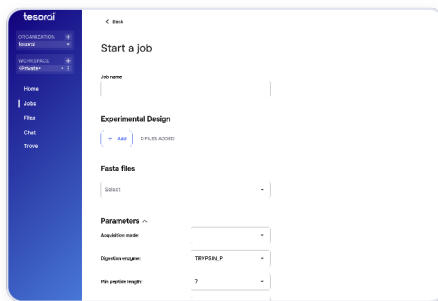


SEARCH · CHAT · TROVE

From raw proteomics data to biological insight

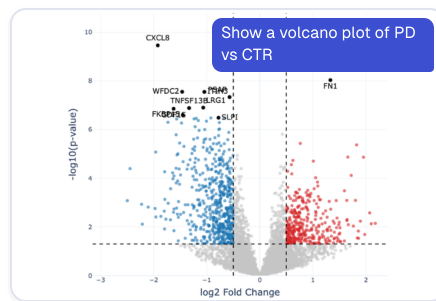
Tesorai brings sensitive mass-spectrometry search, no-code analysis, and public-data exploration into one connected environment.

Search



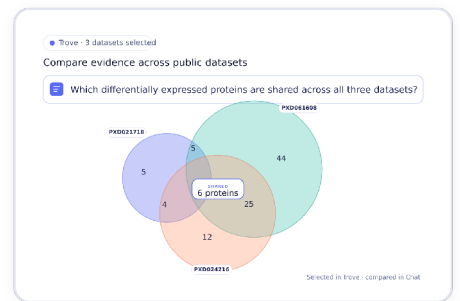
Process raw mass-spectrometry data with sensitive, scalable identification.

Chat



Analyze, visualize, and interpret results through a conversational interface.

Trove



Search thousands of curated public proteomics datasets to extend or validate discoveries.

Raw data

Confident identifications

Analysis & interpretation

Cross-dataset discovery

68% more on average

Peptide identifications than MaxQuant across seven independent benchmark datasets at 1% FDR.²

Up to 10× fewer

False identifications than another leading search engine at the same reported 1% FDR, with comparable sensitivity.³

Sensitivity results from Burq et al.² The false-identification result comes from an independent entrapment analysis with a biotechnology partner and is specific to the evaluated dataset and comparator.³

APPLICATION SPOTLIGHT · UCSF RNA EDITING

Revealing the functional landscape of RNA editing

UCSF researchers combined deep proteomics with Tesorai Search to identify wild-type and RNA-edited peptide sequences across multiple tissues and protease workflows.¹

18×

more protein-verified
RNA-editing sites

Tesorai expanded protein-level evidence from **432 previously reported sites** to **7,998 verified sites** across 2,091 proteins.

10 TB processed in **under 10 hours**. Source: UCSF Quantitative Biosciences Institute · Jack Moen, PhD — "Functional Diversification of the Cephalopod Proteome by RNA Editing" (2025).

Designed for demanding proteomics research

Three connected components take researchers from raw instrument output to biological interpretation, with transparent results at every stage.

Sensitive, scalable search

TESORAI SEARCH

Tesorai Search processes DDA and DIA mass-spectrometry data at scale while maintaining controlled false-discovery rates, identifying 68% more peptides on average than MaxQuant across seven independent benchmark datasets at 1% FDR.²

Analysis through conversation

TESORAI CHAT

Tesorai Chat helps researchers perform quality control, differential analysis, visualization, and biological interpretation using plain-language instructions. Researchers can inspect results, refine analyses, and generate scientific visualizations without building every workflow from code.

Discovery across public data

TESORAI TROVE

Tesorai Trove makes curated public proteomics datasets easier to find and explore. Researchers can locate relevant experiments, investigate biological patterns, and connect new results with existing evidence.

Explore proteomics with Tesorai

See how Tesorai can help you move from raw mass spectrometry data to analysis, interpretation, and discovery.

Explore the platform

Try Tesorai

tesorai.com



References — 1. UCSF Quantitative Biosciences Institute, Jack Moen, PhD, "Functional Diversification of the Cephalopod Proteome by RNA Editing" (2025), tesorai.com/resources/revealing-the-functional-landscape-of-rna-editing · 2. Burq M, Stepec D, Restrepo J, et al. Tesorai Search: Cloud-based Database Search Engine Boosts Identifications for Mass Spectrometry Proteomics With a Pretrained Peptide-spectrum Deep-learning Model. *Journal of Molecular Biology*. 2026;169940. doi:10.1016/j.jmb.2026.169940. · 3. Tesorai, independent entrapment-based validation analysis, tesorai.com/solutions/tesorai-search.