

Polyclonal antibody *de novo* sequencing highlights:

- A complete workflow solution for accurate sequencing the natural activity antibody directly by mass spectrometry
- Multiple-dimensional LC enables reliable and efficient separation of simple antibody mixture from polyclonal antibodies.
- Multiple level mass technology ensures the data quality and verifiable.
- Powered by innovative, deep learning-based data analysis algorithms.
- Characterization of up to 4 antibodies / a fraction of the mixture

PEAKS AB Polyclonal Antibody Sequencing Details

Time	You Provide	We Deliver
4-6 weeks	A fraction of Antibody mixture (>1mg)	<ul style="list-style-type: none">• Top 4 most abundant antibody sequences• Intact mass validation for each• 3-tier Leu/Ile Differentiation• Comprehensive PEAKS AB Report

The best part? BSI's PEAKS AB Service provides complete characterization of antibody mixtures and polyclonal antibodies without a custom database or NGS data.

We deliver fast, accurate and cost-effective results in 6 weeks or less!

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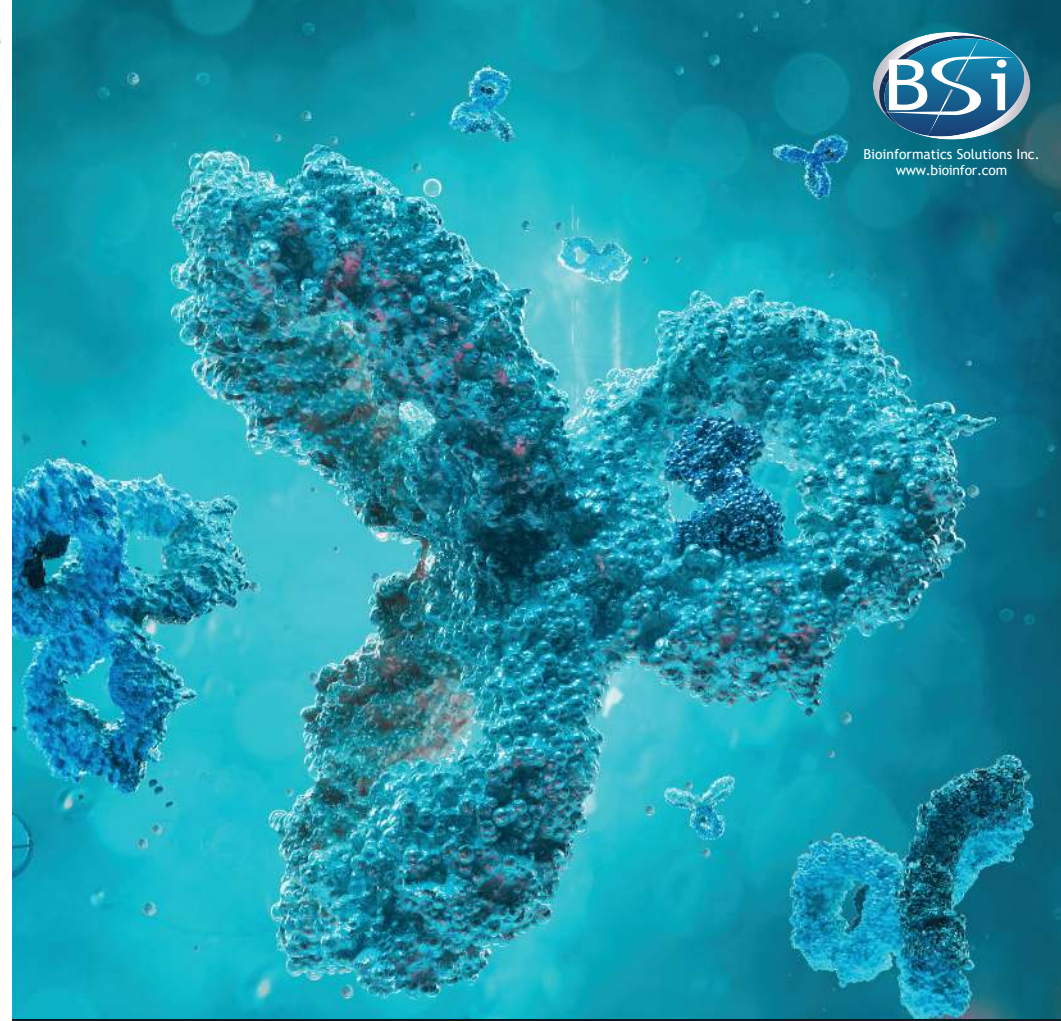
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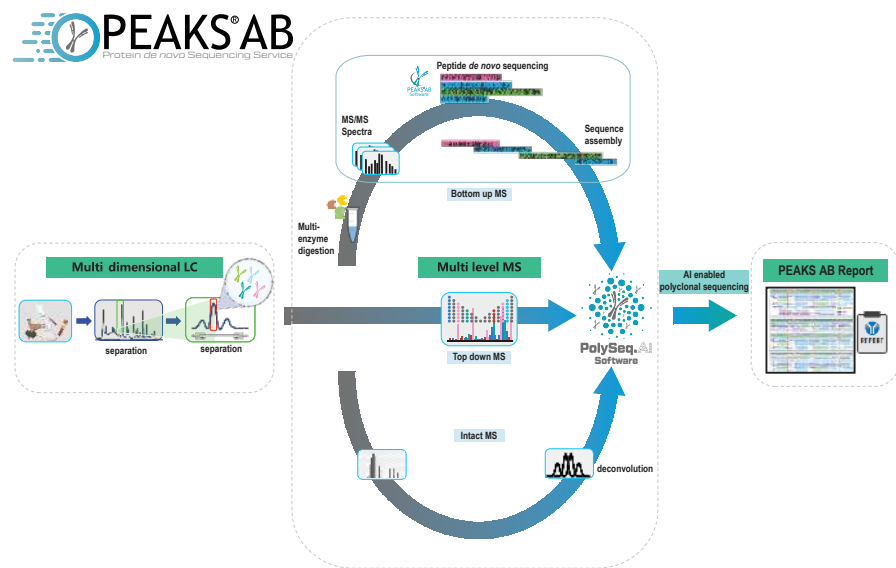


MULTI-DIMENSIONAL LC-MS BASED POLYCLONAL ANTIBODY SEQUENCING



Polyclonal Antibody *de novo* Sequencing Service

Polyclonal antibodies play a critical role in human immunity and their identification has important implications for disease treatment. Unlike monoclonal antibodies, sequencing polyclonal antibodies presents a great challenge due to the complexity of sequence variants. Traditional bottom-up proteomics approaches involved in monoclonal antibody sequencing cannot distinguish between each antibody variant by peptide assembly. To overcome this challenge, intact data combined with top-down proteomics is needed. We have developed a complete workflow that integrates multi-dimensional LC with intact, top-down, and bottom-up data to accurately *de novo* sequence antibody mixtures.



Here, we show an example of sequencing a mixture of 4 antibodies (Adalimumab, Bevacizumab, Rituximab, and Herceptin) without the requirement for a custom database from next-generation sequencing data, to simulate a fraction from multi-dimensional LC separation of polyclonal antibody sample. Integrating intact, top-down, and bottom-up data generates correct sequences of all 4 antibodies. Adalimumab is shown as an example. Figure 1 Intact masses of 4 antibodies mixture matched with the *de novo* sequences: (a) intact, (b) reduced, and (c).

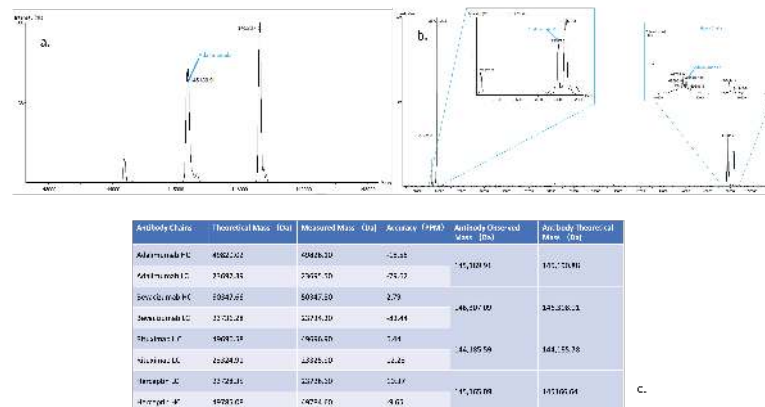


Figure 1 Intact masses of 4 antibodies mixture matched with the *de novo* sequences: (a) intact, (b) reduced, and (c) summary.

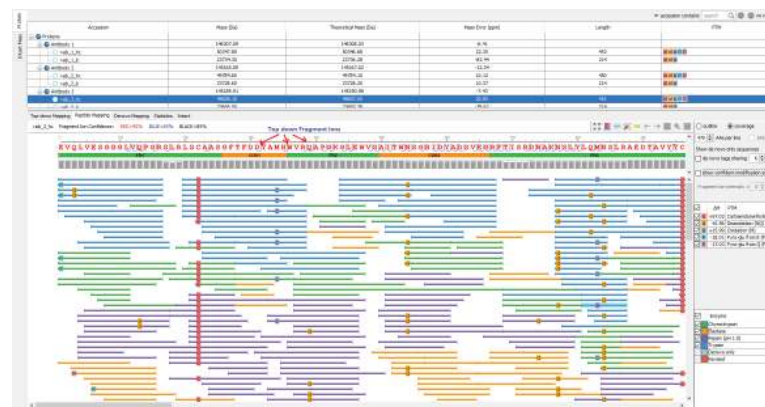


Figure 2 *De novo* sequences with supporting peptides from PEAKS AB Polyclonal antibody sequencing, powered by PolySeq.AI.

This complete solution for sequencing antibody mixtures will be offered under PEAKS AB Polyclonal Antibody Sequencing Service by Bioinformatics Solutions Inc. Mass Spec Lab.