

Intact Mass Analysis

Mass spectrometry is a powerful tool for characterization of proteins.

High accuracy molecular weight determination allows for confirmation of the integrity of the protein sequence and can be used to identify the presence of post-translational modifications or chemical adducts. Intact mass analysis is the perfect complement to Proteos' protein purification services and can be added to any project.

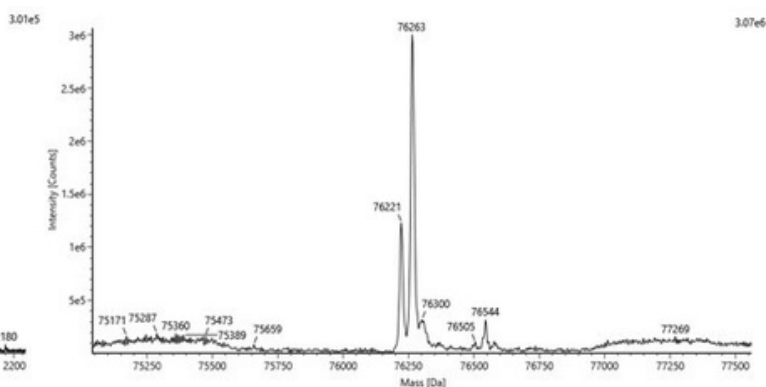
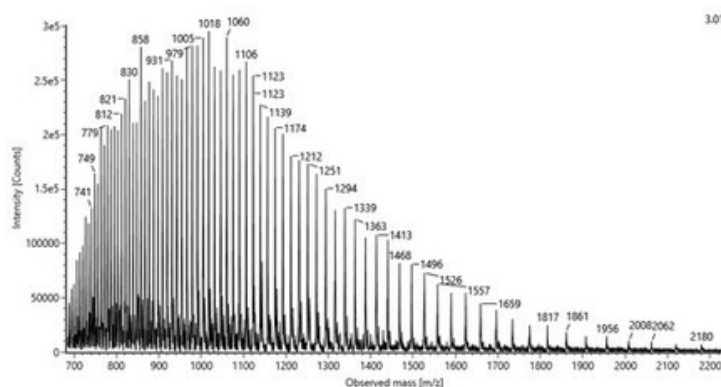
Instrumentation:

Proteos utilizes 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

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)