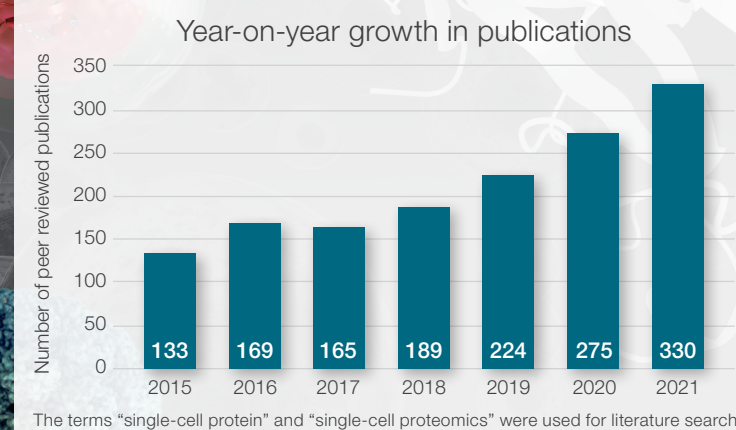


Evolution of modern single-cell proteomics

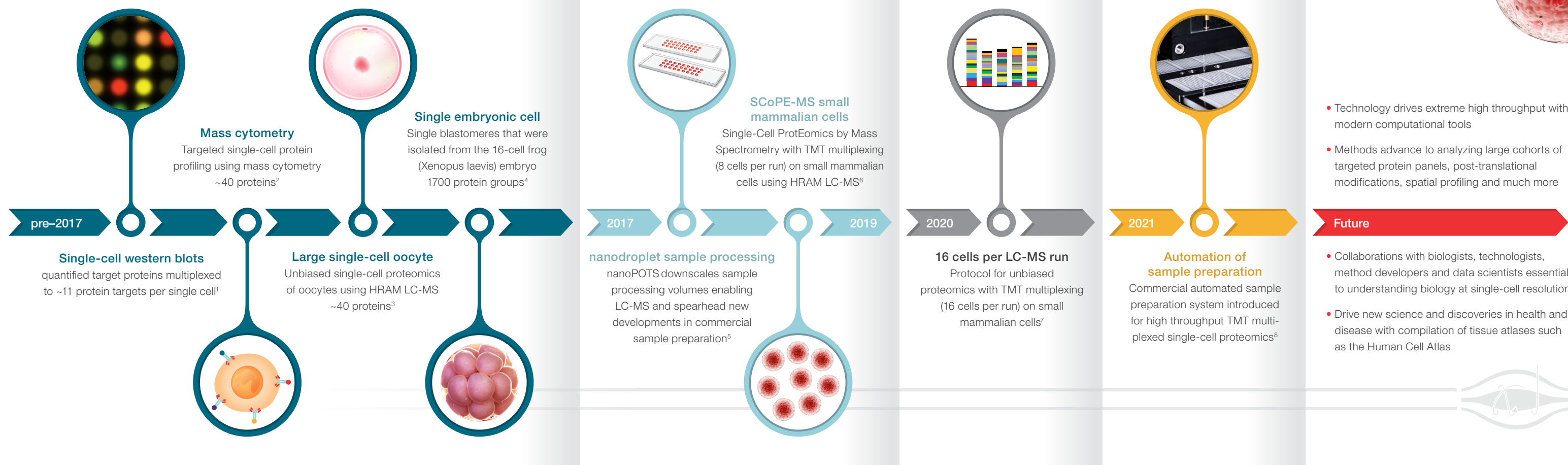
Researchers have been pushing single-cell protein analysis for a long time with techniques such as mass cytometry and single-cell western blotting that rely on targeted markers (e.g., antibodies). With the continued innovation of high-resolution accurate mass (HRAM) Thermo Scientific™ Orbitrap™ mass 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.



A brief chronology



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

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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