



Protein QC

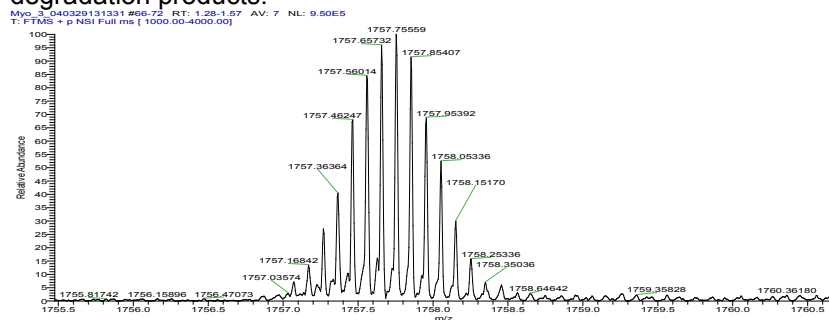
Qualitative LC – MS (/MS) analysis is the method of choice for quality control of proteins. We use high resolution mass spectrometers to identify intact protein masses and peptide fragment fingerprints to determine the amino acid sequence and its modification(s).

BACKGROUND

Liquid chromatography (LC) coupled to a mass spectrometer (MS) makes it possible to separate and accurately measure the m/z of proteins or peptides. HPLC or nano columns aim to retain the molecules and individually release them again during a solvent gradient directly into the MS, where the samples get ionized and measured via their mass to charge ratio (m/z). The raw data can then be analysed by either a deconvolution software for intact protein masses or a database search against known protein sequences for peptide assignment.

TECHNOLOGY

Provide us, the research group Bioanalytics at the TU Vienna, with dry proteins, proteins in solution or even gel bands and we will prepare the samples according to the desired information for intact and/or sequencing analysis. Our experience in the technical equipment has already been proven many times in external projects. Most often we were able to resolve the proteins to their monoisotopic masses or reach 100% sequence coverages. With that we are able to check for impurities, all sorts of mutations, special modifications, protein sizes or degradation products.



OFFER

We professionally assist you in your protein query via mass spectrometry-based sequencing and intact mass analysis, taking CDA/NDA for granted. IP developed in such a project would fully belong to our investor/industrial partner.

EXPERT:

Ruth Birner-Gruenberger, Ph.D.

AVAILABLE FOR:

- Investments
- Joint Research Projects
- Contract Research

DEVELOPMENT STATUS:

Technology Readiness Level 6
(Demonstrated in relevant environment)

IPR:

Can be generated for our industrial partners / investors

KEYWORDS:

LC-MS analysis
Protein sequence
Protein size
Point mutations
Protein stability
Protein purity
Protein modifications
Glycosylation

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