Mass Spectrometry based Proteome Analyser - Platform	**Category: D. Particle Exposure Assessment** **Institute: VITO** **Location: Center for Proteomics, Groenenborgerlaan 171, 2020 Antwerp, Belgium** **Contact Details of Technology Expert:** **Inge Mertens** **Phone: +32 (0)3 2653387** **Fax: +32 (0)3 2653697** **E-mail: inge.mertens@vito.be**

Short technology description/Overview *(approx 300 words)*:

The LTQ-velos Orbitrap hybrid mass spectrometry platform is a combined mass spectrometer consisting of a dual pressure-cell linear ion trap followed by a fourier-transform ion trap analyser, and is further upgraded with an electron-transfer dissociation fragmentation option. This instrument can be hyphenated with a high-field asymmetric-waveform ion mobility spectrometer, a two-dimensional ultra high-pressure nano-liquid chromatography set-up, and/or a chip-based nano-electrospray interface. This combination makes it a versatile state-of-the-art toolbox for contemporary high-quality proteome analysis.

The set-up allows for high mass accuracy and high mass resolution resulting in a precise and accurate peptide mass measurement with a reduced false positive identification ratio. The implementation of FAIMS allows to selectively enrich for multiple charged ions and an enhanced signal-to-noise ratio. The robotic nano LC-ESI interfaces allow for an increased sensitivity, throughput and autonomy. The different fragmentation techniques include low energy 'ion trap' collision induced dissociation (CID) and high energy 'QTOF-like' CID that can be put into force for structural elucidation of the peptide backbone and to gather peptide sequence information. Post-translation modification information with respect to the nature of the modification, as well as topochemical information can be obtained using electron transfer dissociation (ETD).

The platform makes it possible to:

- Perform parallel MS and MSn analysis
- Analyse complex peptide samples used for bottom-up protein identification
- *De novo* peptide sequencing
- Obtain structural information of post-translation modifications using MSn
- Obtain positional information of post-translation modifications, e.g. phosphorylation or glycosylation, using ETD
- Obtain quantitative information using high energy CID combined with isobaric labeling for differential protein profiling and molecular marker discovery
- Characterize proteins using top-down protein identification

Main Features (Equipment Capabilities):

- Resolving power of >100,000
- Mass accuracy better than 1 ppm
- Multiple fragmentation techniques: CID, HCD and ETD
- Ion charge state selection
- MS*n* analysis (n<= 10)
- Parallel MS and MS*n* analysis
- On-line 2D nano ultra high-pressure LC analysis

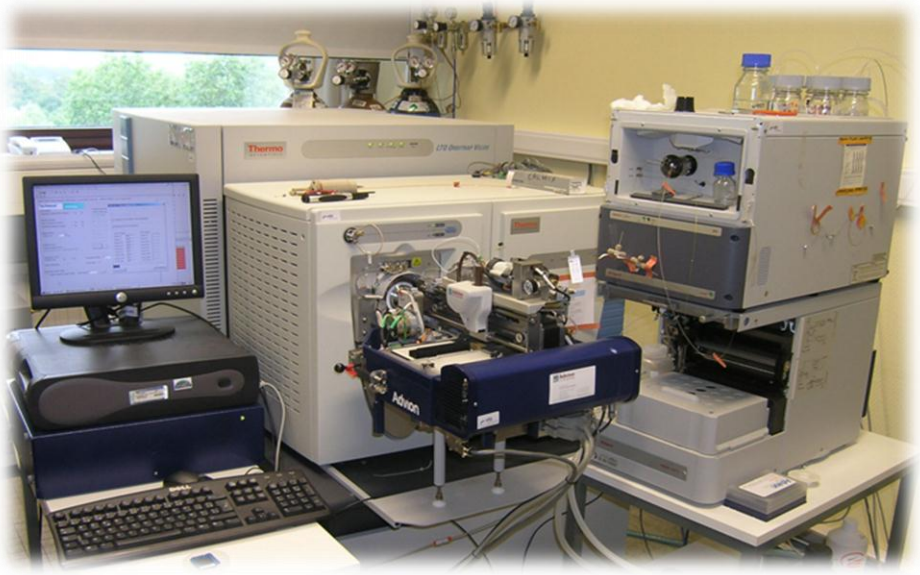
Typical Samples & Images:

Limitations and Constraints:

- Protein/peptide sample should be prepared according to a strict protocol and should not contain polymers, detergents and/or large quantities of salts
- Final sample volume should be between 20 nanoliter and 20 microliter
- Sample concentrations are typically between 10 nanogram and 10 microgram

Material examples:

- Protein/peptide extracts from plant/animal cell cultures or tissue for differential protein profiling
- Protein/peptide extracts from human/animal matrices (eg blood, lacrimal fluid, saliva, urine...) for molecular marker screening
- Protein/peptide samples for structural elucidation of post-translation modifications



Any further Information: