

Identify more peptides from your single-cell data

Analyze single-cell and low-input mass spectrometry data with Tesorai Search. Run database searches in your browser, with identification gains demonstrated in NanoPOTS and DISCO benchmarks.

Make more of limited starting material

Tesorai Search uses a pretrained model to score peptide-spectrum matches, with target-decoy false discovery rate control. NanoPOTS and DISCO benchmarks demonstrate additional identifications compared with FragPipe.

Scale your analysis without managing compute

Run single-cell and low-input database searches through your browser. Tesorai handles processing in the cloud, without search software to install or local compute infrastructure to maintain.

HOW IT WORKS

- 01 UPLOAD YOUR DATA**
Add mass spectrometry files and select a sequence database.
- 02 CONFIGURE AND RUN**
Set search parameters and run the search in the cloud.
- 03 REVIEW YOUR RESULTS**
Explore peptide and spectrum identifications.

BENCHMARK RESULTS · TESORAI SEARCH VS. FRAGPIPE

More identifications from the same single-cell spectra

NANOPOTS · ONE-CELL CONDITION

29% more unique peptides

than FragPipe, pooled across 10 one-cell runs.



Unique peptides · Williams et al. NanoPOTS, MCF10A

DISCO · ONE-CELL CONDITION

37% more identified MS2 spectra

than FragPipe, by MS2 identification rate.



MS2 identification rate · Lamanna et al. DISCO

Compared with FragPipe at 1% FDR, with match-between-runs disabled for both tools. NanoPOTS counts are pooled across runs. See benchmark details overleaf.

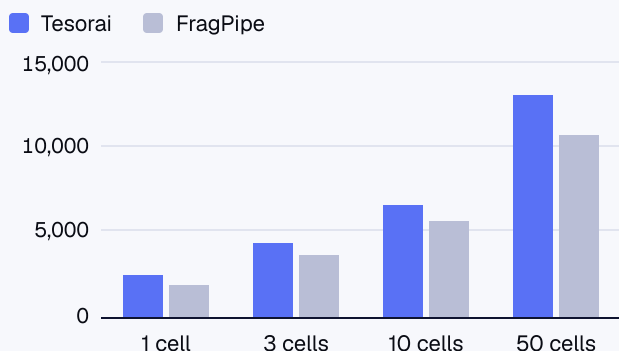
BENCHMARK DETAILS

Gains across inputs and datasets

Reanalysis of two public single-cell datasets, compared with FragPipe at 1% FDR. Match-between-runs was disabled for both tools, so gains reflect identifications from the acquired spectra.

NANOPOTS · WILLIAMS ET AL. [3]

Unique peptides by cells per run

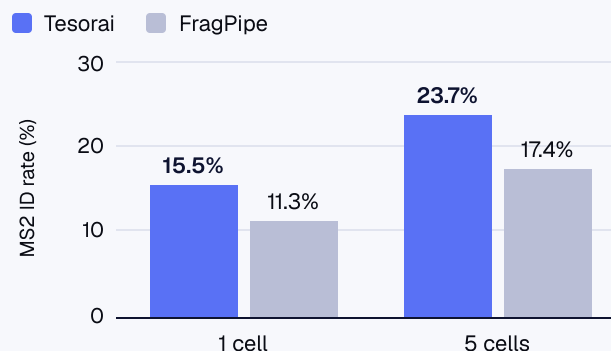


Cells per run	FragPipe	Tesorai	Gain
1	1,910	2,472	+29%
3	3,611	4,301	+19%
10	5,620	6,614	+18%
50	10,720	13,030	+22%

Counts are pooled across runs within each input condition, not per-cell averages. One cell: 10 runs; 3, 10 and 50 cells: 4 runs each.

DISCO · LAMANNA ET AL. [2]

MS2 identification rate



Tesorai also identified more unique peptides: 6,273 vs. 5,713 at one cell and 10,729 vs. 9,598 at five cells.

Three runs per condition. Tesorai counts exclude decoys and non-human contaminants. Gain is relative to FragPipe. [4]

Benchmarks measure peptide and spectrum identification sensitivity, not protein counts. NanoPOTS: MCF10A, MassIVE MSV000085230. DISCO: PRIDE PXD019958, Thermo Q Exactive HF-X. Both searched a human Swiss-Prot database with default Tesorai settings; FragPipe v22.0 used strict trypsin specificity and peptide lengths of 7–63 amino acids. [1]

Try Tesorai on your single-cell dataset

Start an analysis in your browser, or talk with us about your sample type, acquisition method and search setup.

[Start an analysis](#)
[Discuss your workflow](#)
tesorai.com

[1] Burq M, et al. Tesorai Search. *J Mol Biol* (2026), Fig. 2 and supplementary methods and tables. doi:10.1016/j.jmb.2026.169940

[3] Williams SM, et al. Automated coupling of nanodroplet sample preparation with LC-MS for high-throughput single-cell proteomics. *Anal Chem* 92, 10588–10596 (2020). doi:10.1021/acs.analchem.0c01551

[2] Lamanna J, et al. Digital microfluidic isolation of single cells for -Omics. *Nat Commun* 11, 5632 (2020). doi:10.1038/s41467-020-19394-5

[4] Tesorai Search benchmark analysis of DISCO dataset PXD019958. Target identifications exclude decoys and non-human contaminants; MBR disabled for both tools.