Intact Mass Analysis

Mass spectrometry is a powerful tool for protein characterization.

High accuracy molecular weight determination allows for confirmation of the integrity of protein sequences and can identify the presence of post-translational modifications or chemical adducts. Intact mass analysis is the perfect add-on to complement our protein purification services.

Instrumentation:

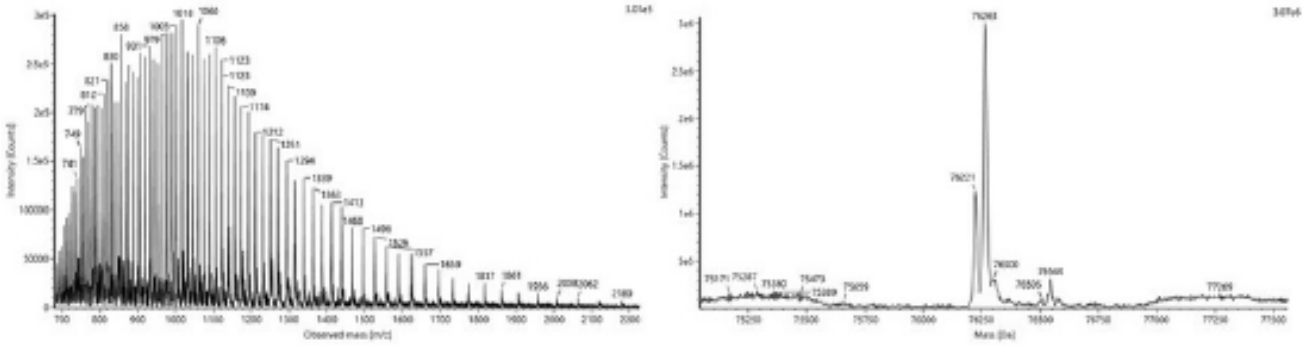
We utilize the Waters BioAccord LC-MS, an electrospray ionization-time of flight (ESI-TOF) mass spectrometer for intact mass determination of proteins and antibodies. The instrument is self-optimizing to ensure consistent, high-quality data output.

Common PTM and adducts detectable by intact mass:

- Phosphorylation/dephosphorylation
- Acetylation
- Glycosylation
- Disulfide bond formation
- Removal of initiator Met residue
- β-ME and glutathione adducts
- Biotinylation

Email info@proteos.com to connect with our scientists.

Intact Mass Data



Theoretical MW: 79222.98 Da

Experimental MW	Delta Mass	Presumed PTM
76221 Da	-2 Da	disulfide bond (-2 Da)
76263 Da	+40 Da	disulfide bond (-2 Da) acetylation (+42 Da)