

AP-MALDI HRMS analyses and imaging at LIST

MASSTECH's European Demo and Application Lab

06/06/2019

Gilles Frache

- LIST
 1. AP-MALDI coupled to LTQ/Orbitrap
 2. AP-MALDI HRMS analyses (applications and workflows)
 3. AP-MALDI HRMS imaging (applications and workflows)
- Conclusions & Take home messages:

LUXEMBOURG INSTITUTE OF SCIENCE AND TECHNOLOGY (LIST)

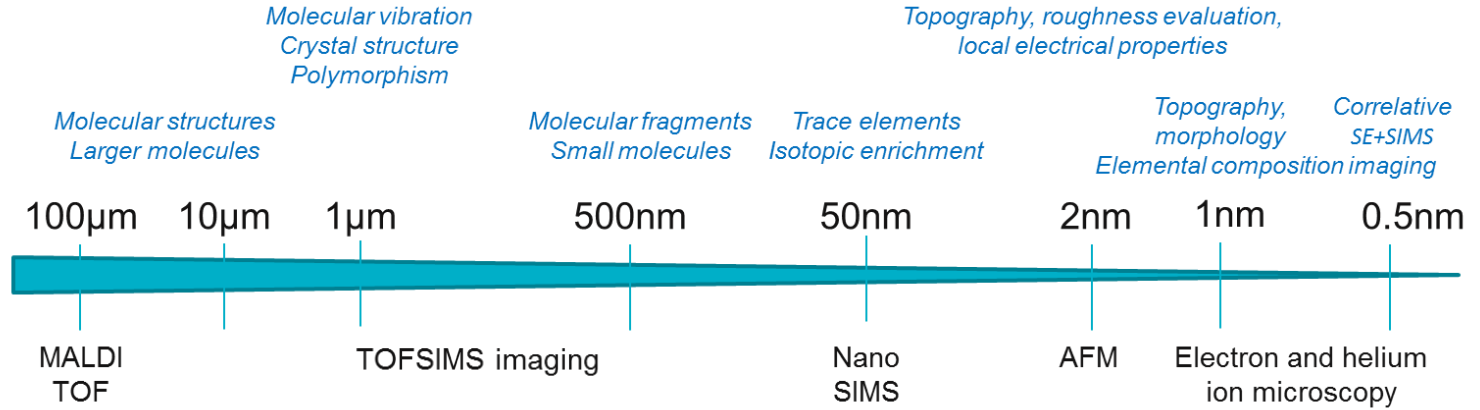
- RTO of 600+ employees, 80+ PhD students, 40 nationalities
- Three main RDI departments:
 - Environmental Research and Innovation (ERIN)
 - IT for Innovative Services (ITIS)
 - Materials Research and Technology (MRT)
 - 4 Main RDI activities:
 - Nanomaterials/Nanotechnology
 - Bio-based & Functional Polymers
 - Scientific Instrumentation & Coatings Process Engineering
 - Composites
- One Transversal Platform: Materials Characterization, Testing, Prototyping and Composites manufacturing



→ European Application & Demo lab

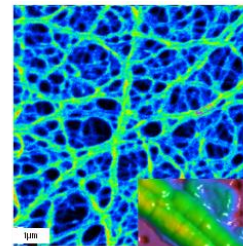
ANALYTICAL IMAGING AT LIST

From micro- to nano- scale

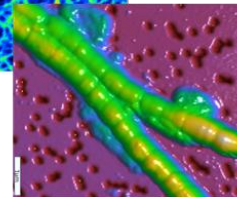


Molecular imaging

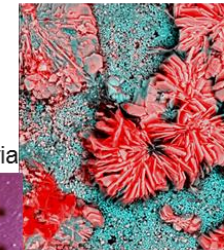
Nanofiber



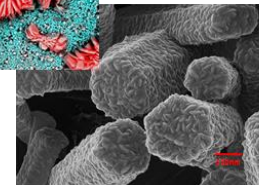
Bacteria



Corrosion

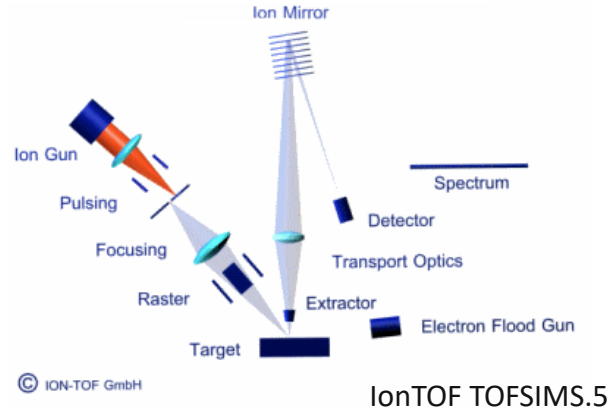
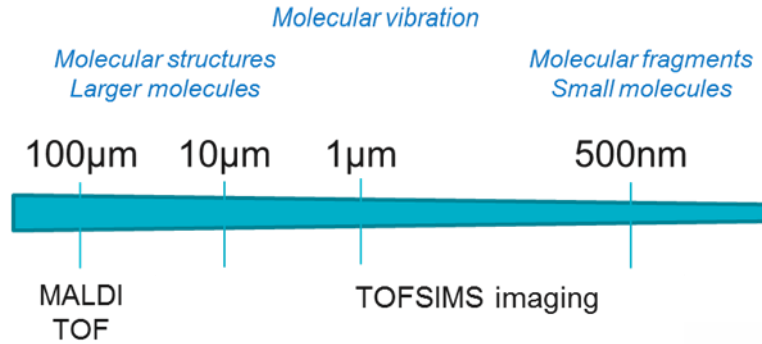


Catalyst on nanowires



ANALYTICAL IMAGING AT LIST

Molecular imaging



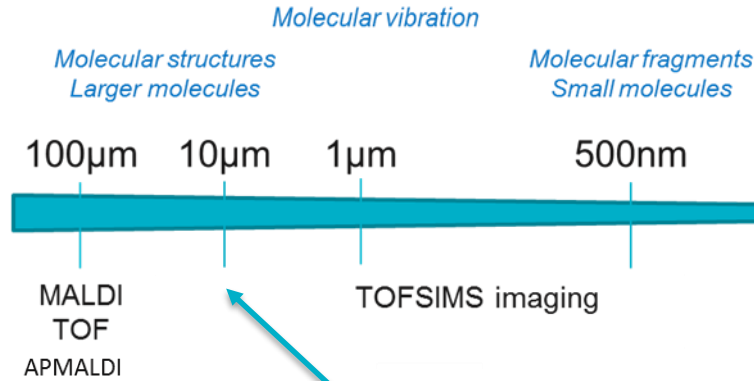
- Pulsed primary ion gun focused down to 400nm
- Very fast TOF analyser (kHz)
- No sample preparation



- Strong ionization (high fragmentation rate)
- Moderate mass resolution (unreliable assignments of m/z signals)

ANALYTICAL IMAGING AT LIST

Molecular imaging

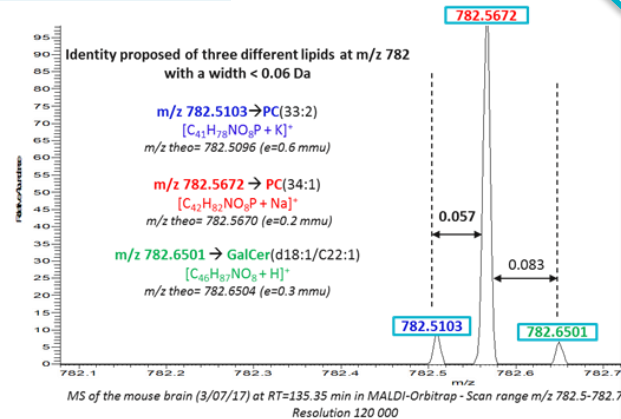


- Softer Ionization → MALDI
 - Reliable identification
 - Exact mass
 - Structural analysis
- LTQ/Orbitrap

- Keep LC/HRMS capability
- Masstech AP-MALDI PDF+ (2012)

- AP-MALDI Imaging capability?
- Masstech AP-MALDI PDF+ (2012)

- Masstech AP-MALDI (ng) UHR



AP-MALDI Imaging with high resolution in mass and space

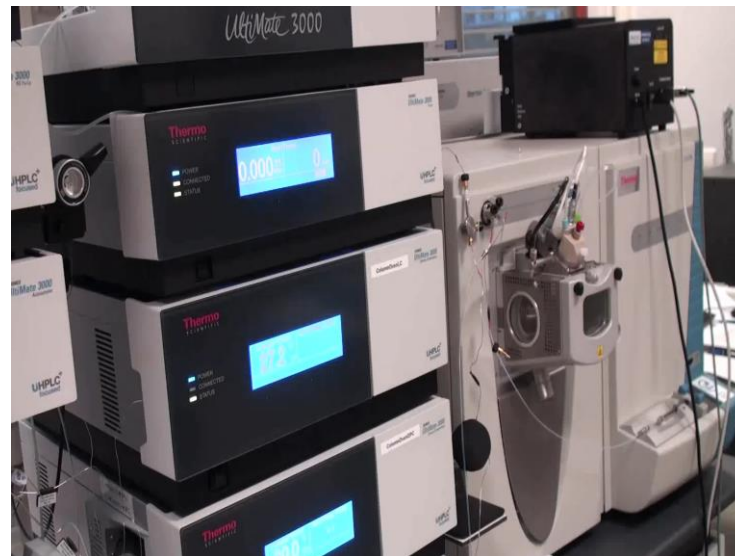
AP-MALDI HRMS



- Benefits of LTQ/Orbitrap :
 - Hybrid mass spectrometer : 2 analyzers
 - Full scan Orbitrap → accurate (but slow)
 - Full scan LTQ → faster (but less accurate)
 - SIM, SRM, → targeted analysis
 - MS/MS, DDA, DIA, → highly informative!
 - AP interface (multiple ionization techniques (ESI, APCI, nanospray, DART...))

- Benefits of AP-MALDI :
 - Flexibility
 - Performances

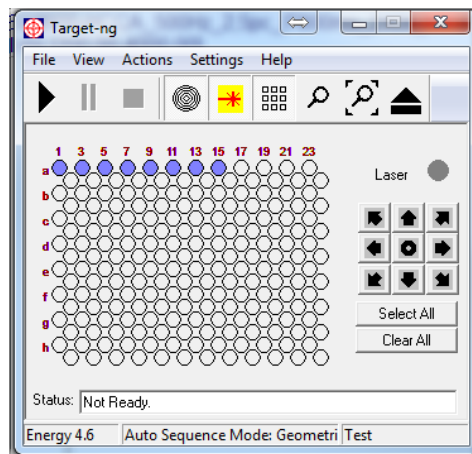
→MALDI analysis and imaging with HRMS analyzer



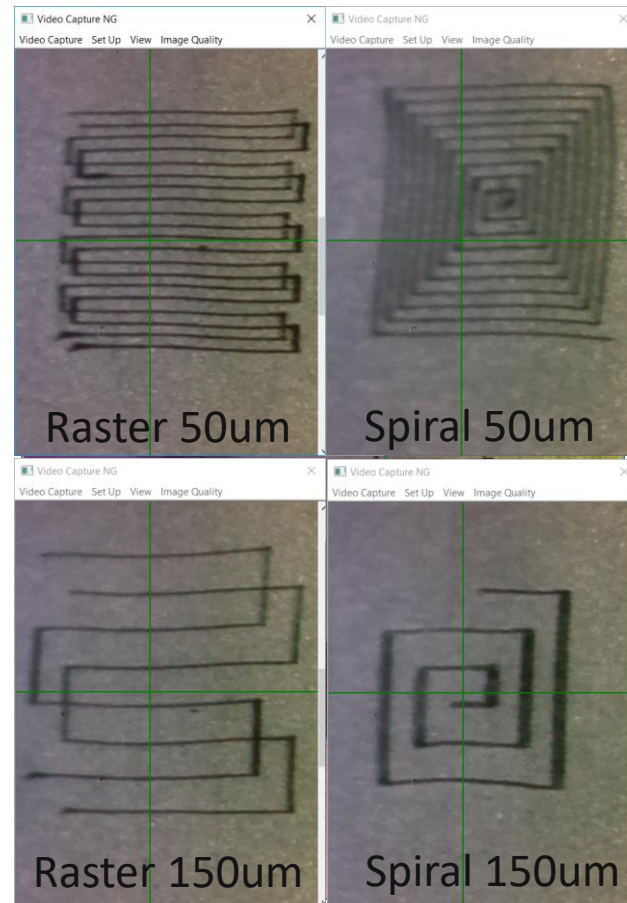
AP-MALDI HRMS ANALYSES

Software: Data acquisition

- Masstech Target®

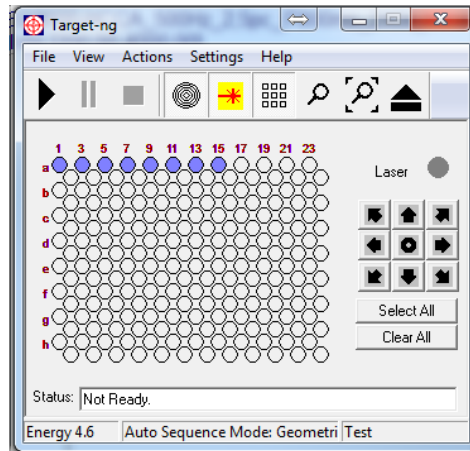


- Spiral or raster motion with tuneable parameters
- Tuneable Laser frequency and Energy
- Irradiation of each sample spot with internal or external timing with tuneable duration



Software: Data acquisition

- Masstech Target®



- Spiral or raster motion with tuneable parameters
- Tuneable Laser frequency and Energy
- Irradiation of each sample spot with internal or external timing with tuneable duration

- Thermo Xcalibur:

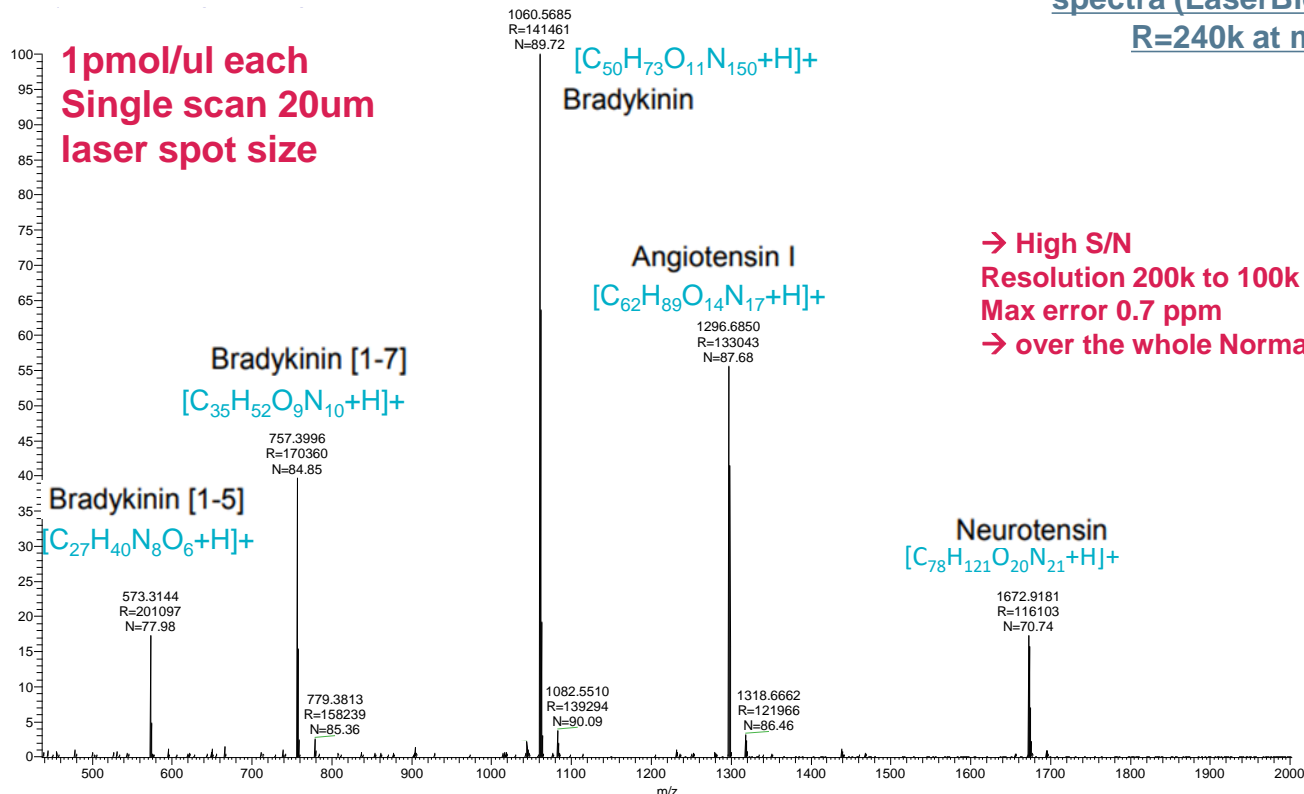
- Selection of the analyzer (LTQ or Orbitrap)
- Single or multiple scan events (full scan, SIM, SRM) or method (DDA, DIA)
- Mass range
- Acquisition started
 - Either from Tune window (all sample spectra in one RAW file)
 - Or from Xcalibur sequence editor (each sample spectrum in one RAW file)

AP-MALDI HRMS ANALYSES

Applications : peptides

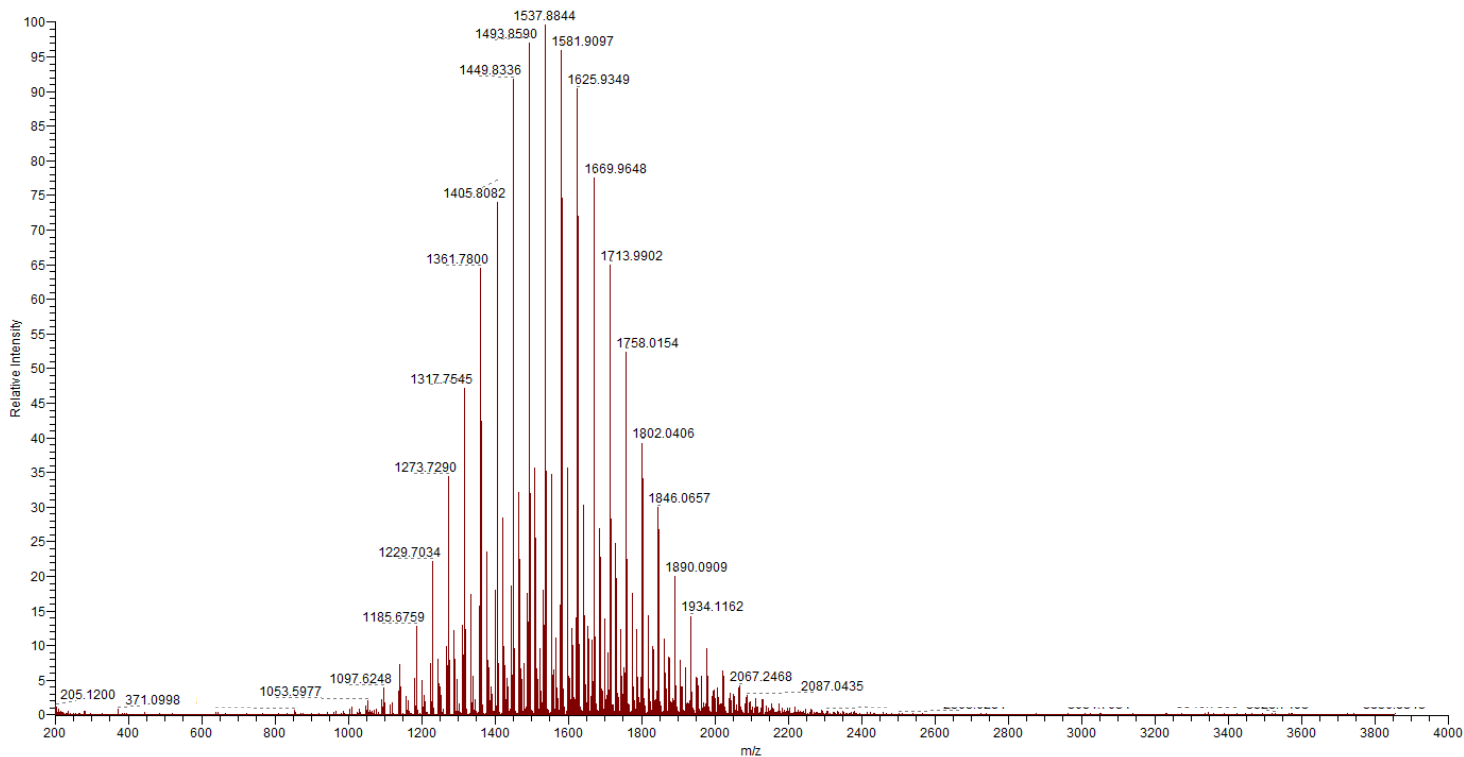
Experimental AP-MALDI HRMS spectra (LaserBioLabs Mix5)

R=240k at m/z400:



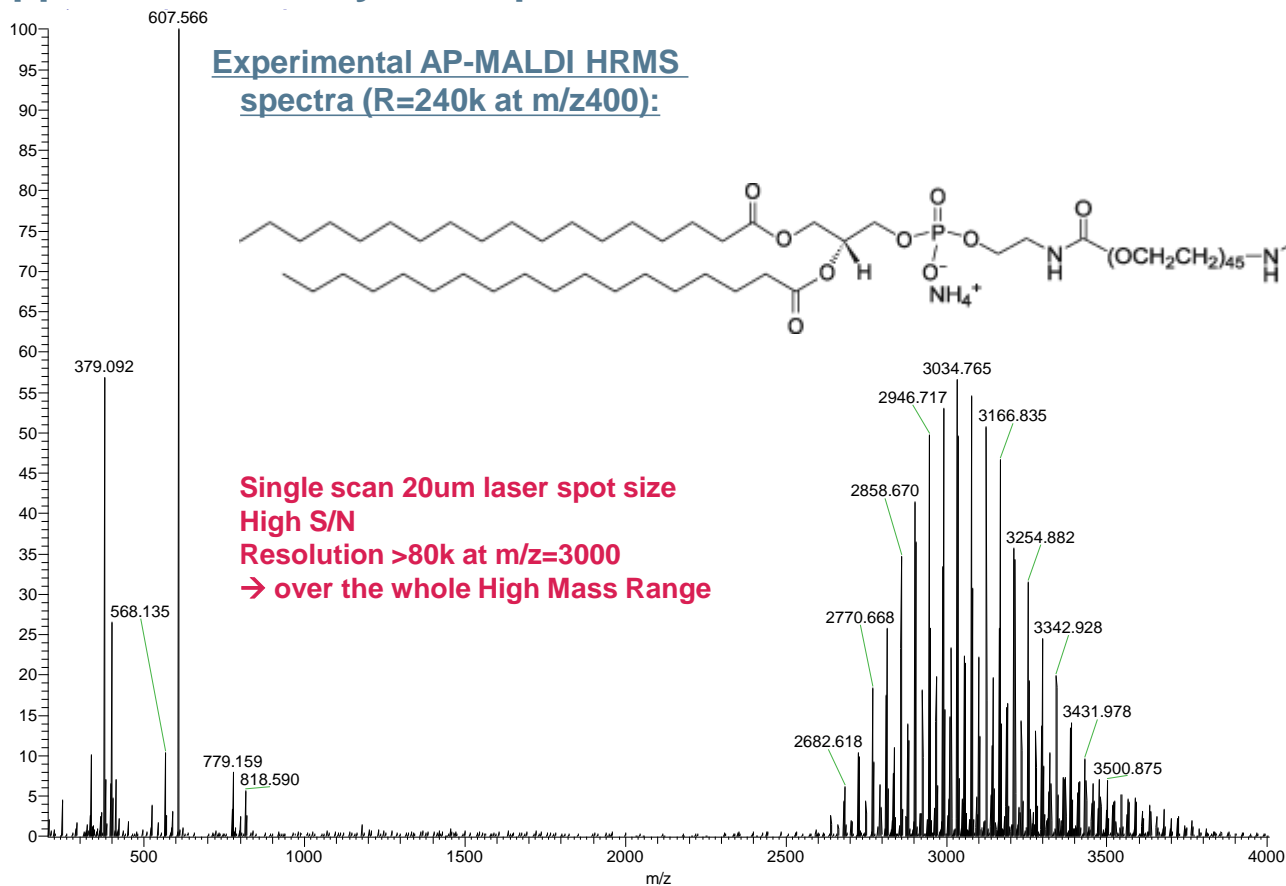
AP-MALDI HRMS ANALYSES

Applications: PEG-1500



AP-MALDI HRMS ANALYSES

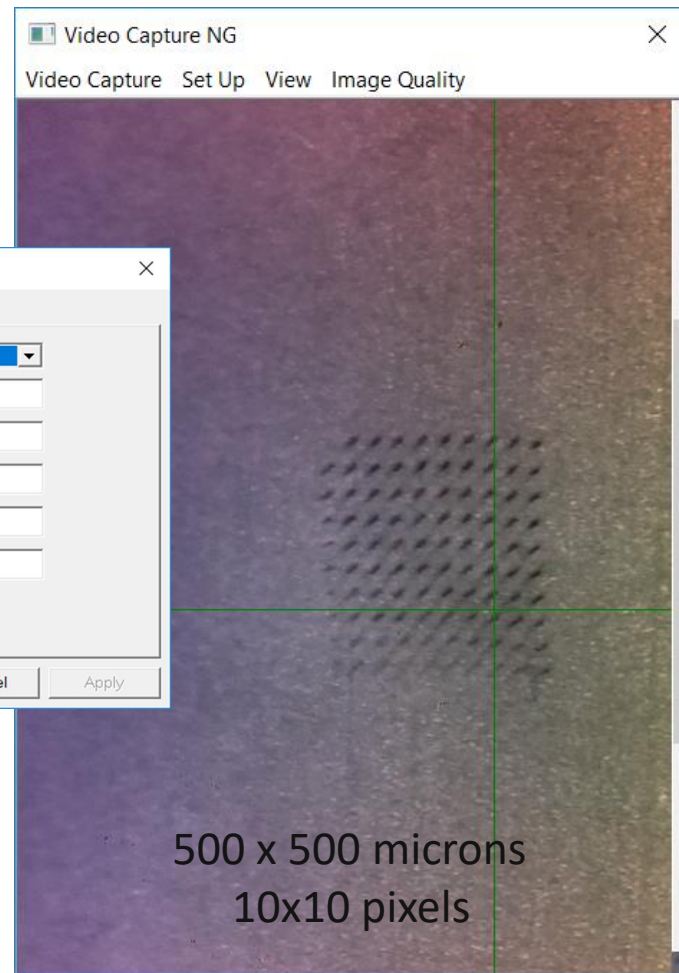
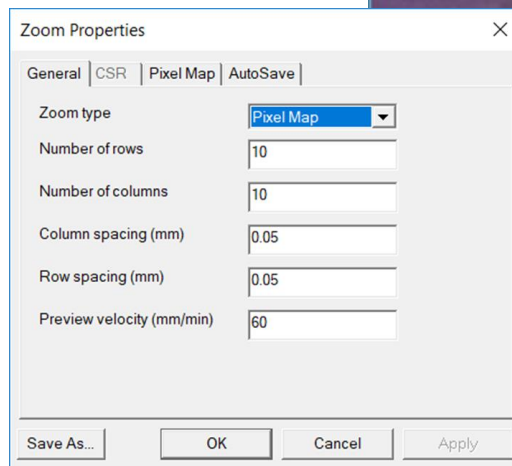
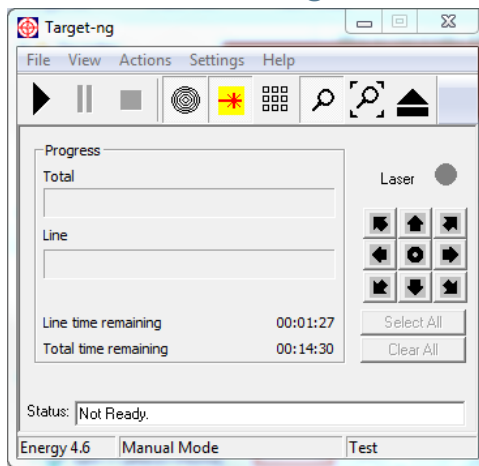
Applications: PEGylated lipid / functionalized PEG



AP-MALDI HRMS IMAGING

Software: Image acquisition

- Masstech Target®



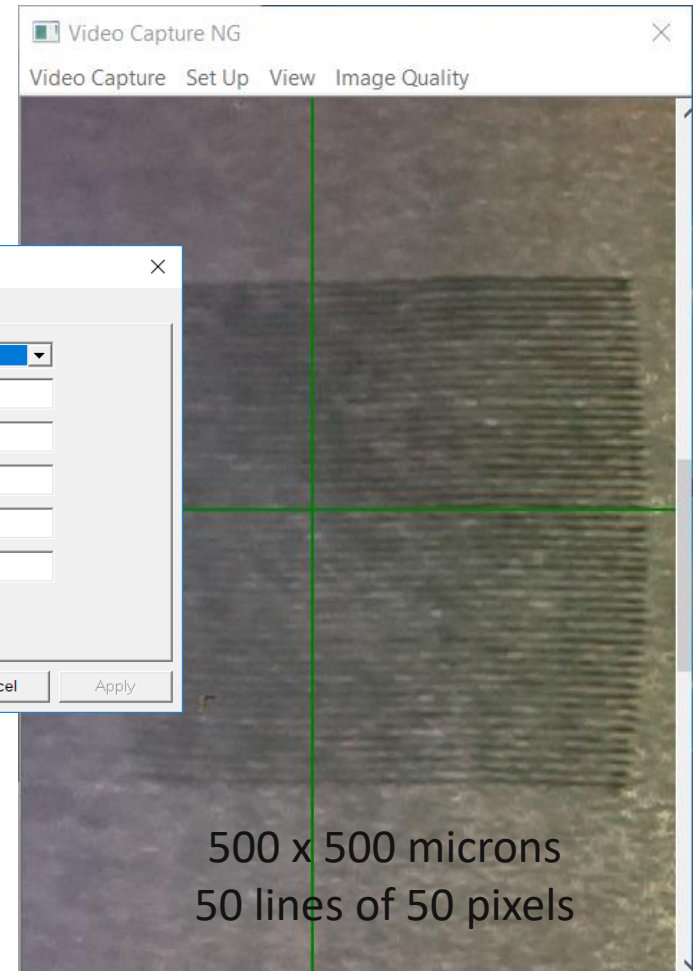
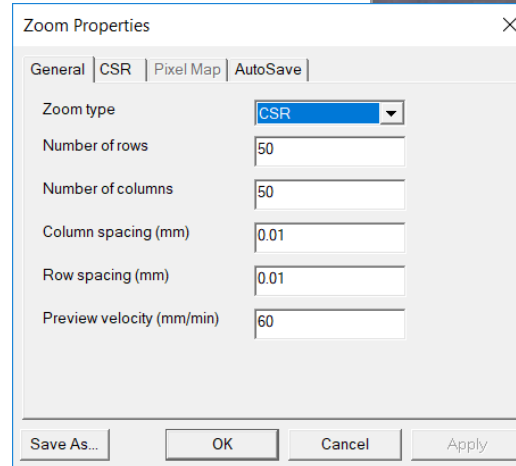
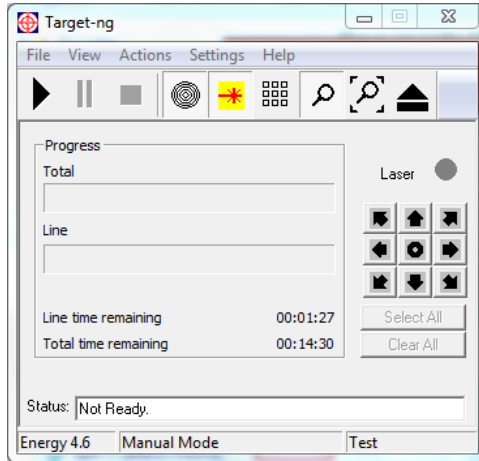
- **PixelMap** : Irradiation of each pixel position
- Constant Speed Raster (CSR) motion: Irradiation of continuous lines (sampled by the mass spectrometer into a given number of pixel per line)

500 x 500 microns
10x10 pixels

AP-MALDI HRMS IMAGING

Software: Image acquisition

- Masstech Target®



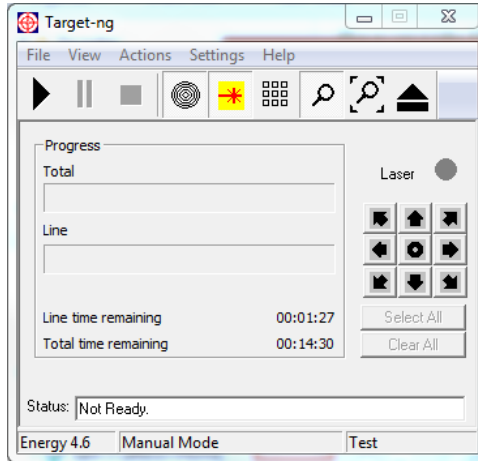
- PixelMap : Irradiation of each pixel position
- **Constant Speed Raster (CSR) motion:**
Irradiation of continuous lines (sampled by the mass spectrometer into a given number of pixel per line)

500 x 500 microns
50 lines of 50 pixels

AP-MALDI HRMS IMAGING

Software: Image acquisition

- Masstech Target®



- PixelMap : Irradiation of each pixel position
- Constant Speed Raster (CSR) motion:
Irradiation of continuous lines (sampled by
the mass spectrometer into a given
number of pixel per line)

- Thermo Xcalibur:

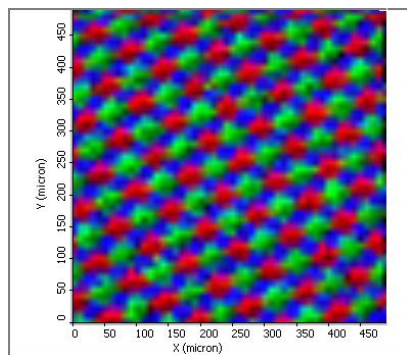
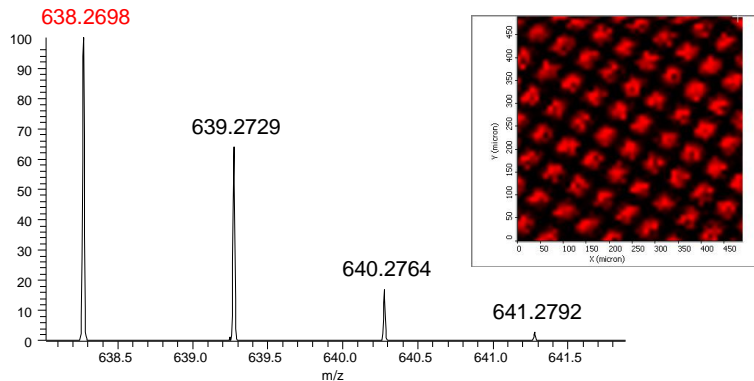
- Selection of the analyzer (LTQ or Orbitrap)
- Single or multiple scan events (full scan, SIM, SRM) or method (DDA, DIA)
- Mass range
- Acquisition started using synchronization cable, and stopped after duration (estimated by Target software)

- Thermo ImageQuest:

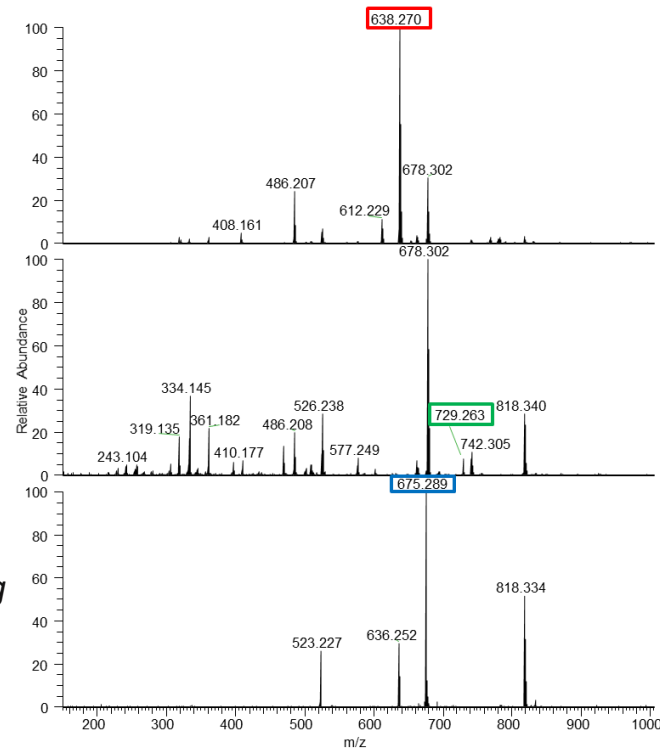
- Combines Raw files (+ Target xml position file) into MALDI images
- Alternatively, imzML open source format can be used.
→ MSI Reader, DataCube Explorer, SCILS..

APMALDI HRMS IMAGING

Application to OLEDs imaging



500um x 500um
AP/MALDI(ng) UHR imaging
of a portion of an OLED
display (R: m/z=638.2685,
G: m/z=729.2635,
B: m/z=675.2890)



→ AP-MALDI HRMS imaging
at 10 micron lateral resolution

Whole brain imaging



Sagittal mouse brain cryo-section

Sample preparation (Univ Swansea)

APMALDI imaging :

- CSR mode
- 30 micron resolution
- 350x230 = 80500 pixels

Orbitrap

- full scan (300-1200)
- 30k or 60k
- 1.5 to 2.5 pixels/second

6.5 GB, 15hrs @60k

APMALDI HRMS IMAGING

Whole brain imaging

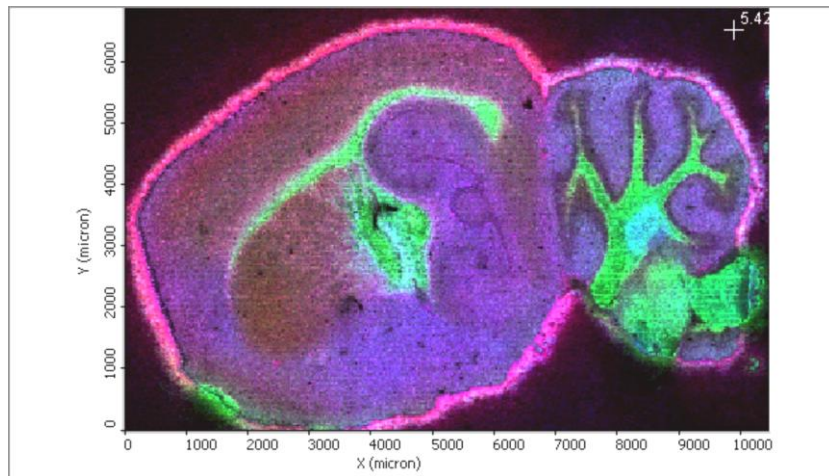
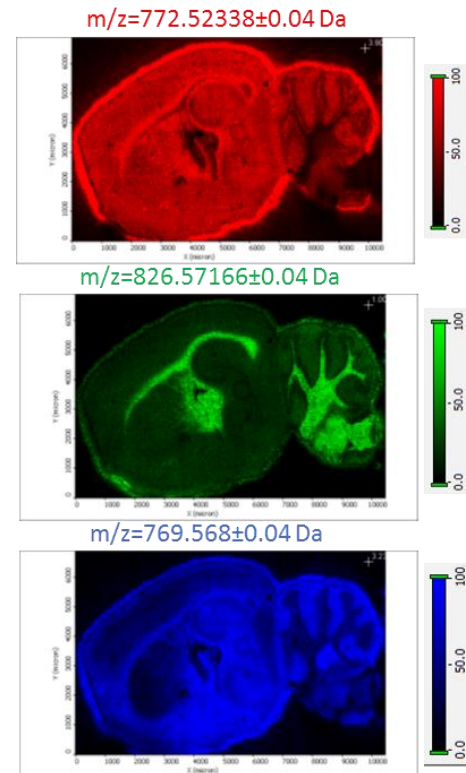
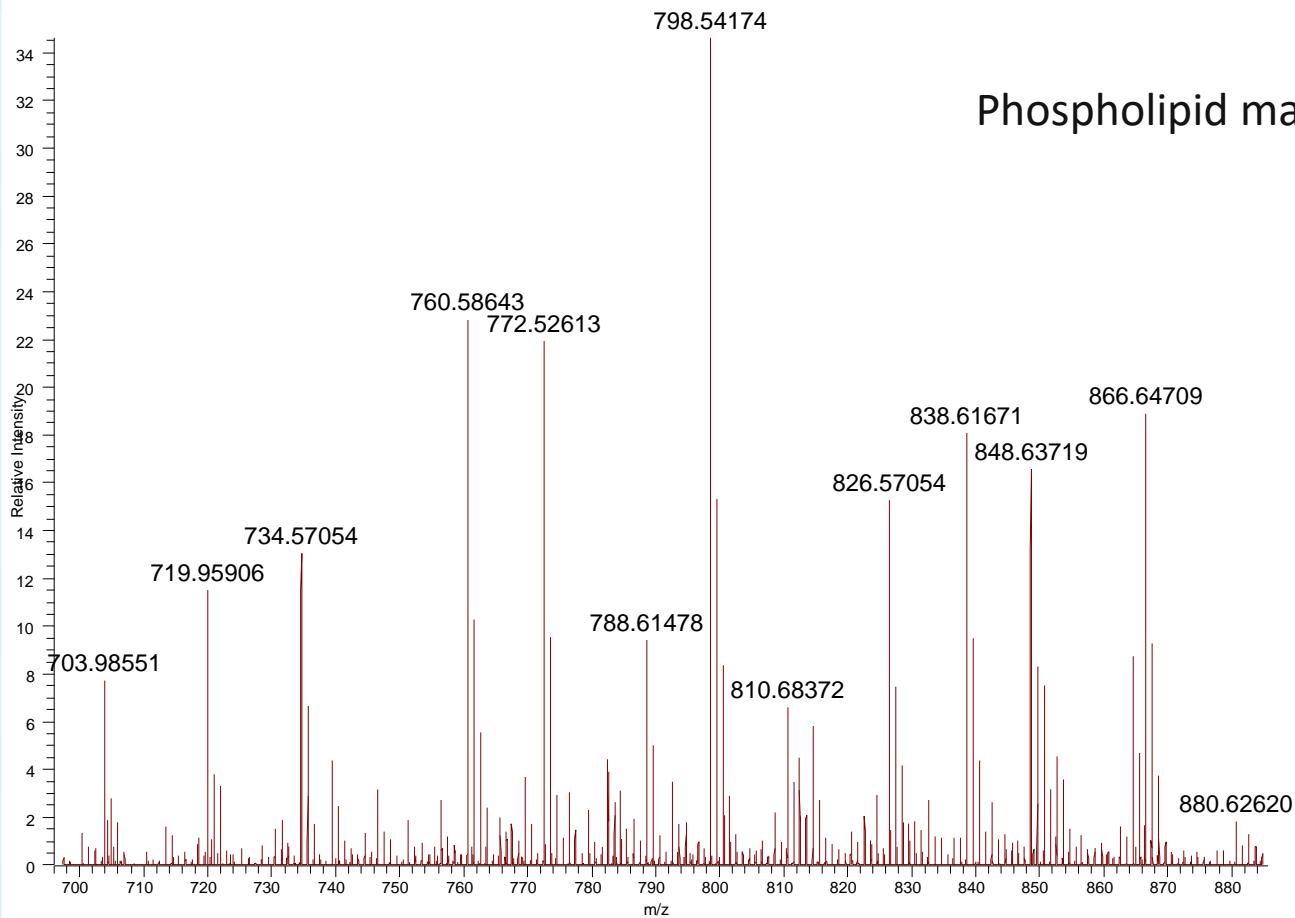


Fig.3: Overlaid AP-MALDI HRMS images of 3 lipids with a mass tolerance of 0.04Da (red: $m/z=772.52338$, green: $m/z=826.57166$, and blue : $m/z=769.568$) obtained using ImageQuest software



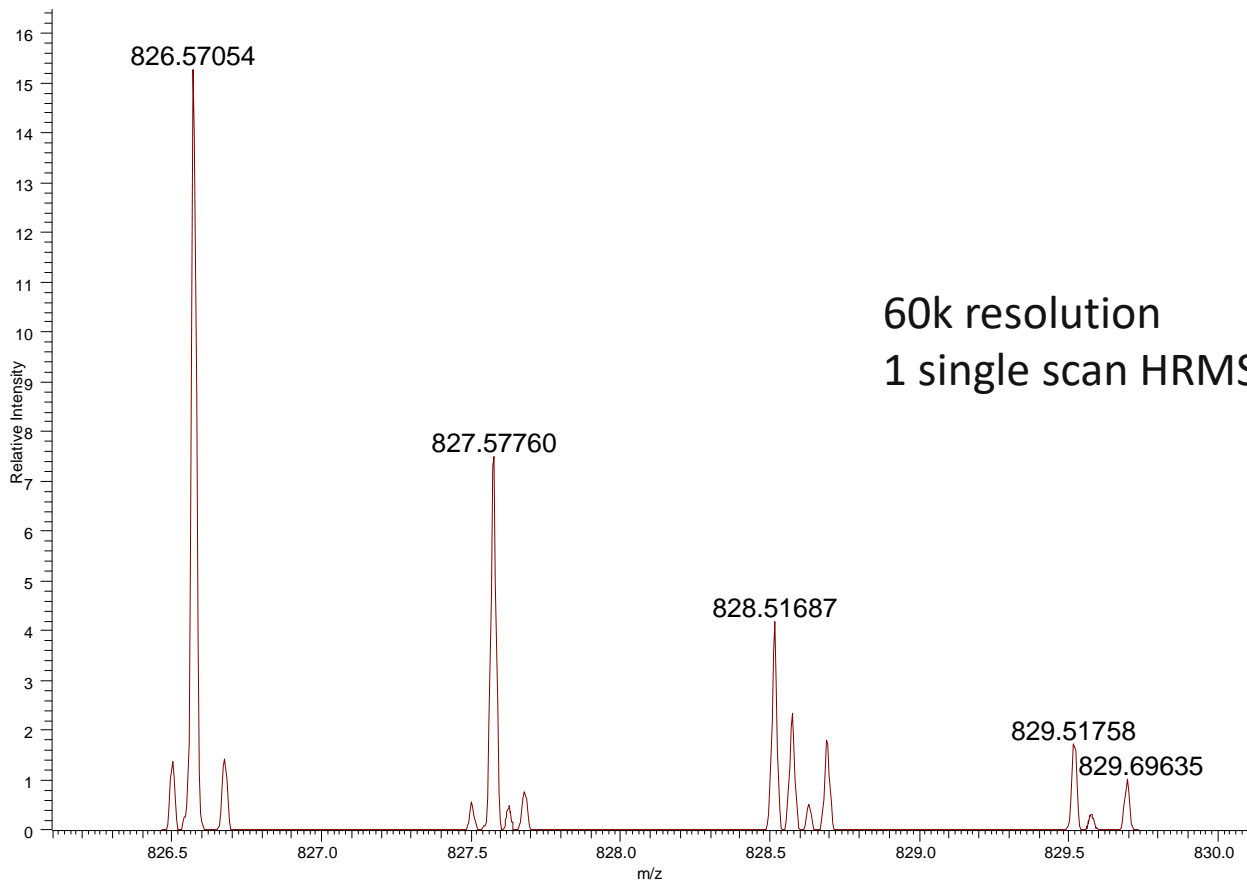
SINGLE SCAN / SINGLE PIXEL HRMS

#49898 AV:2 ST:0.62 uS: 1 NL: 2.83E4



SINGLE SCAN / SINGLE PIXEL HRMS

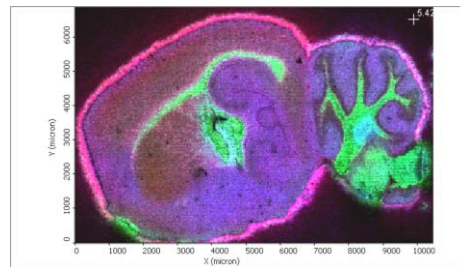
#49898 AV:2 ST:0.62 uS:1 NL:2.83E4



APMALDI HRMS IMAGING

Whole brain imaging

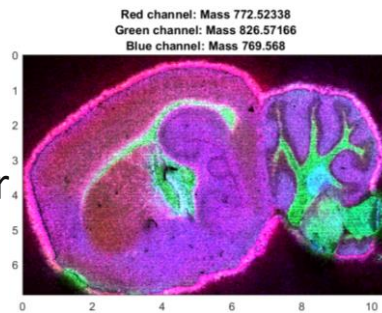
Thermo
RAW file
+ Target
XML file



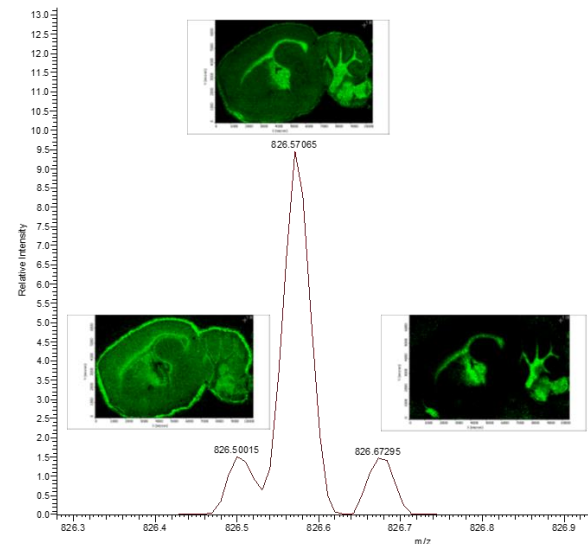
Thermo ImageQuest

Thermo
RAW file
+ Target
XML file

imzML
converter



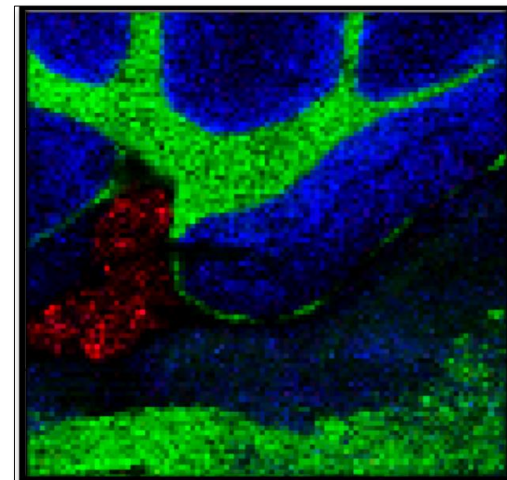
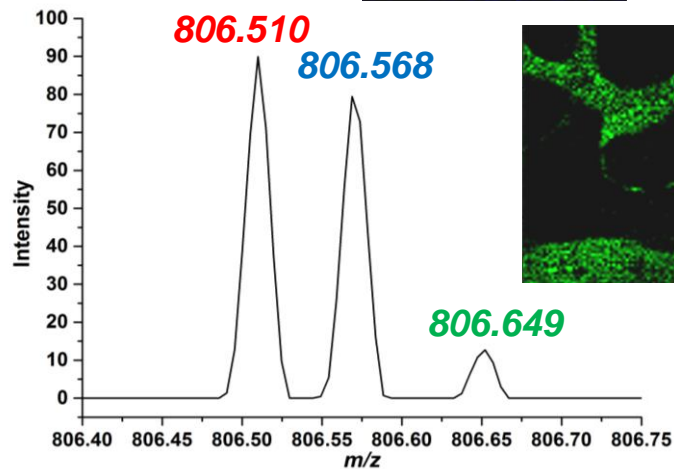
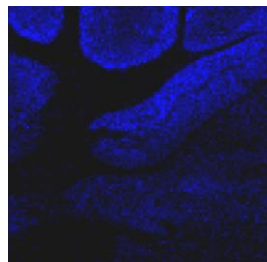
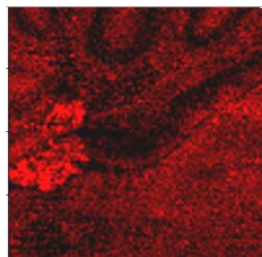
MSI Reader



Single pixel mass spectrum showing 3 intact lipids in a 0.3Da mass window

APMALDI HRMS IMAGING

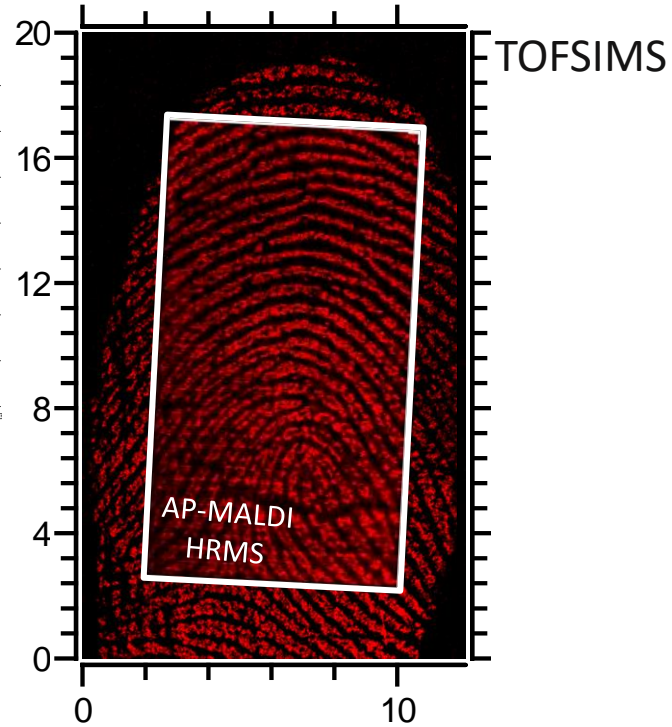
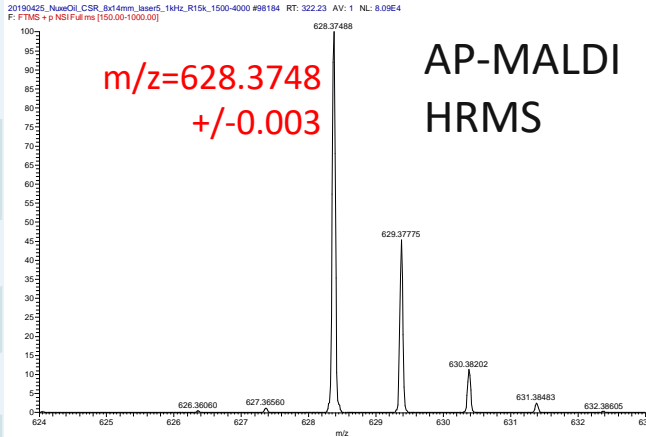
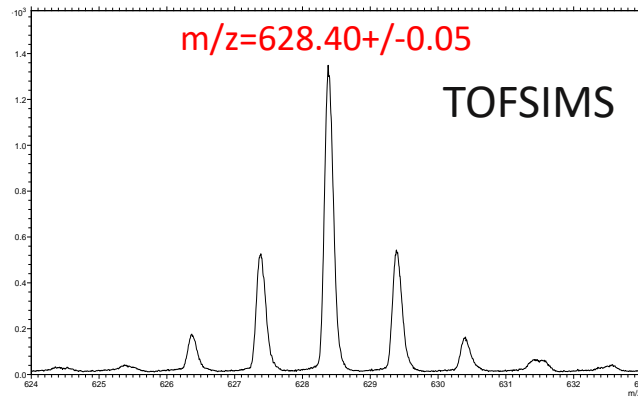
Down to 10 micron lateral resolution



RGB Overlay

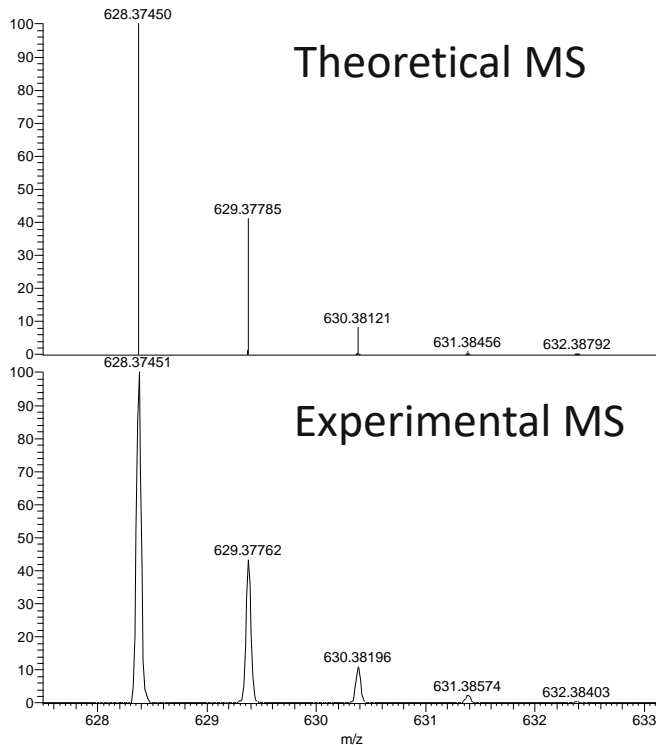
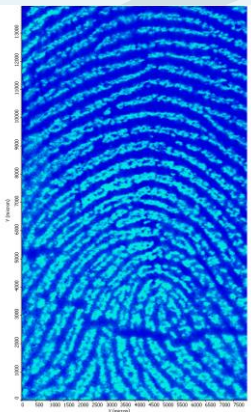
MULTIMODAL IMAGING

Skin applications



AP-MALDI HRMS IMAGING

Accurate Formula assignment

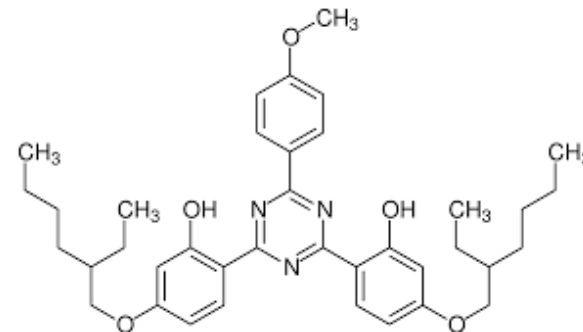


NL:
6.45E5
C₃₈H₅₀O₅N₃
C₃₈H₅₀O₅N₃
pa Chrg 1

$$628.37450 = [C_{38}H_{49}N_3O_5 + H]^+$$

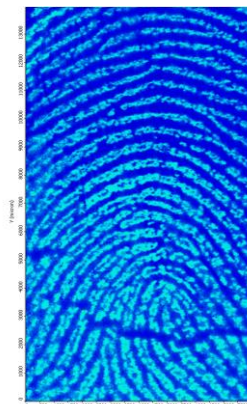
NL:
6.69E4
20190425_NuxeOil_CSR_8x1
4mm_laser5_1kHz_R15k_150
0-4000#309 RT: 1.00 AV: 1
T: FTMS + p NSI Full ms
[150.00-1000.00]

Bemotrizinol ?

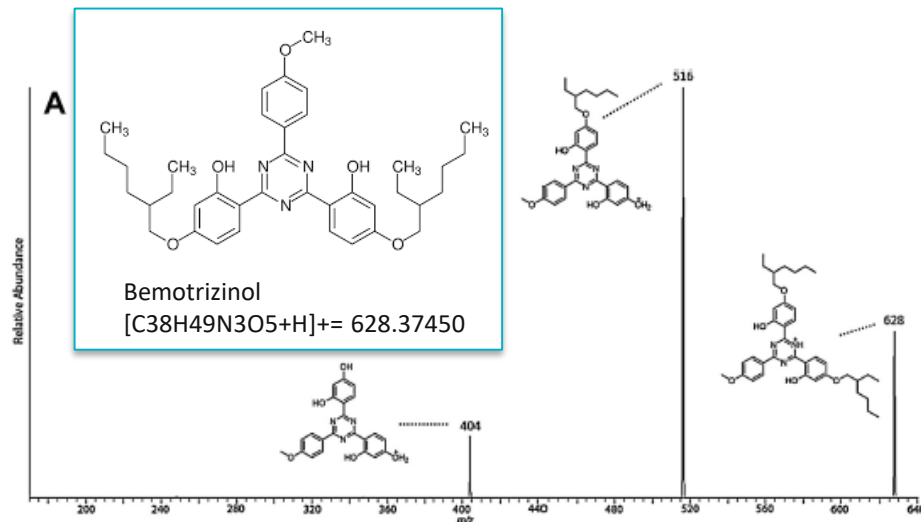


AP-MALDI MS/MS IMAGING

Structural confirmation and/or Targeted imaging



Bemotrizinol ?

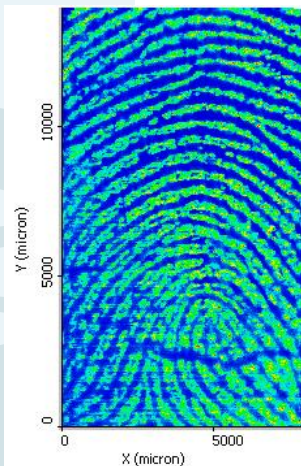
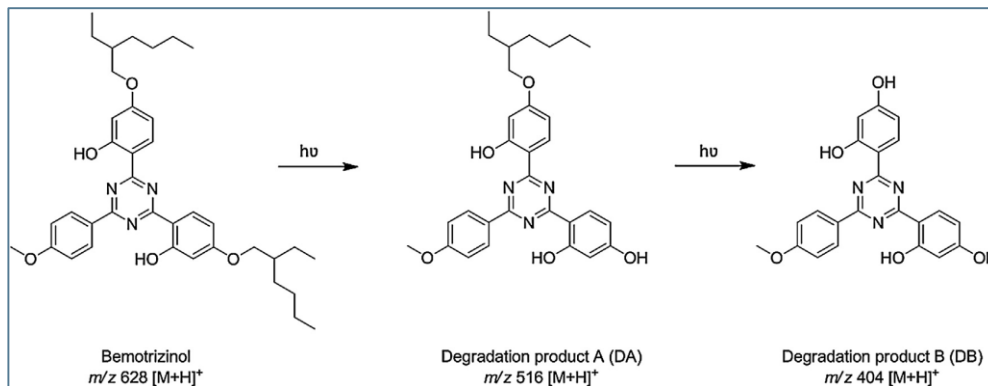


Collision-induced dissociation (CID) spectrum of (A) Bemotrizinol

→ Possible application : Structural confirmation of active ingredient by Multiscan imaging (Fullscan + SRM)

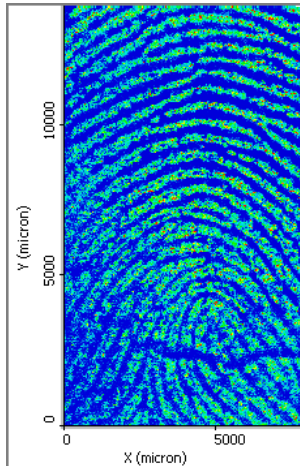
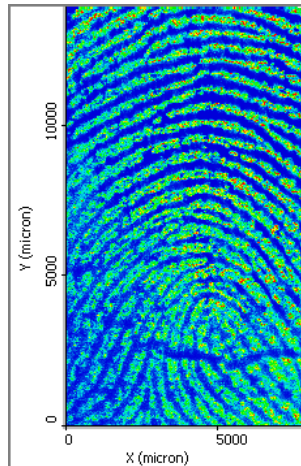
EFFECT OF AGING (UV)

Degradation products



← Bemotrizinol
Max=2e5

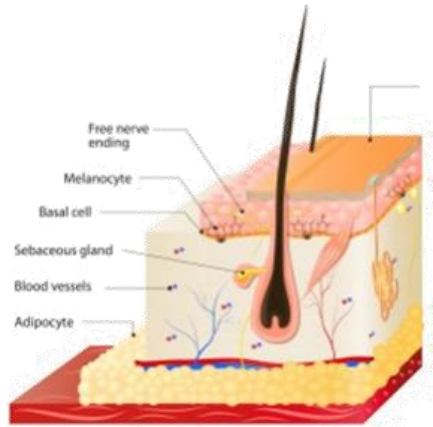
Degradation pdt #1 →
 $[C_{30}H_{33}N_3O_5+H]^+$
 $m/z=516.24930$
Max=1.6e3



← Degradation pdt #2
 $[C_{22}H_{17}N_3O_5+H]^+$
 $m/z=404.12410$
Max=1.6e3

OUTLOOKS

Correlative molecular imaging HRMS on skin

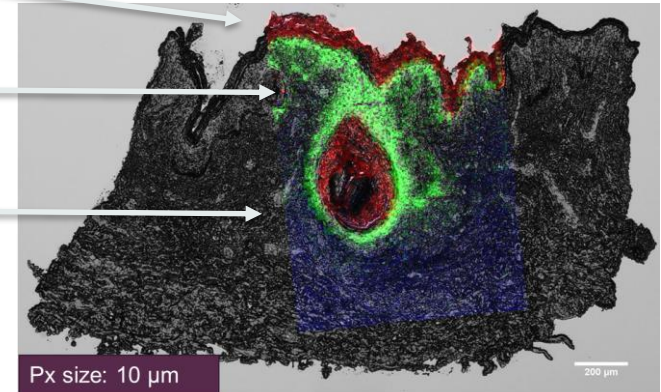


Stratum corneum

Epidermis

Dermis

Hypodermis



■ Ceramide m/z 386.399

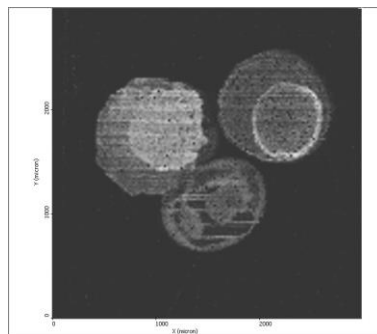
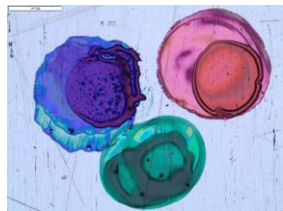
■ Phosphoethanolamine PE(36:2) m/z 744.553

■ Peptide m/z 582.273

→ Application to penetration studies, skin diseases

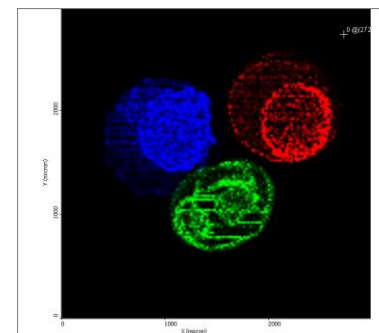
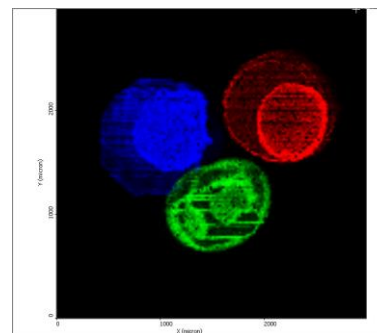
COMBINED MODE OF ANALYSIS

Fullscan (120k Orbitrap) + 3 MS/MS (LTQ)



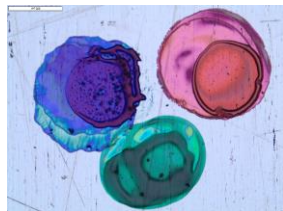
AP-MALDI HRMS
imaging
(Orbitrap@120k)
 $m/z=443.23257$
 $m/z=385.26263$
 $m/z=478.32063$

AP-MALDI MS/MS
imaging (LTQ-MSMS
scan, @CID:60):
 443.23 , 385.26 , 478.32
→ structural confirmation

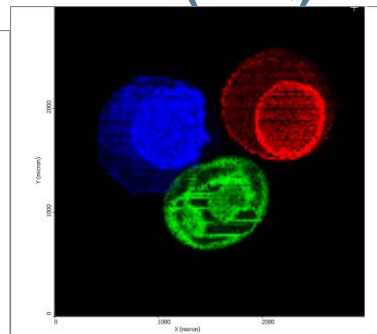
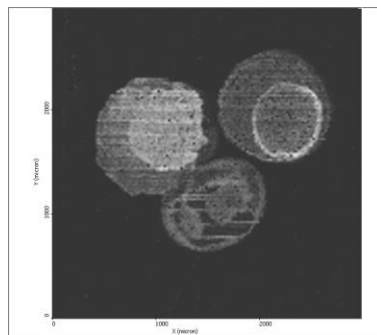


COMBINED MODE OF ANALYSIS

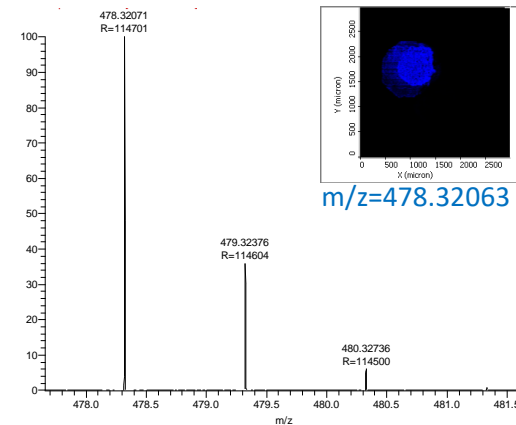
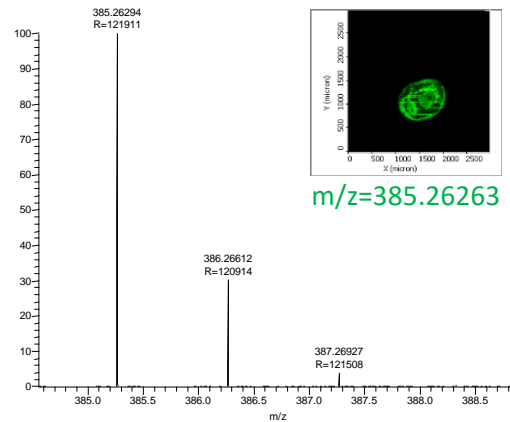
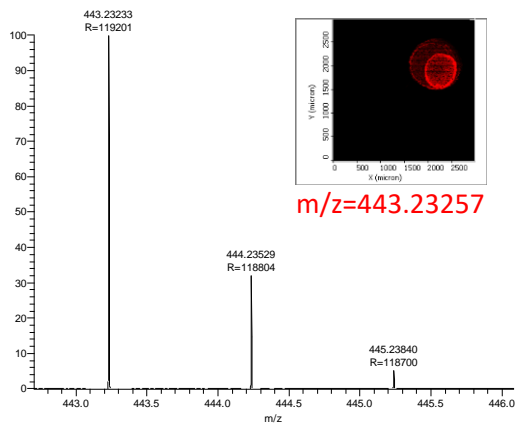
Fullscan (120k Orbitrap) + 3 MS/MS (LTQ)



MR(443.23157)
MR(385.26263)
MR(478.32063)

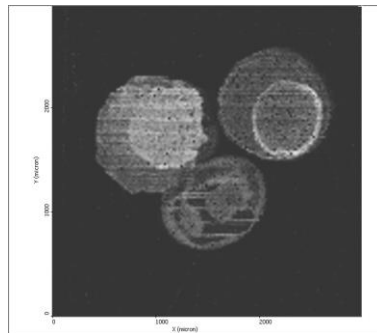
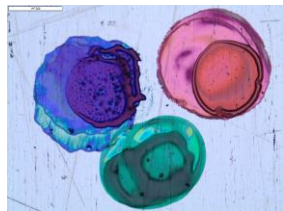


AP-MALDI HRMS
imaging
(Orbitrap@120k)
 $m/z=443.23257$
 $m/z=285.26263$
 $m/z=478.32063$

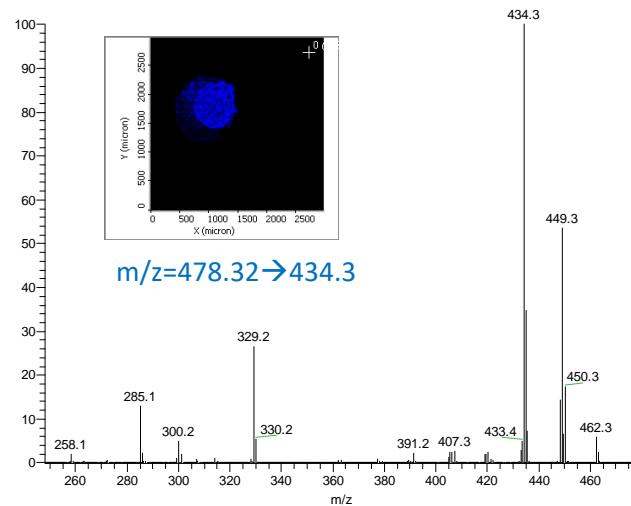
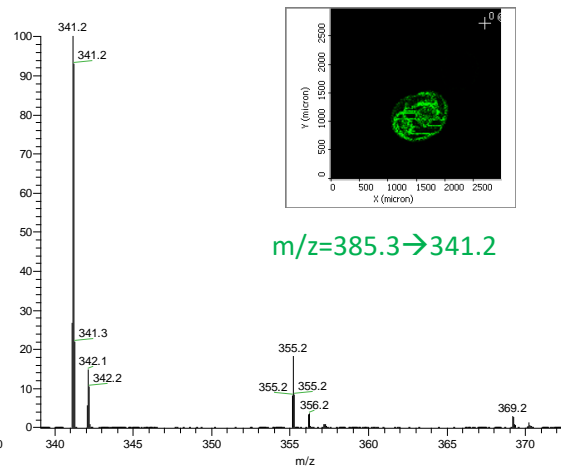
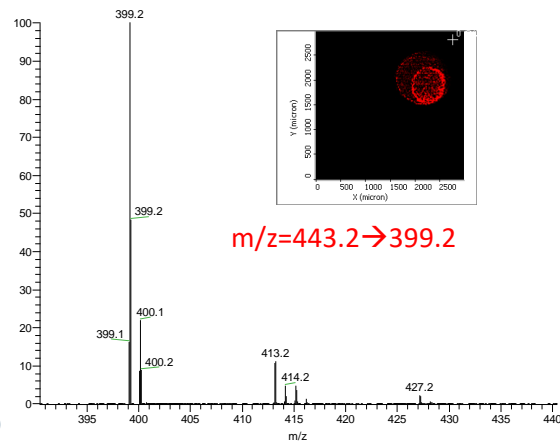
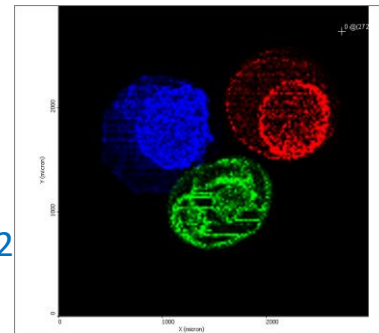


COMBINED MODE OF ANALYSIS

Fullscan (120k Orbitrap) + 3 MS/MS (LTQ)



AP-MALDI MS/MS
imaging (LTQ-MSMS
scan, @CID:60):
443.23, 385.26, 478.32



- **Masstech AP-MALDI (ng) UHR** source :
 - provides high performances MALDI analysis and imaging (sensitivity and lateral resolution)
 - cost-effective add-on module for LCMS instruments, ideally coupled to high-end HRMS instrument
 - flexible: ESI-APMALDI swap is done within a few minutes, the HRMS can still work in LC/HRMS configuration.

ACKNOWLEDGEMENTS



Richard Lee
Vladimir Doroshenko
Eugene Moskovets
Konstantin Novoselov



Sue Kennerley



Dana El Assad
Morgane Janin
Jérôme Bour
Jessica Desport

- Pr. William Griffiths, Swansea University
- Dr. Carine Jacques Jamin (Laboratoires Pierre Fabre Dermo-cosmetique)
- Pr. Maria Lorena Cordero Maldonado (LCSB, Uni Luxembourg)

