## General Proteomics

At Bioinformatics Solutions Inc., we focus on proteomic analysis using mass spectrometry and bioinformatics to provide comprehensive identification and characterization of peptides/proteins and post translational modifications (PTM).

HIGHLIGHTS:
- Protein identification and peptide mapping
- Analysis of PTMs and sequence variants
- Antibody–drug conjugate analysis (with or without antibody sequencing)
- Intact mass analysis
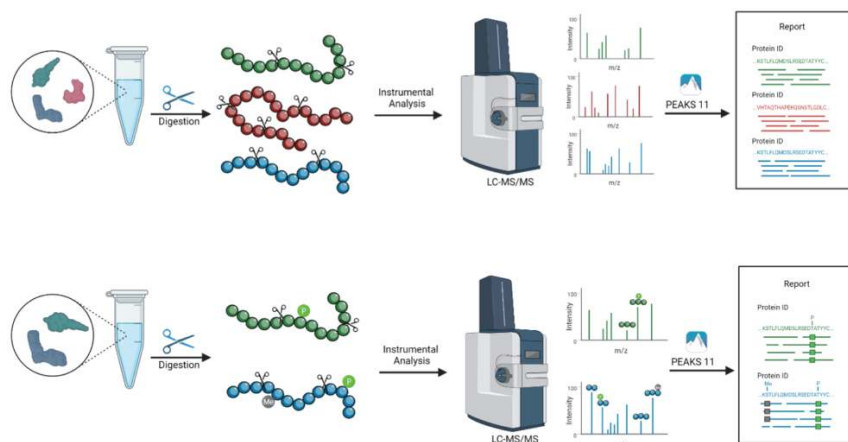
Why use our service?

With over 20 years experience in the proteomics research community, we understand the importance and value of antibody, proteomics and glycomics research to advance our understanding of the complexity underlying biological systems. We provide fast turnaround times, complete confidentiality, and guaranteed results through cost-effective and efficient mass spectrometry solutions for a wide range of industries.

Contact us for a personal consultations to develop your project, and perform all experiments in a professional, accurate, and timely manner.

BSi

Service LAB

PROFESSIONAL CRO FOR MASS SPEC-BASED LABORATORY

PEAKS AB® Protein *de novo* Sequencing

Protein de novo sequencing is the process of determining the amino acid sequence of a protein, directly from the target protein using mass spectrometry and advanced software solutions.
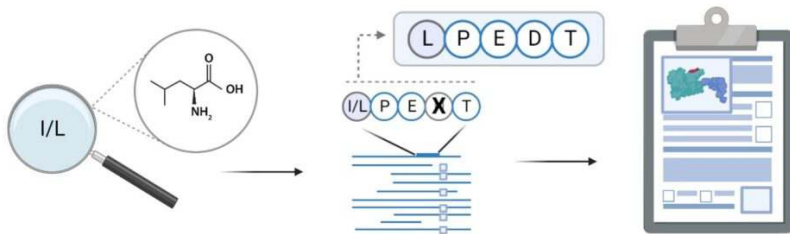

Step 1 — Top-down: Reduction and deglycosylation + LC-MS + deconvolution = intact masses
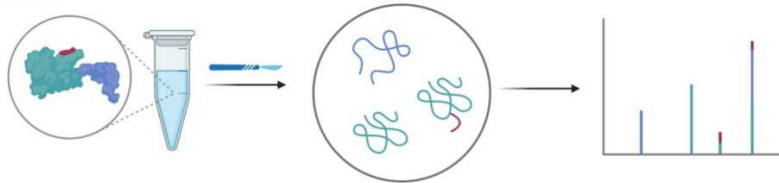
Step 2 — Bottom-up: Multi-enzyme digestion + LC-MS/MS + *de novo* sequencing + sequence assembly
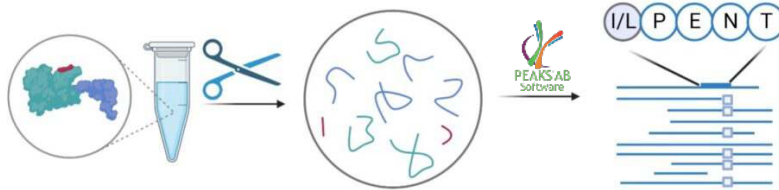
Step 3 — Analysis: Ile vs. Leu (EThcD MS) + manual analysis + match to intact = 100% coverage
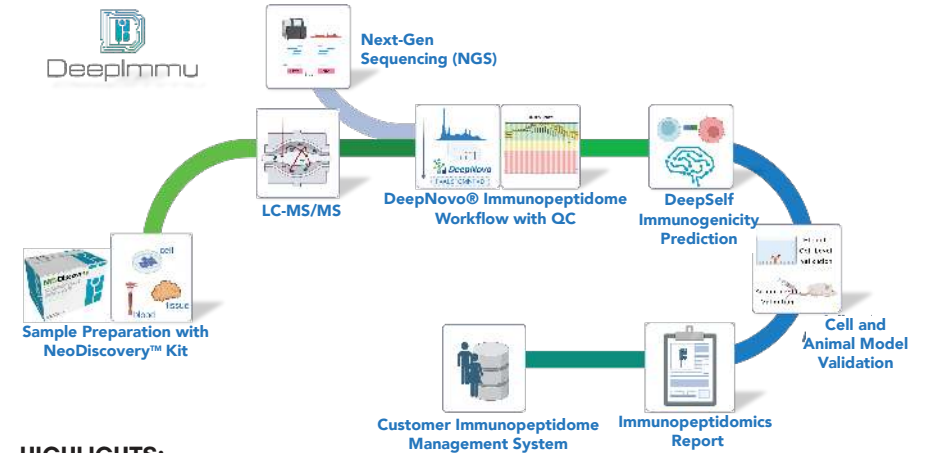
HIGHLIGHTS:
• End-to-end sequencing in <2 weeks
• 100% sequence coverage and absolute accuracy
• Full length heavy and light-chain antibody sequencing for all species, isotypes and allotypes
• Validation by Intact Mass
• 3-tier Leu vs. Ile Differentiation using an advanced EThcD MS method, enzyme digestion specificity and homology database analysis
• Sequencing of non-antibody proteins
• Analysis of PTMs and sequence variants, in-depth glycan profiling (upon request)
• Manual verification, detailed reports and consultations with our expert scientists

DeepImmu® Immunopeptidomics Discovery

For our Immunopeptidomics service we perform cell lysis, MHC peptide purification, LC-MS/MS, peptide identification, sequence motif generation, and binding affinity and immunogenicity prediction. This service also includes quality control tests to ensure accurate results. Our advanced software algorithms and PEAKS DeepNovo Peptidome workflow provides accurate, sensitive, and reproducible results for immunopeptide identification and quantification.
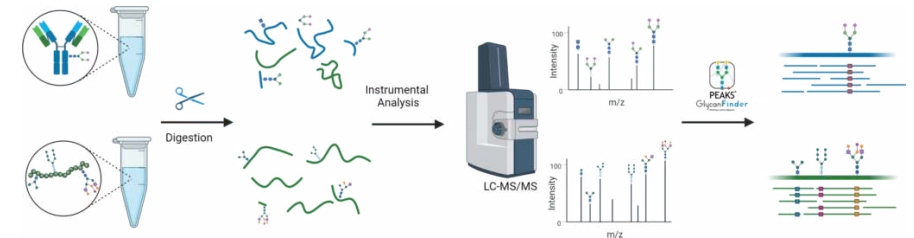

HIGHLIGHTS:
• Fast turnaround times (2-3 weeks)
• Comprehensive platform for qualitative and quantitative analysis of immunopeptidome
• Proprietary MHC immunopeptide purification / enrichment method
• Accurate peptide sequencing enabled by AI-driven DeepNovo® algorithm
• Immunogenicity prediction / scoring using the DeepSelf model
• Sequence motifs for HLA alleles, predicted immunopeptides and their length distribution chart included in results, comprehensive report

PEAKS® GlycanFinder

In this service we identify N- and O-linked glycans along with protein glycosylation sites using PEAKS® GlycanFinder. We process in-solution or in-gel samples and offer glycopeptide enrichment for more complex samples.

HIGHLIGHTS:
• Fast turnaround times (1-3 weeks)
• In-depth glycan profiling and glycopeptide analysis
• Identification and quantification of N- and O-linked glycans with structural resolution
• De novo sequencing for finding unknown glycans
• Includes proprietary glycopeptide enrichment methods
• Enabled by PEAKS® GlycanFinder software and deep learning-based algorithms