

BSI lab services now offers in-depth glycoproteomics and glycan profiling! Complete results and full report in 2-3 weeks!

Depending on the sample type (purified protein or protein mixture / complex sample), our clients will receive either Glycan Report I or Glycan Report II, along with the experimental raw data. Customized reports can be delivered on request.

- **Glycan Report I (for purified proteins):**

a full glycoprotein sequence, intact mass results with peak annotation to top glycoforms, peptide mapping of N-linked and/or O-linked glycopeptides, list of all identified glycans and their glycosylation sites, MS2 spectra of top supporting glycopeptides.

- **Glycan Report II (for complex samples / glycoproteomics):**

glycoprotein sequences, peptide mapping of N-linked and/or O-linked glycopeptides to top 5 identified glycoproteins, list of all identified glycans and glycoproteins (provided as .csv file), MS2 spectra of top supporting glycopeptides for the top 5 glycoproteins identified.

See our application notes based on experiments run in our lab to learn more about our **PEAKS® GlycanFinder Service at BSI**



Characterisation of N-linked glycosylation patterns of IgG antibodies in PEAKS GlycanFinder



N-glycan and O-glycan Profiling of Fetuin by single LC-MS/MS run



Identifying different glycan profiles of CD33 expressed in HEK293 and CHO cells



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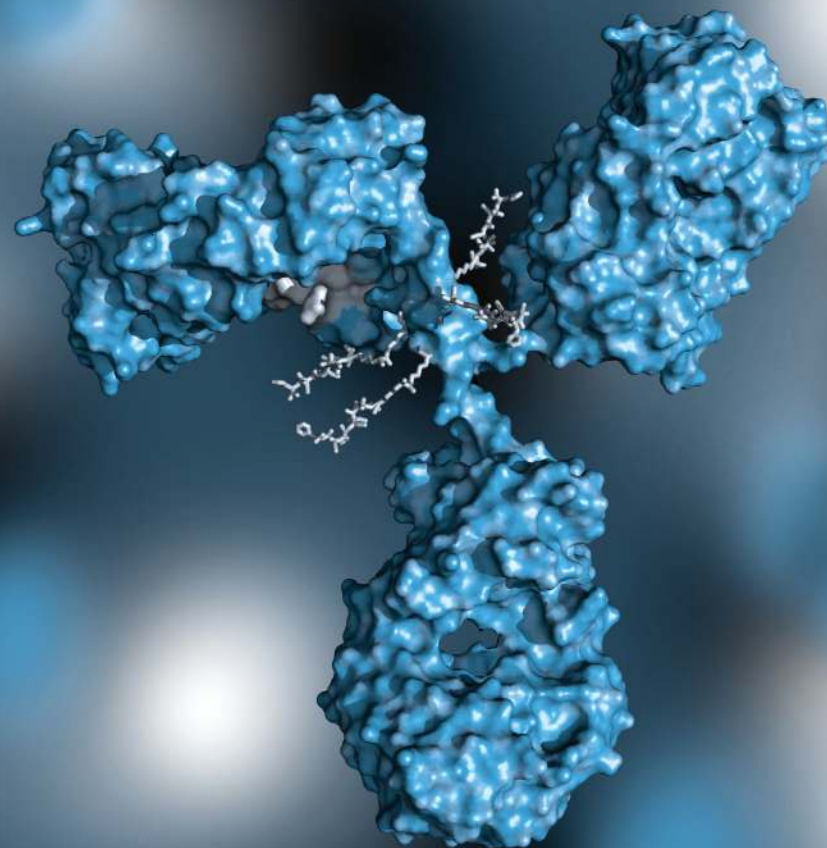
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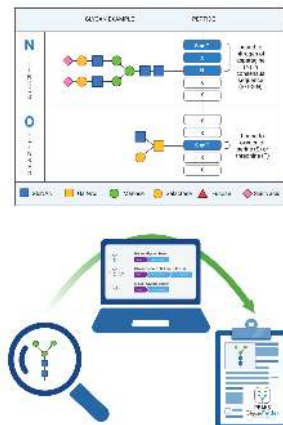
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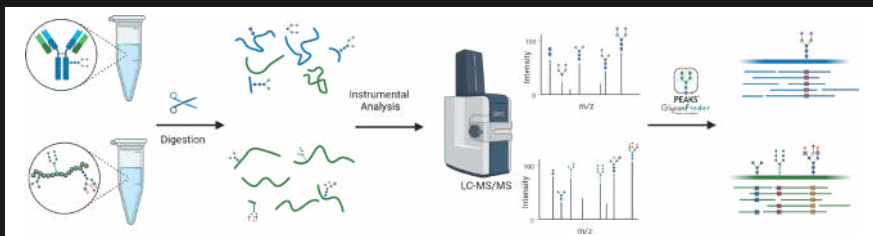
Glycans are a heterogeneous group of carbohydrate-based structures that can be linear or branched and are attached to the side chain of amino acids within glycoproteins. Glycosylation is one of the most common post-translational modifications (PTMs) and refers to the covalent attachment of monosaccharides or complex carbohydrate chains (glycans) to proteins. These universally present PTMs directly affect protein structure, function and stability, and play a critical role in numerous biological processes. Therefore, an in-depth analysis of glycans and glycosylation sites is pivotal for protein characterization under various conditions and for the development of novel therapeutics.



Glycans can be categorised as N-linked, bound to the nitrogen atom of asparagine (N), or O-linked, bound to the oxygen of serine (S) or threonine (T) side chains. PEAKS® GlycanFinder software was designed to overcome most common challenges in LC-MS/MS glycoproteomics, including macro- and micro-heterogeneity where there may be multiple glycosylation sites per peptide and multiple structures with the same glycan composition. PEAKS® GlycanFinder accurately identifies glycosylation sites and scores candidates for structural resolution. Glycan *de novo* sequencing alleviates the limitations of the incompleteness of the glycan database.

PEAKS® GlycanFinder Service

The BSI Service Lab offers PEAKS® GlycanFinder service that combines our LC-MS/MS expertise and optimized protocols with our advanced PEAKS® GlycanFinder software to identify N- and O-linked glycans along with glycosylation sites in purified proteins or complex samples. We process in-solution or in-gel samples and offer proprietary glycopeptide enrichment technology for more complex samples.



HIGHLIGHTS

- Comprehensive analysis and detailed reports in 2-3 weeks
- In-depth glycan profiling and glycopeptide analysis
- Glycan identification for purified proteins and complex samples
- Comprehensive identification of glycosylation sites
- Identification and quantification of N-linked and O-linked glycans with structural resolution
- *de novo* sequencing for finding unknown glycans
- Includes proprietary glycopeptide enrichment methods
- Enabled by the PEAKS® GlycanFinder software platform and deep learning-based algorithms

PEAKS® GlycanFinder provides two types of workflows to analyse glycoproteomics. There are identification and quantification workflows available, including Glycan Site Profiling and Glycan Sample Profiling.

