

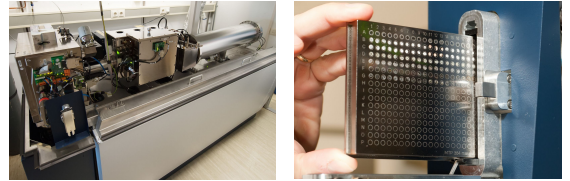
## Maldi-TOF/TOF-MS

<https://search.researchequipment.wur.nl/SearchDetail.aspx?deviceid=6dde0ecb-1b66-48ca-aa5c-1cc6358fbf4b>

### **Brand**

Bruker

### **Type**



### **Contact**

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### **Organisation**

Agrotechnology & Food Sciences Group

### **Department**

Food Chemistry

### **Description**

Matrix assisted laser desorption/ionisation - time of flight mass spectrometry (MALDI-TOF MS) is a rapid, accurate and sensitive technique for providing molecular weight information of compounds like proteins, peptides, oligonucleotides, nucleic acids and carbohydrates.

Its relative high tolerance towards contaminations (e.g. salts), makes it a valuable technique, complementary and competitive to other mass spectrometric techniques having other ionisation principles. The mass accuracy of the UltraFlextreme is 1 - 5 ppm and the mass resolution goes up to 40000 in reflector mode. The range of molecular weights, which can be analysed by routine with MALDI-TOF MS varies from ca. 100-150.000 Da, although in rare cases proteins with a Mw above 1 MDa have been analysed successfully. With the UltraFlextreme it is also possible to perform MS/MS on every peak in the spectra using the TOF/TOF option.

#### Principle

Sample material, co-crystallised with a matrix compound, is irradiated with laser light (334 nm). The matrix molecules adsorb the energy and transfer this energy to the molecules of interest under the addition of a proton (proteins and peptides) or sodium ion (carbohydrates). After ionisation, the molecules are accelerated by the voltage difference between the sample plate and the grid wire. All ions receive the same amount of energy and, therefore the flight time to the detector is correlated with the m/z ratio of the ion. To calculate the molecular mass (Mw) from this m/z ratio, the charge of the formed ion should be taken into account.

### **Technical Details**

Supplier: Bruker Daltonics (Bremen Germany)

Specifications: Bruker UltraFlextreme

- 1 kHz smartbeam-II™ laser technology enables ultra-high data acquisition speed in both MS and MS/MS-mode
- Laser focus diameters down to 10 μm for high spatial resolution imaging without pixel overlap
- Wide mass range resolving power up to 40,000 due to proprietary PAN™ technology
- FlashDetector™ combined with new 4 GHz digitizer provides 1 ppm mass accuracy for highest confidence
- MALDI Perpetual™ Ion Source with laserbased self-cleaning in minutes. It's pushbutton concept for removing sample and matrix debris is indispensable for kHz operation

## ***Applications***

- "standard" Proteomics
- Identification of glycopeptides/proteins
- Identification of phosphopeptides/proteins
- Analysing intact proteins (up to 150 kDa)
- Sequencing of peptides and proteins (DeNovo Sequencing)
- Profiling and identification of charged and neutral oligosaccharides
- Identification of phytonutrients (Saponins, Polyphenols etc)
- Identification of bacteria (with BioTyper)