

From raw HLA-IP data to candidate antigens in hours, not weeks

Search large immunopeptidomics datasets with accessible, scalable workflows built for discovery across standard and custom protein databases.

01 CREATE A FIT-FOR-PURPOSE FASTA

Create or use a custom protein sequence database relevant to the biological question.

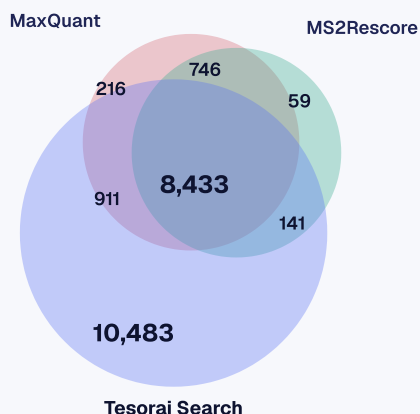
02 SEARCH RAW MASS SPECTROMETRY DATA

Configure and run large HLA-IP searches without assembling or managing dedicated compute infrastructure.

03 REVIEW AND INTERPRET RESULTS

Explore identified peptides, compare conditions, and generate analysis-ready outputs.

GREATER SENSITIVITY AT CONTROLLED FDR



Tesorai Search identified 19,968 peptides in the Neuroblastoma cohort, including 10,483 not recovered by MaxQuant or MS2Rescore.

1% peptide-level FDR — Tesorai Search

5% peptide-level FDR — MaxQuant and MS2Rescore

Supplementary Figure 2 restricts the comparison to high-confidence identifications using Andromeda score >70 and Tesorai score >5. Adapted from Li et al., A pan-cancer atlas of therapeutic T cell targets, bioRxiv, 2025.

CASE STUDY · IMMUNOVERSE

Building a pan-cancer atlas of therapeutic T-cell targets

The ImmunoVerse team used Tesorai to reprocess a large public immunopeptidomics collection, accelerating a workflow that previously required weeks of computation.

2,500+

Raw HLA-IP files processed

< 5 hours

Total analysis time, for a workflow previously requiring weeks



Read the ImmunoVerse user story

~60% more peptides
identified

All validated peptides
recovered

0 incorrect identifications
found during manual review

Results shown are specific to the ImmunoVerse analysis and dataset.

CUSTOM PROTEIN DATABASES

Expand the search space, not the turnaround time

Tesorai makes it possible to create and search custom FASTA databases tailored to the biological question, bringing study-specific protein sequences into the same scalable workflow used for large standard-proteome searches.



In the same workflow

- Create or use a study-specific FASTA
- Configure immunopeptidomics-appropriate search parameters
- Move directly into downstream review and analysis
- Search expanded protein sequence databases
- Process large raw-data collections in the cloud

ADDITIONAL VALIDATION · SALOMONIS LAB

~4 TB

Of raw data

~4,000

Files

~7 hours

Total compute time

~100,000Proteins in custom FASTAs
Approximately 4× the canonical proteome

"We extensively leveraged Tesorai to reprocess the public ImmunoVerse immunopeptidomics collection... completing the analysis in approximately 7 hours of total compute time... The superior accuracy of these predictions were reflected in comparison to ours and other prior validation studies."

Nathan Salomonis

Salomonis Lab, Cincinnati Children's Hospital

Explore immunopeptidomics with Tesorai

See how Tesorai can help you search raw HLA-IP data, work with custom FASTAs, and move from spectra to candidate antigens faster.

[Explore the application](#)[Try Tesorai](#)tesorai.com[Explore immunopeptidomics](#)