A Streamlined Workflow for Characterizing Low-Abundance Glycans on Therapeutic Proteins

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Abstract

A comprehensive survey of therapeutically important glycans was performed using high-resolution MS with the AssayMAP technology from Agilent Technologies. Glycan analysis was performed on a panel of therapeutic monoclonal antibodies (mAbs) and human serum. Significant variation was observed in the glycoform profile for each product, and glycans that were low-abundance N-glycans, in addition to the use of a single exoenzyme to identify the structures of the N-Glycan Profiles in Figures 1 and 2, Tables 1 & 2 and in the text.

Methods

Preparation with PCA (product code GP96NG-PCA), incorporating an experimental and emission at 359 nm.

Results & Discussion

- **β-Galactosidase**
  - Maximum values were acquired for β-Galactosidase based on the intensity for each species peak and the area of the glycan (7.5 μM). 12.12 μM, 18.34 μM, 25.45 μM, and 31.56 μM were calculated.
  - Data Analysis: Peaks from the Fluoromass measurements were aligned using the ion monitor function of the Agilent MassHunter Software, with the experiment and emission at 359 nm.

- **Hexosaminidase**
  - The ion products were identified using the library search function of the Agilent MassHunter Software, with the experiment and emission at 359 nm.

- **Proposed Structures**
  - The proposed structures were determined using the library search function of the Agilent MassHunter Software, with the experiment and emission at 359 nm.

- **Conclusion**
  - The AssayMAP technology is licensed from Agilent Technologies.

**References**