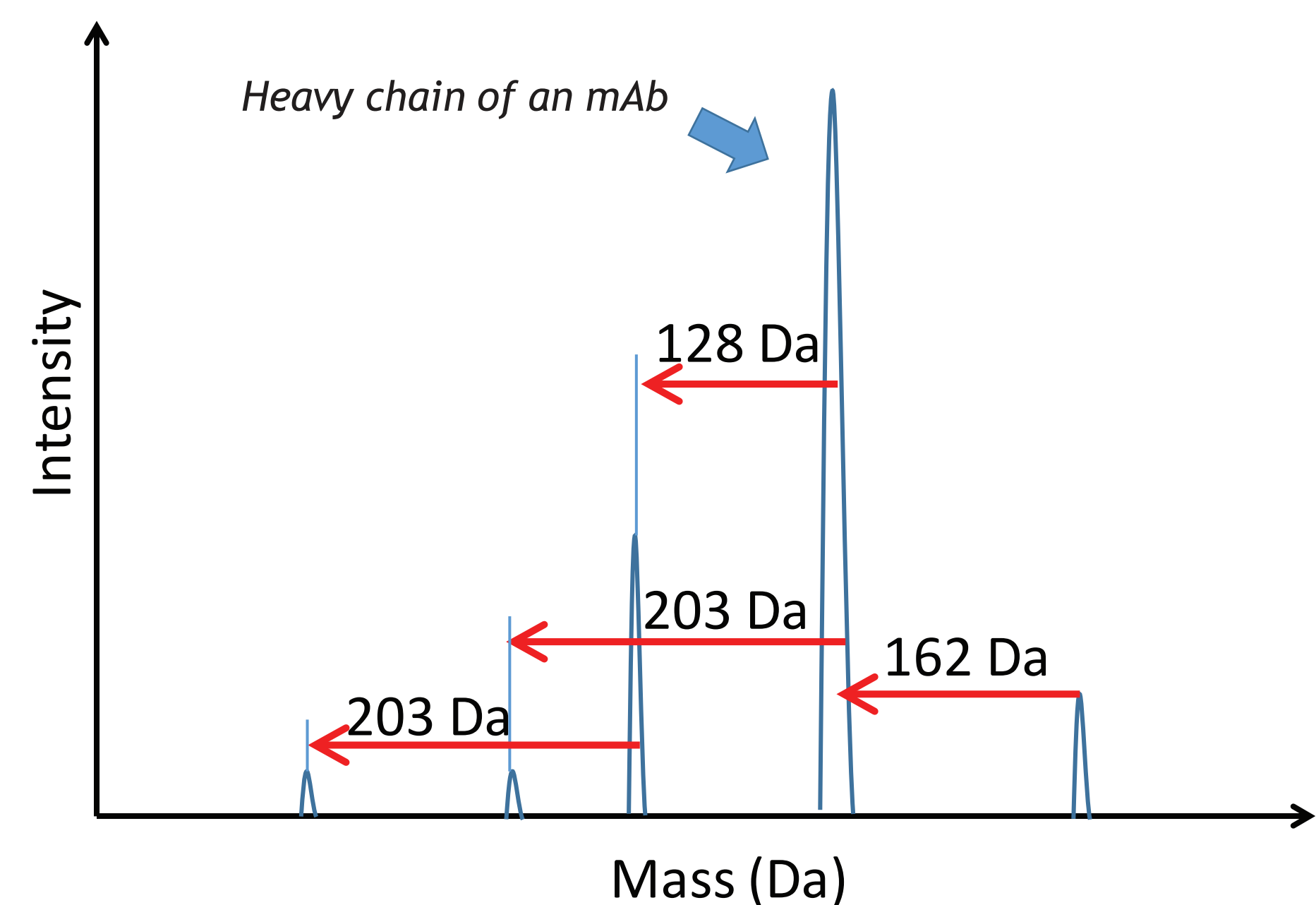


## Summary

Studies of therapeutic proteins, especially monoclonal antibodies (mAbs), require the accurate and complete protein sequences and comprehensive characterization before the proceeding of downstream applications. It has been proven that current LC-MS technologies can provide accurate and sensitive solutions for both mAb sequencing and characterization. However, it is difficult to transfer LC-MS/MS data to mAb knowledge without the assistance from a powerful software tool. Based on our experiences in LC-MS/MS-based antibody protein sequencing and proteomics studies, we have developed a novel algorithm for our software platform, PEAKS AB®. This unique software tool can easily carry out *de novo* protein sequencing to get accurate antibody protein sequences, provide qualitative and quantitative analysis functions for sequence variants and post-translational modifications (PTMs), including N-linked glycans, and identify cross-linked peptides with disulfide bridges.

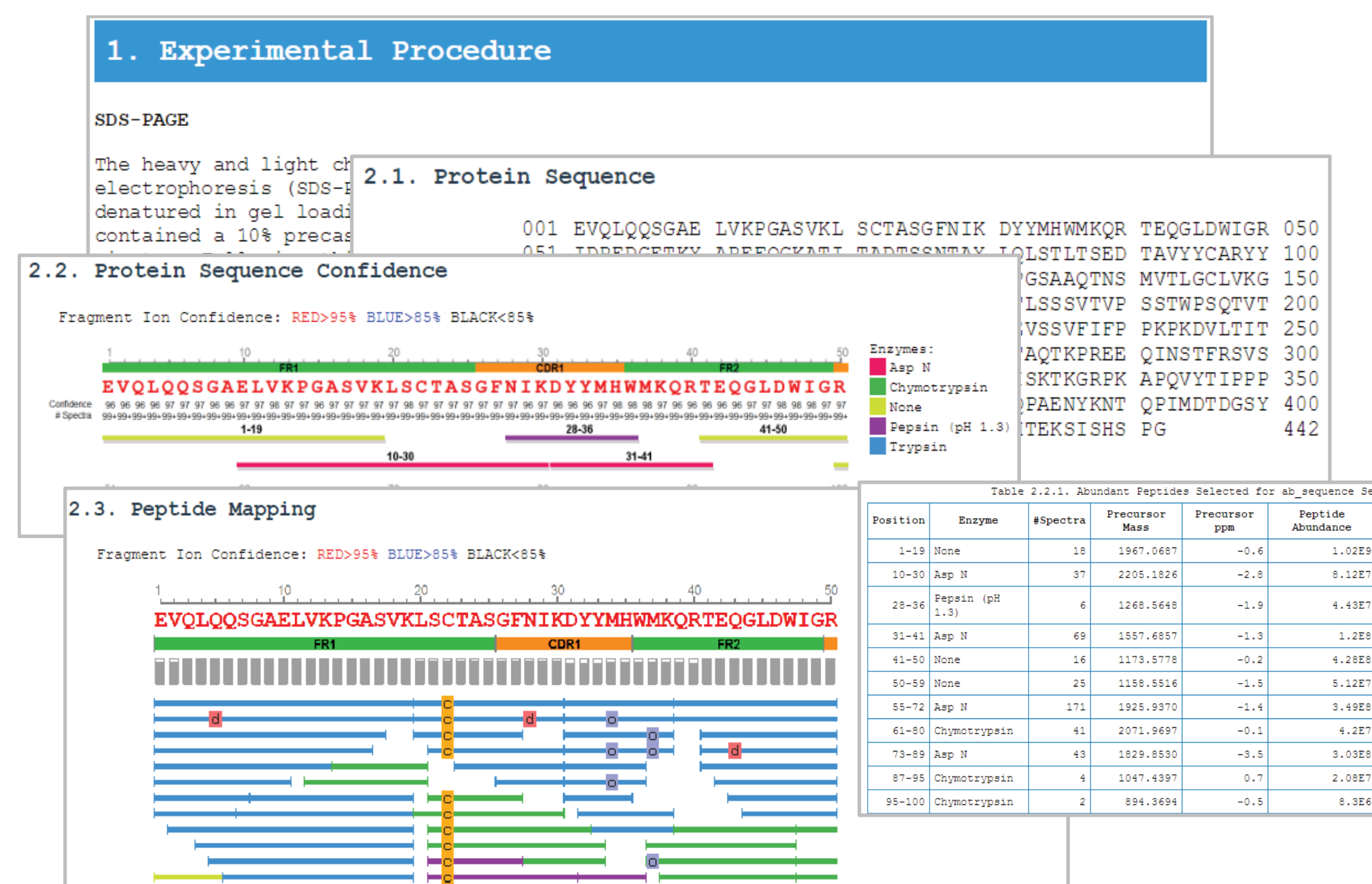
## Intact Mass Measurement

Intact mass measurement provides another means to validate the assembled protein sequences, assist with determining the C-terminal lysine truncation, and identifying different N-linked glycan forms.



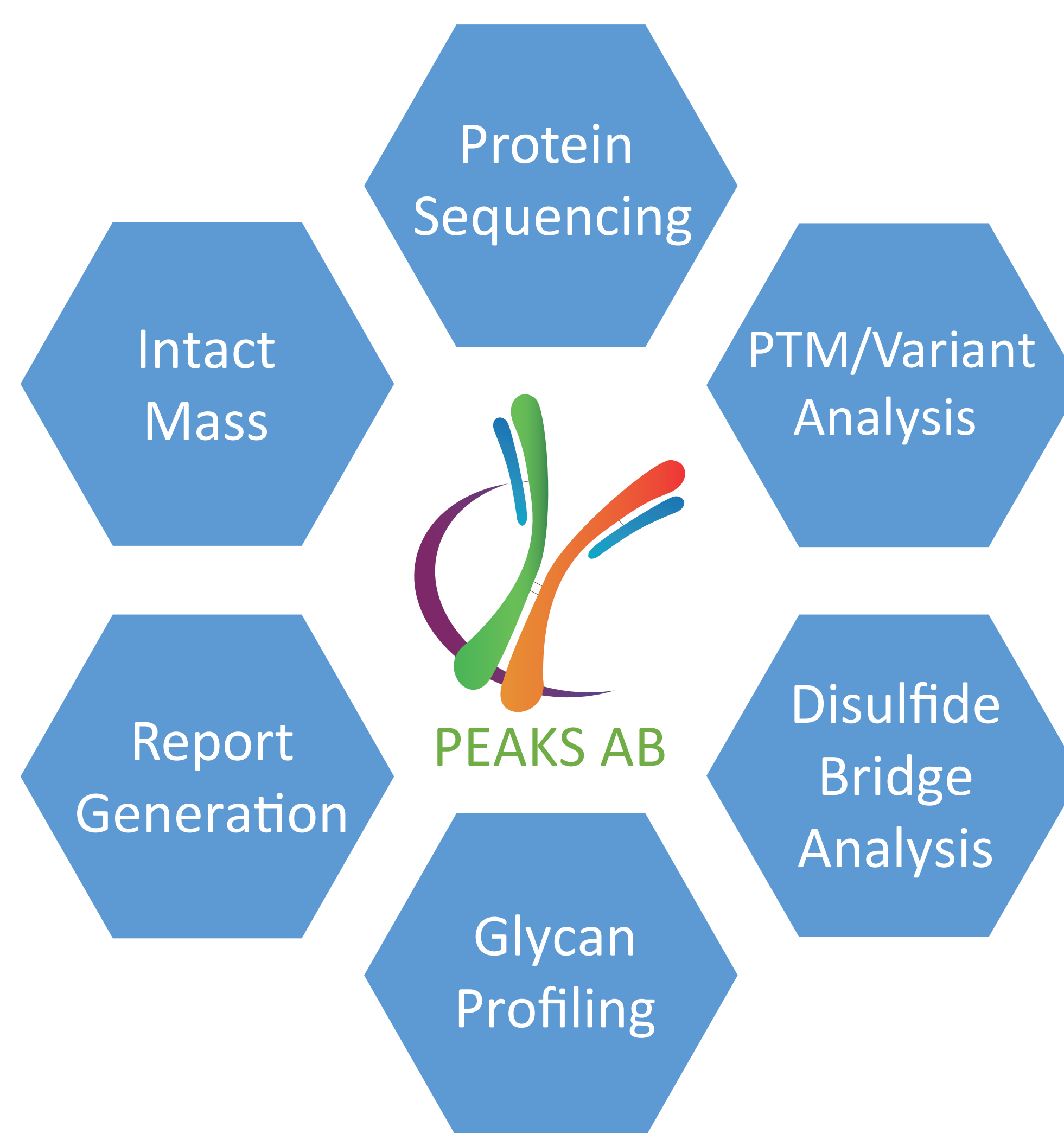
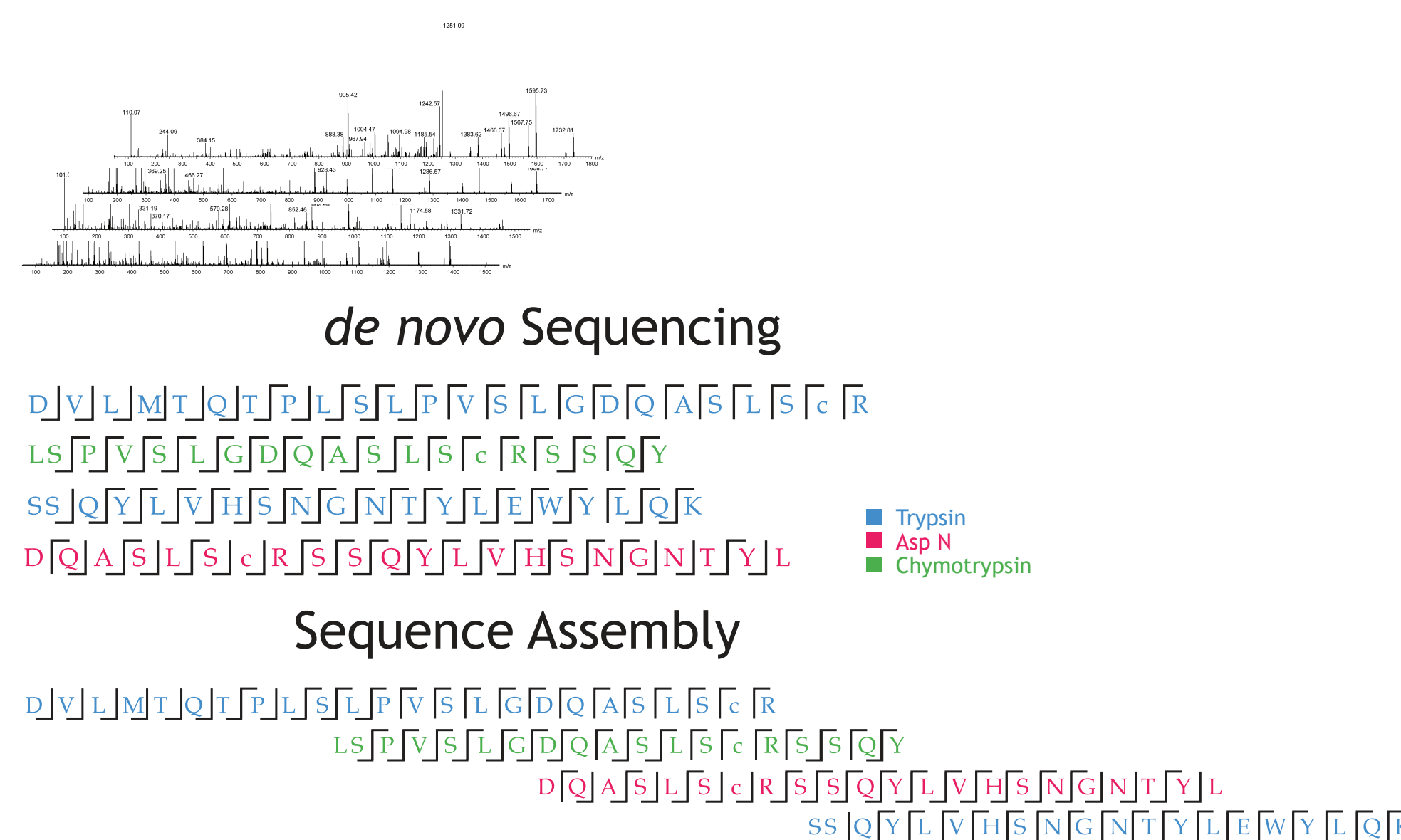
## Comprehensive Report Generation

PEAKS AB® Software provides a comprehensive reporting function that can easily customize and generate reports from mAb analysis results.



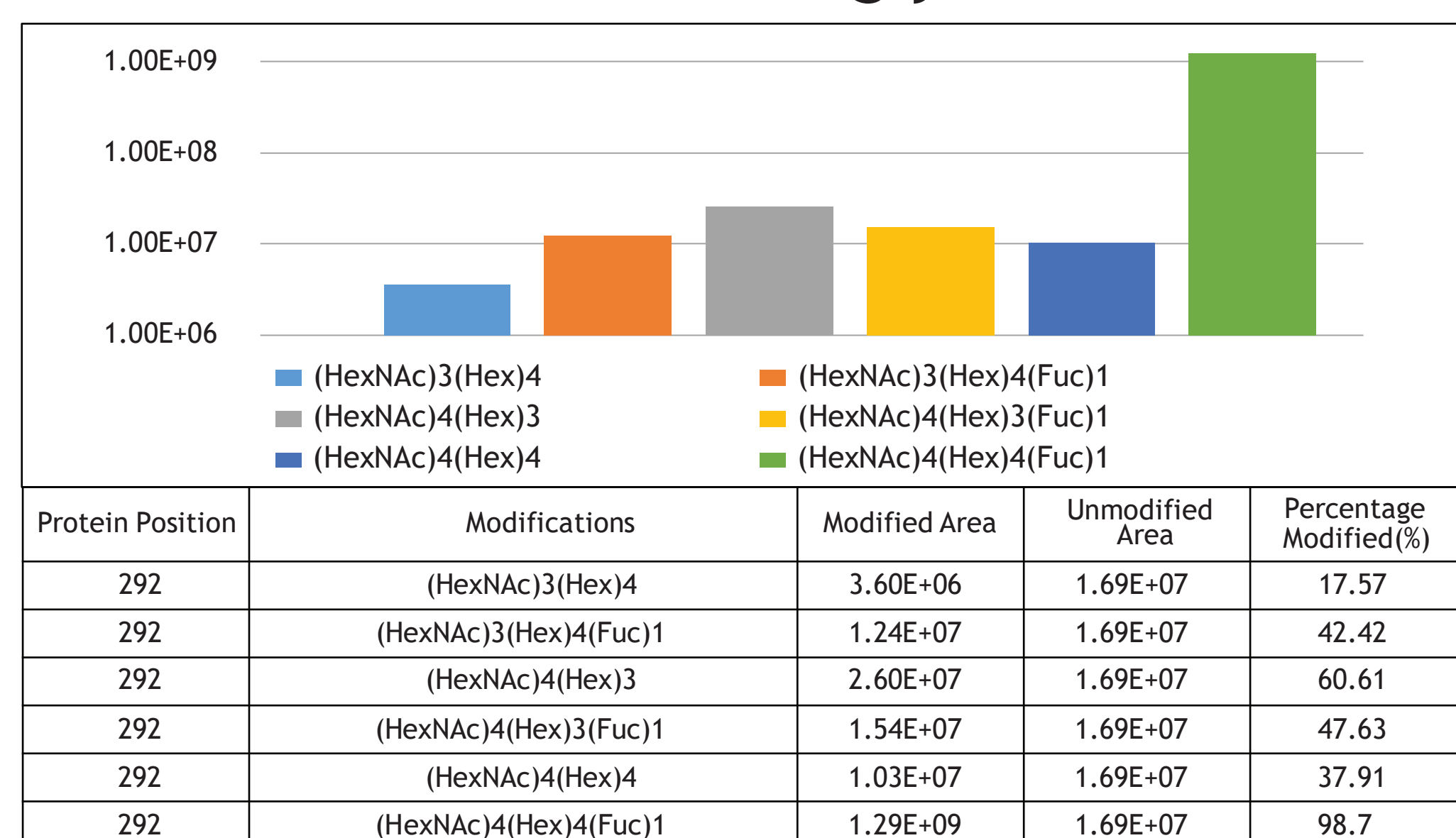
## de novo Protein Sequencing

PEAKS AB® uses our novel algorithm, ALPS [1], to assemble *de novo* peptide sequences into a full protein sequence of each chain.



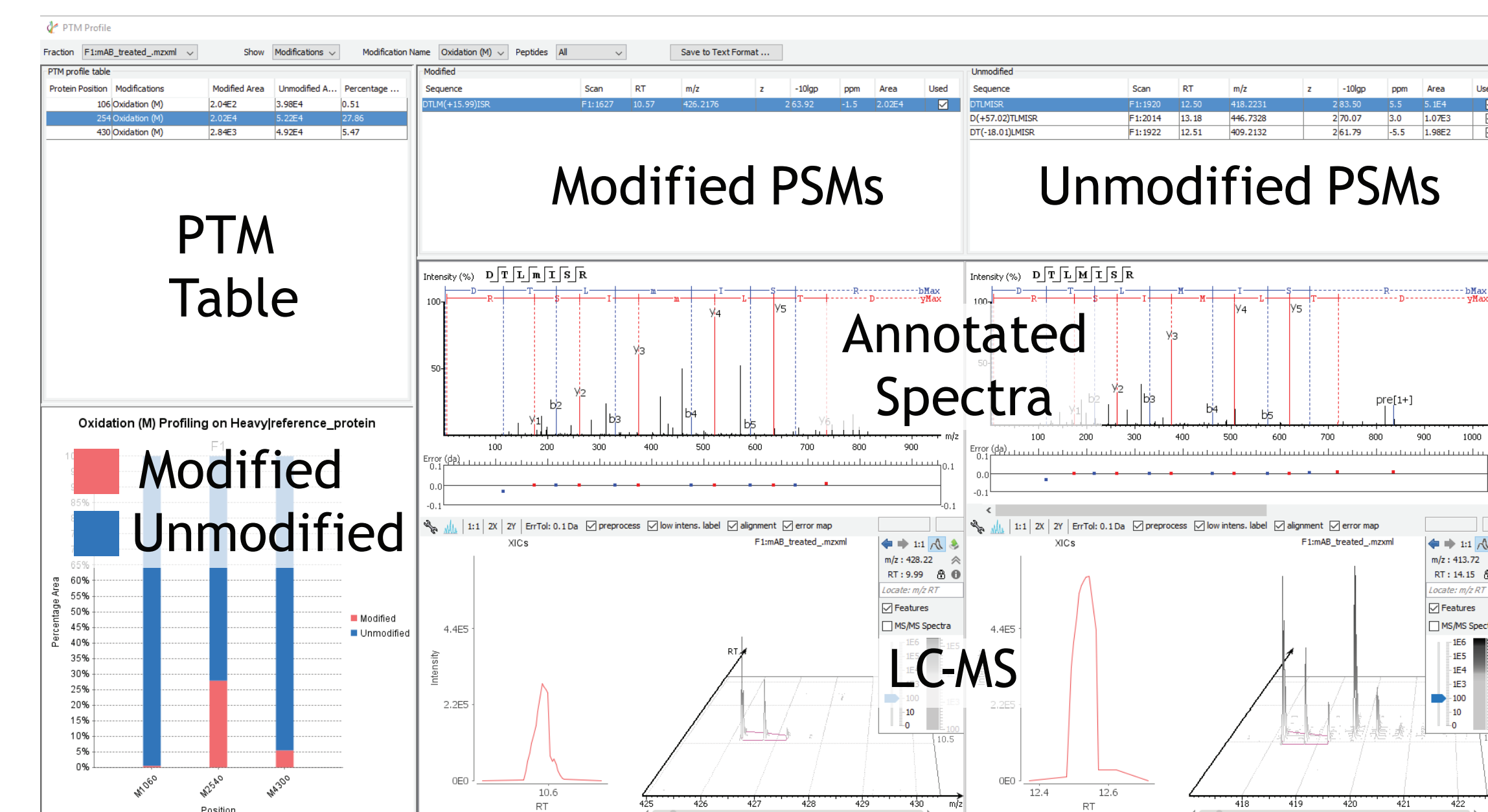
## Glycan Profiling

PEAKS AB® provides the identification of N-linked glycans and quantitative information of different glycan forms.



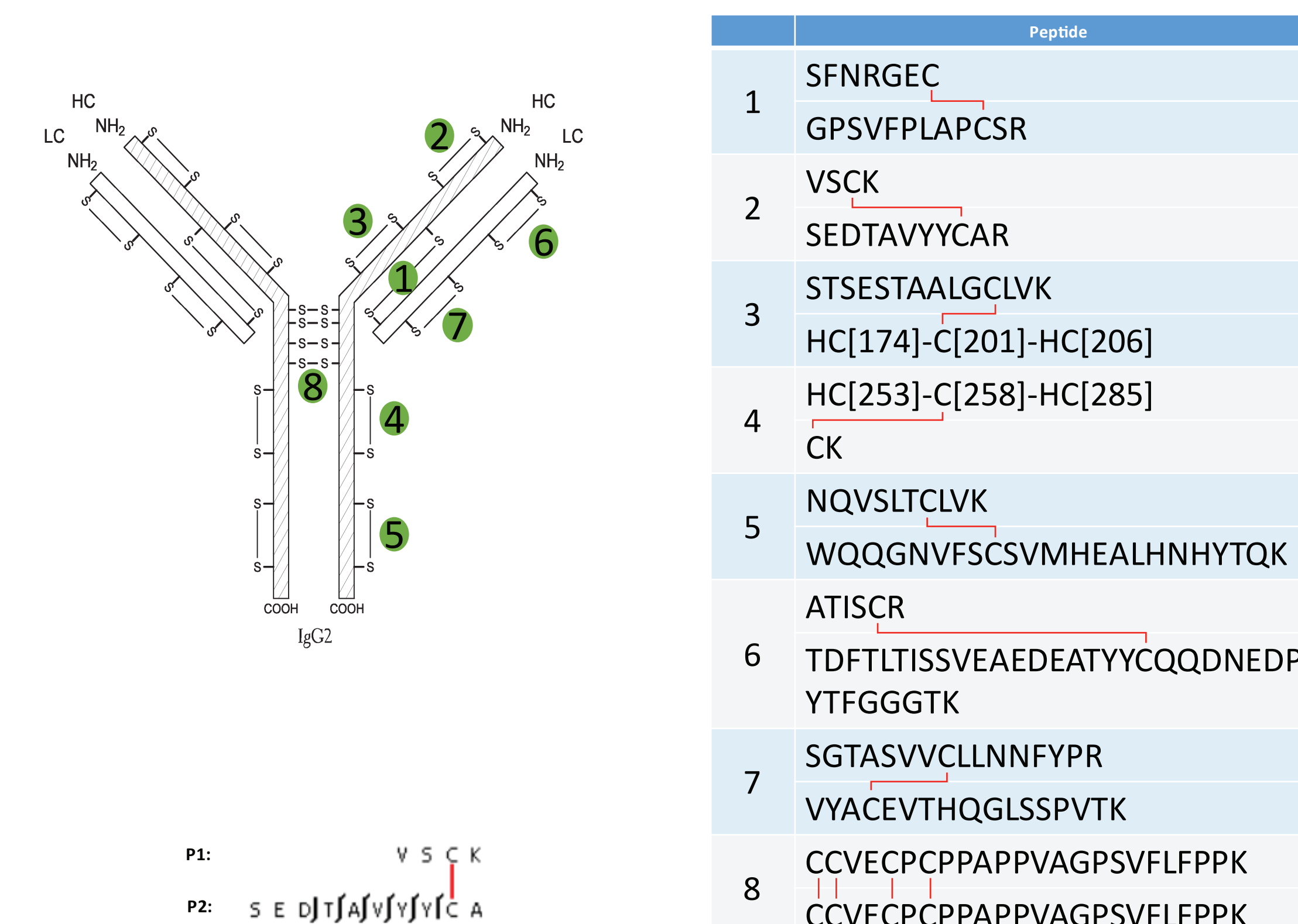
## PTM/Variant Analysis

PEAKS AB® identifies PTMs and sequence variants using its PEAKS PTM and SPIDER modules. The abundance of each modification is extracted from LC-MS and the quantitative analysis result is shown in an informative PTM profiling view. The qualitative and quantitative analysis result can be easily exported for further analysis.



## Disulfide Bridge Analysis

Cross-linked peptides with disulfide bridges can be identified by PEAKS AB® using the MS/MS data generated from a non-reduced antibody sample.



## References:

[1] Tran, N.H. et al. Complete De Novo Assembly of Monoclonal Antibody Sequences. Scientific Reports. 01/09/2016.