Mass Spectrometry Solutions Using LC/MS/MS and HRMS for Oligonucleotides and Biologics

Biologics | Fast TAT | HRMS | LC/MS/MS | Oligonucleotides | RNA Therapeutics

pyxant LABS

BIOANALYTICAL CONTRACT RESEARCH

Once traditionally a platform for small molecule analysis, mass spectrometry is now applied to the development of biologic methods. Over the past several years, Pyxant Labs has been applying its decade of experience with chromatography methods to the development and validation of LC/MS/MS and high-resolution mass spectrometry (HRMS) analytical methods for oligonucleotides and biologics.

Our bioanalytical experience applying LC/MS/MS and HRMS methodologies to oligonucleotides and biologics includes:

- Over a decade of experience developing methods, validating, and assaying for oligonucleotides
- Vast biologics diversity, spanning from small (1 kDA) therapeutic peptides to large (900 kDa IgM) proteins
- A wide range of sample preparation methods, from simple protein precipitation to complex affinity capture enrichment techniques
- Development and validation of mass spectrometry assays using surrogate peptides produced by proteolytic digestion of proteins for quantitation
- Semi-quantitative analysis of intact proteins (>10 kDa)
- Characterization of antibody-drug conjugates (ADCs) using high-resolution mass spectrometry (HRMS)

Benefits of High-Resolution Mass Spectrometry

HRMS can measure proteins intact (Top-Down MS) or surrogate peptides after digestion.

HRMS also has advantages over ligand binding assays (LBA), since the development time to produce suitable capture and detection reagents is eliminated. In addition, the need to develop multiple LBA methodologies for assessment of post-translational modification can be eliminated.

The additional benefits of HRMS for drug development is highly specific, including the ability to accurately measure masses to a resolution of 0.0001 Da or greater, and the ability to simultaneously quantify multiple proteins. HRMS also has the ability to measure post-translation modification of proteins within the same analytical run and can elucidate the ratio of modified and unmodified states of proteins.