-cell proteomics

Researchers have been pushing single-cell protein analysis for a long time with techniques such as mass cytometry and single-cell western blotting that rely on targeted markers (e.g., antibodies). With the continued innovation of high-resolution accurate mass (HRAM) Thermo Scientific[™] Orbitrap[™] mass spectrometry, we have moved from analyzing large single cells such as oocytes to small mammalian cells.

As pioneers and innovators in proteomics research, Orbitrap mass spectrometry has led the way to defining the modern era of unbiased single-cell proteomics with the ability not only to analyze in much greater depth per cell (>3000 proteins), but also multiplexing to maximize throughput and sensitivity (>200 cells per day) so that we can truly move away from inferring proteins from mRNA levels.

The future of single-cell proteomics is bright as illustrated with the growing number of publications per year and we look forward to driving innovations in single-cell proteomics that unlock the potential of analyzing large cohorts of targeted protein panels, post-translational modifications and much more.



1. Hughes, AJ., et al. Nature methods 11.7 (2014): 749-755

2. Fisher, Daniel AC., et al. Leukemia 31.9 (2017): 1962–1974

3. Virant-Klun, I., et al. Molecular & Cellular Proteomics 15.8 (2016): 2616-2627 4. Lombard-Banek, C., et al. Angewandte Chemie 128.7 (2016): 2500-2504

Discover more at thermofisher.com/singlecellproteomics

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Year-on-year growth in publications 350 300 250 200 150 100 50

The terms "single-cell protein" and "single-cell proteomics" were used for literature sear

- Technology drives extreme high throughput with modern computational tools
- Methods advance to analyzing large cohorts of targeted protein panels, post-translational modifications, spatial profiling and much more

Future

- Collaborations with biologists, technologists, method developers and data scientists essential to understanding biology at single-cell resolution
- Drive new science and discoveries in health and disease with compilation of tissue atlases such as the Human Cell Atlas

- 5. Zhu, Y., et al. Nature Communications 9.1 (2018): 1–10
- 6. Budnik, B., et al. Genome biology 19.1 (2018): 1–12
- 7. Végvári, Á., et al. Single-Cell Protein Analysis 2022: 113-127
- 8. https://www.cellenion.com/applications/single-cell-proteomics/

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