What We Require

Cell Line	Tissue Sample	Blood Sample
> 10⁷	> 10 mg	2 mL

What We Provide

1. Qualitative results of immunopeptides & corresponding protein information list	2. Predicted immunopeptides ranked by immunogenicity scores
3. Immunopeptide length distribution chart	4. Sequence motifs for HLA alleles
5. QC test results	6. Comprehensive report

QC Western Results

QC:Predicted RT Regression Function

Length Distribution Chart

Motif Analysis

Immunogenicity Ranking

Elispot Validation (optional)

DeepImmu
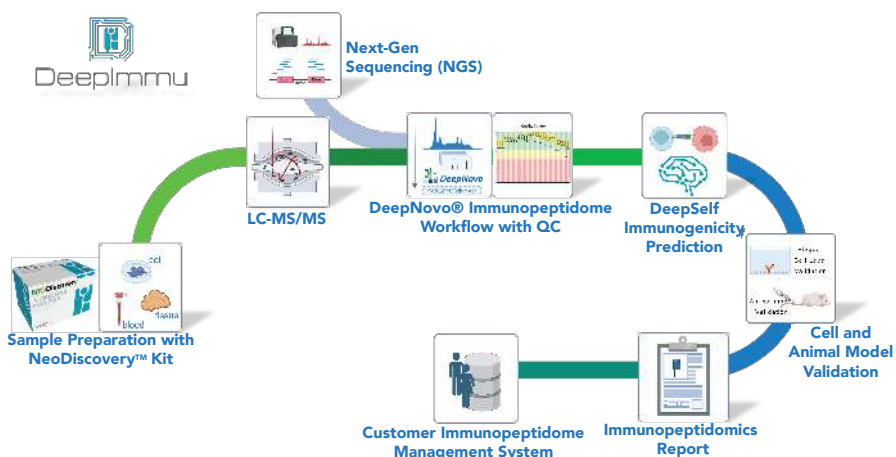
Immunopeptidomics Discovery Service

The display of peptide antigens on cell surfaces by the major histocompatibility complex (MHC) molecules, in humans also known as the human leukocyte antigen (HLA), plays an important role in adaptive immunity through recognition by T cells. Identifying and characterizing antigens displayed specifically on infected cells or tumors is a critical step for the development of immunotherapies and cancer vaccines.
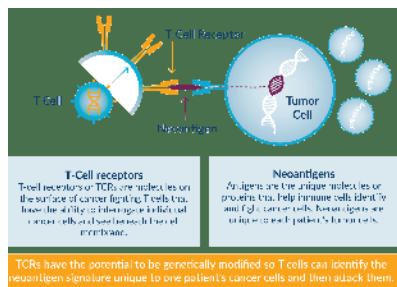
The standard method to do this involves extraction of the these presented peptides, followed by their qualitative and quantitative analysis using high-performance liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS). BSI first reported in 2020 that personalized deep learning of individual immunopeptidome to identify neoantigens for cancer vaccines has greatly improved the efficiency of discovering neoantigens with immunogenicity.

DeepImmu® Immunopeptidomics Discovery Service offers a comprehensive solution from MHC immunopeptide purification, LC-MS/MS acquisition, DeepNovo® algorithm-based sequencing for peptide identification, DeepSelf immunogenicity prediction, to neoantigen screening and immunogenicity validation.


Key Service Advantages

- **DEEP COVERAGE:** Up to 30000+ immunopeptidome, breaking through the limitation of 10 mg tissue (5000+ peptides)
- **ASSURANCE:** High reproducibility of experiments, high efficiency of immunopeptide enrichment, high quality of mass spectrometry acquisition, and QC throughout the workflow
- **ACCURACY:** AI-driven algorithm, more accurate
- **SPEED:** Whole service return time 2-3 weeks

Immunopeptidomics Discovery Service Details

Standard sample preparation and high-resolution mass spectrometers

Standard sample preparation and efficient MHC-bound peptidome enrichment kit provides high experimental reproducibility, and the most advanced high-resolution mass spectrometers with expert teams results in high data quality with lower CV across technical replicates.

number of peptides and binders within < 5% CV from 6 technical replicates
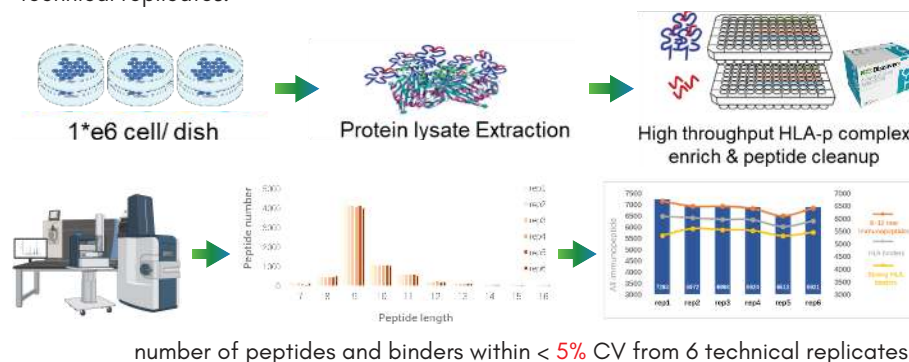
DeepNovo® algorithm-based immunopeptidome discovery

AI-driven DeepNovo Peptidome workflow substantially expanded the reference HLA Ligand Atlas, increasing the number of HLA-I peptides by two-fold and the number of HLA-II peptides by 46%.
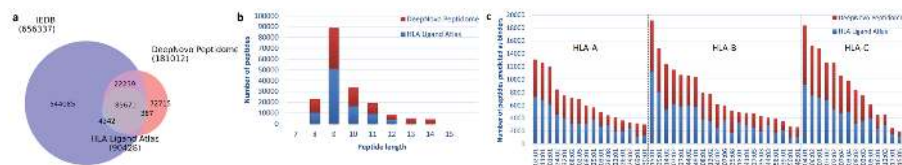
a-c: Venn diagram, length distribution, and NetMHCpan predicted binders of HLA-I peptides.

DeepSelf immunogenicity prediction
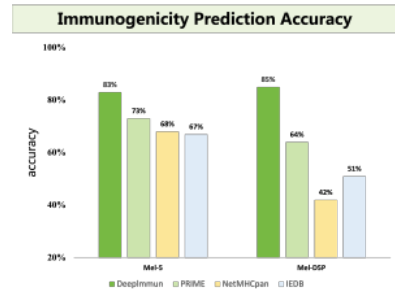
DeepSelf: a personalized model for immunogenicity prediction based on the central tolerance of T cells.

Areas under the receiver operating characteristic curves (ROC-AUC) of the prediction tools on each individual patient. The higher, the more accurate.