

AP/MALDI COUPLED TO ORBITRAP INSTRUMENTS : RECENT DEVELOPMENTS

Gilles Frache

Luxembourg Institute of Science and Technology (LIST)

gilles.frache@list.lu

03.06.2025



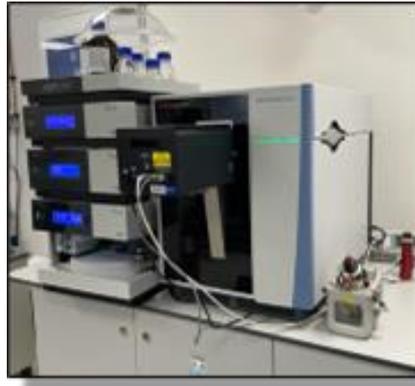
MASSTECH AP/MALDI UHR ION SOURCE

Benefits

- Compatible with various high-resolution LC/HRMS models



AP/MALDI on Orbi Elite 2012-2022 (LIST)



AP/MALDI on Exploris 480 (LIST)

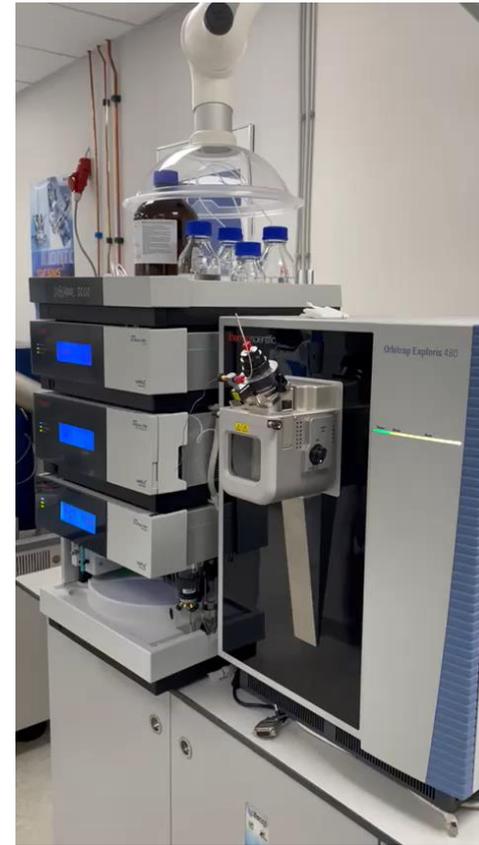


AP/MALDI on ASTRAL
(demo in INSA Toulouse)

MASSTECH AP/MALDI UHR ION SOURCE

Benefits

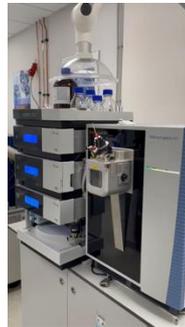
- Swap ESI to AP/MALDI within a minute
- Compatible with various high-resolution LC/HRMS models
- Fully integrated design
 - a solid-state Nd:YAG (355nm 100-10000Hz), Laser Safety compliant, focus below 10 μm
 - all electronics, optics,
 - 5 μm accuracy sample stage with AB OptiTOF192 plate and Video camera



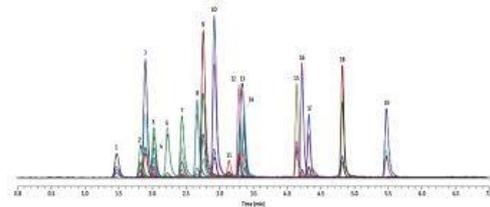
Orbitrap Bulk + Spatial multiomics Workflow



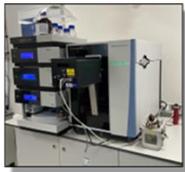
Extracts



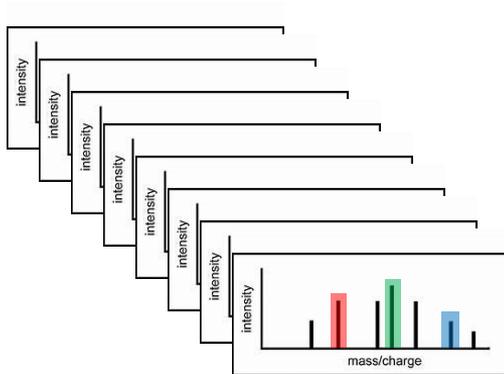
LC/Orbitrap HR MS/MS analyses
(FS, DDA, DIA, tMS2, AcquireX)



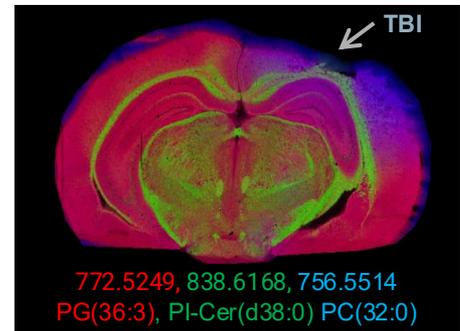
Cryo-sections



AP/MALDI Orbitrap HR MS imaging
(FS, DDA, DIA, tMS2)



m/z1 m/z2 m/z3

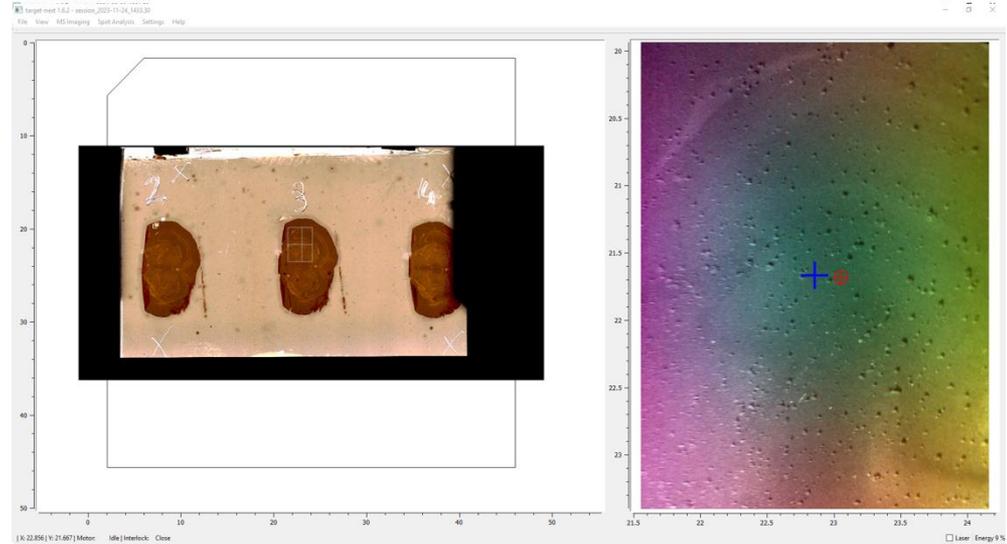


New Target Control software

Key features

- Optical preview

Either a tile preview (stitching of video images) or import optical image from external device



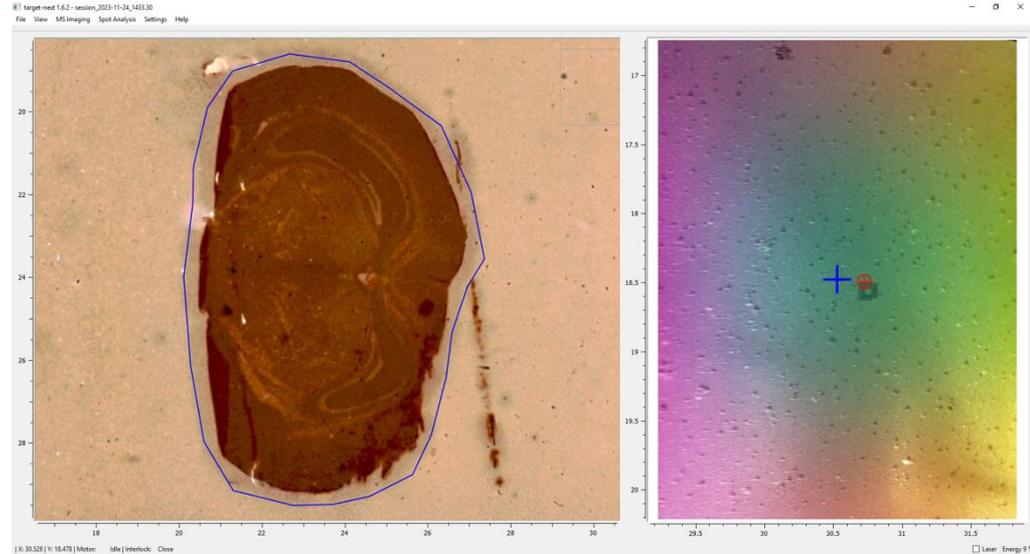
Target Next Control software

Key features

- Select the Regions of interest (ROI)

Free-shape or rectangular imaging area definition

Zoom in for accurate ROI definition

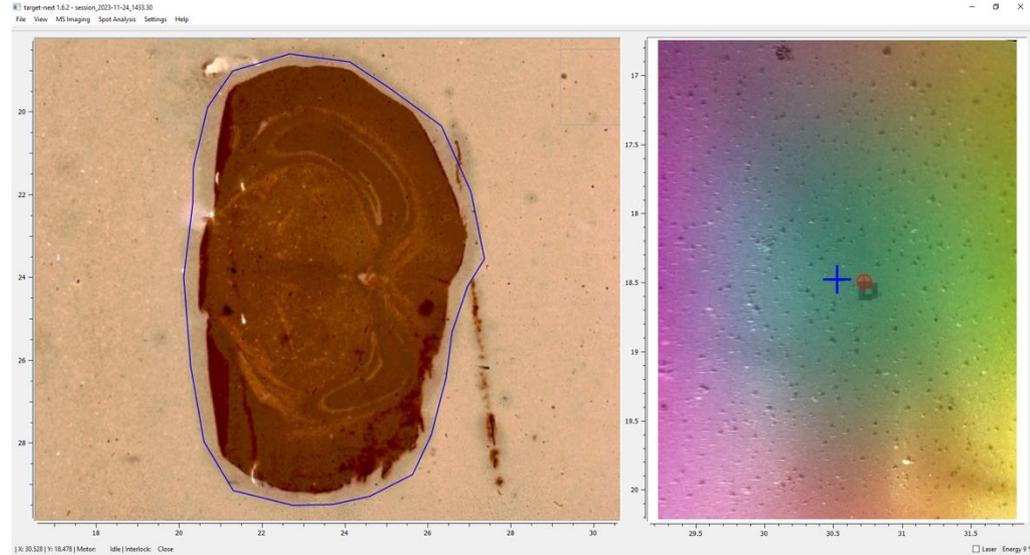
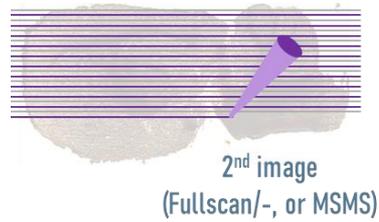
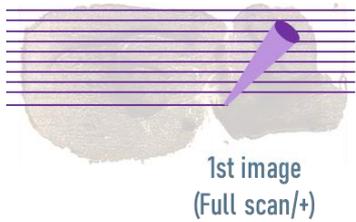


Target Next Control software

Key features

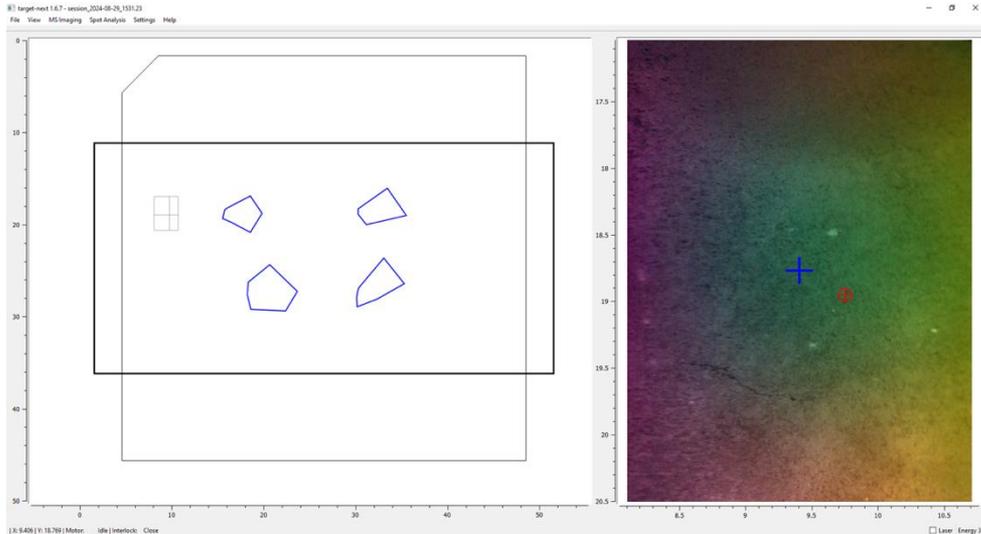
- Successive images from 1 section

Cloning of image areas (interline imaging)



Target Next Control software

Definition of ROIs

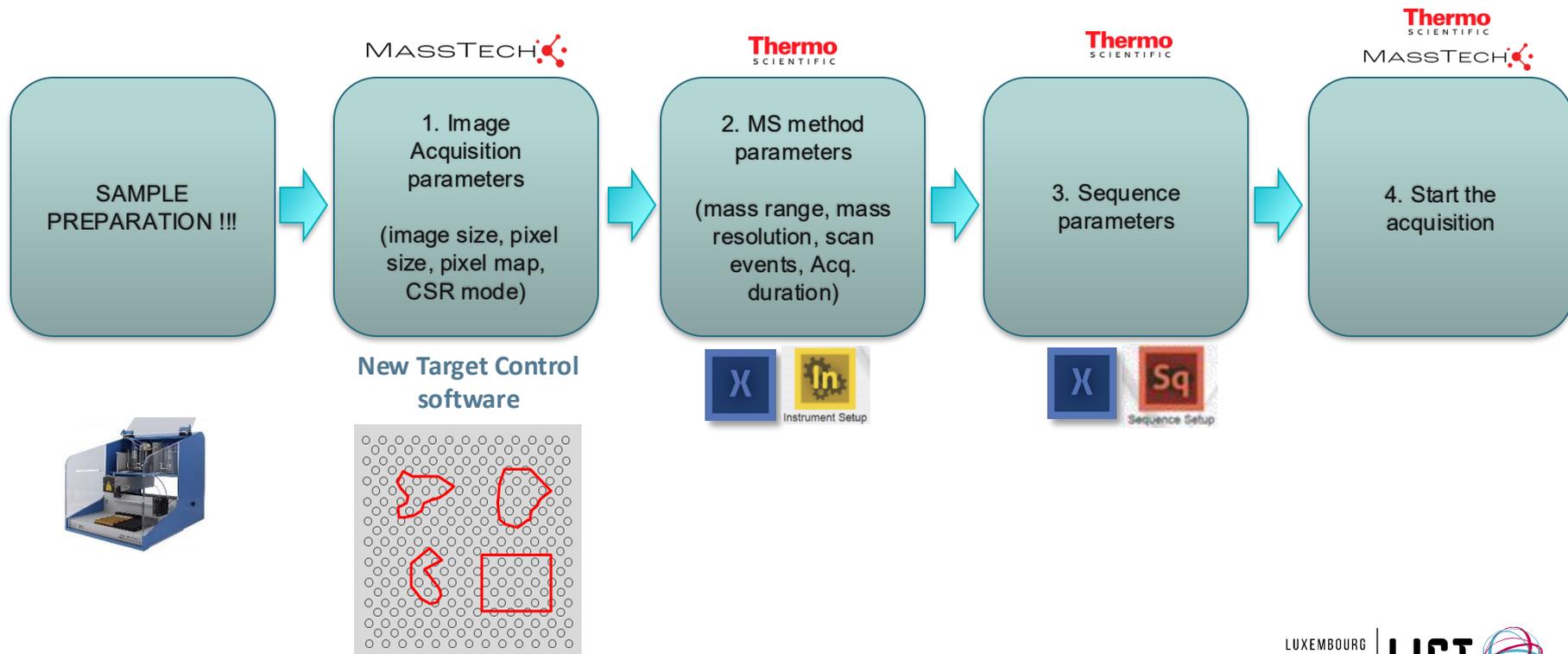


Calculated acquisition duration according to MSI parameters (pixel size, dimensions and MS scan rate)

Name	Laser Energy (%)	Enforce Rect	Resolution (mm)	Velocity (mm/sec)	Pixel Duration (sec)	Duration (s)
1 ROI 1	3	<input type="checkbox"/> false	0.015	0.0285	0.526316	379.1
2 ROI 2	3	<input type="checkbox"/> false	0.015	0.0285	0.526316	451.1
3 ROI 3	3	<input type="checkbox"/> false	0.015	0.0285	0.526316	726.3
4 ROI 4	3	<input type="checkbox"/> false	0.015	0.0285	0.526316	520.9

Buttons: Equalize Duration, +, Up, Down, Clone, Remove, Close

APMALDI imaging workflow



AP/MALDI imaging workflow

MASSTECH 

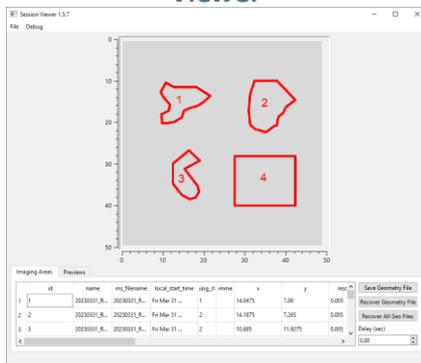
5. Position file (*.xml)

MASSTECH 

6. Conversion to
imzML files (optional)

7. Data analysis

New Target Session
viewer

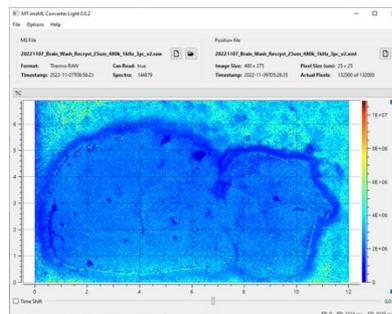


Dedicated software
tool for creation of
position files (xml) for
each image area

→ ROI_1.xml
→ ROI_2.xml
→ ROI_3.xml
→ ROI_4.xml



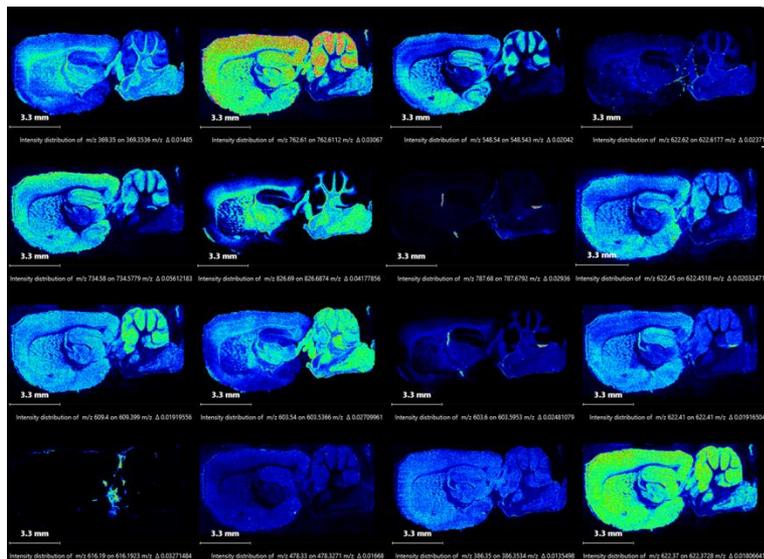
APMALDI imaging workflow



New dedicated software tool
for conversion of raw + xml
files into imzML format
(TIC preview)

→ ROI_1.imzML

APMALDI imaging workflow



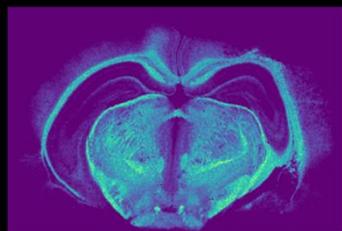
Many data handling solutions:

- Thermo Xcalibur (QuanBrowser, FreeStyle, ImageQuest),
- Lipostar/Pyxis (MassAnalytica), SCILS, Mozaic (Spectroswiss), MSI reader, METASPACE, MZmine
- ...



Masstech APMALDI UHR / Thermo Exploris 480, positive ion mode

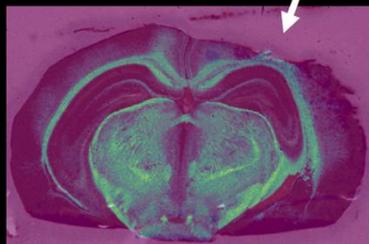
Matrix=1,5-Diaminonaphthalene, 20 um/pixel, R=45000@m/z200, 9.9 pixel/s, 4h15 total acquisition,
Pyxis Viewer software, TIC normalization



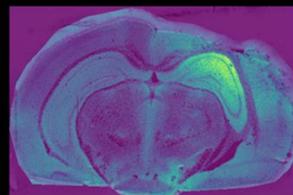
m/z=866.6462
e.g. [PI-Cer(d18:0/22:0)+H]⁺



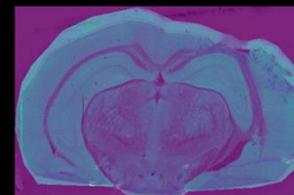
Optical image
(PrimeScan, GT Vision Ltd scanner)



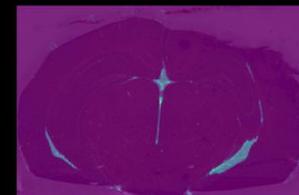
m/z=866,6462 +
optical image



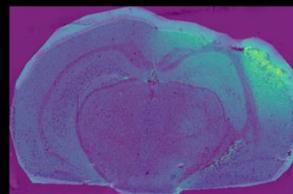
m/z=754.5904



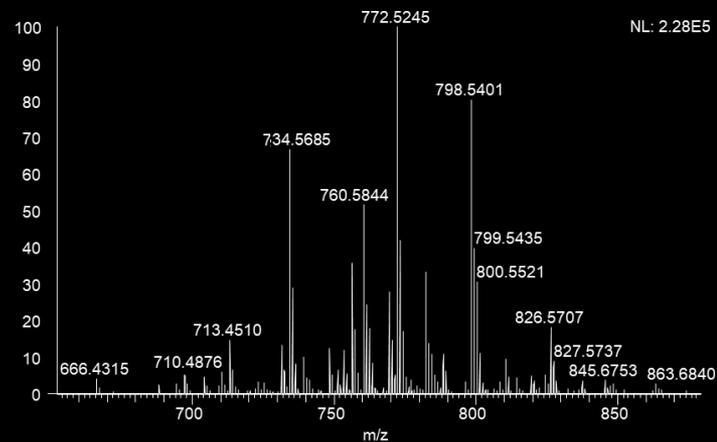
m/z=734.5686
e.g. [PC 32:0+H]⁺



m/z=703.5741
e.g. [SM 34:1;O2+H]⁺



m/z= 758.5625



AP/MALDI coupled to the Orbitrap Astral



AP/MALDI on ASTRAL (INSA Toulouse)



METABOHUB

Infrastructure nationale
en métabolomique et fluxomique

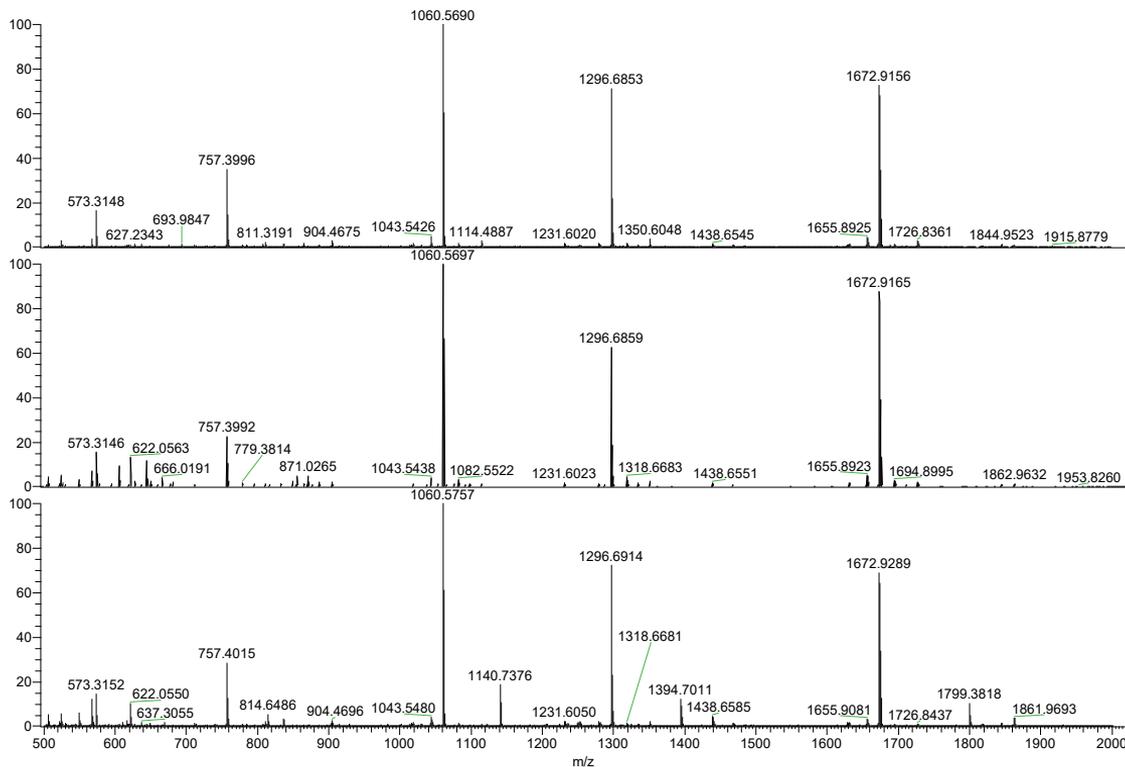
ThermoFisher
SCIENTIFIC

LUXEMBOURG
INSTITUTE OF SCIENCE
AND TECHNOLOGY



PEPTIDE MIX5

Average MS / E1%@3kHz



NL: 4.50E6
20250218_Test_Mix5_E1_3kHz_12
0kOT-isd50_20250218105640#2-
58 RT: 0.01-0.31 AV: 57 T: FTMS +
c ESI sid=50.00 Full ms
[500.0000-2000.0000]

OT 120k
(Elapsed scan time = 210ms)

NL: 1.31E6
20250218_test_mix5_e1_3kHz_480
kot-profile#34-51 RT: 0.57-0.86
AV: 18 T: FTMS + p ESI Full ms
[500.0000-2000.0000]

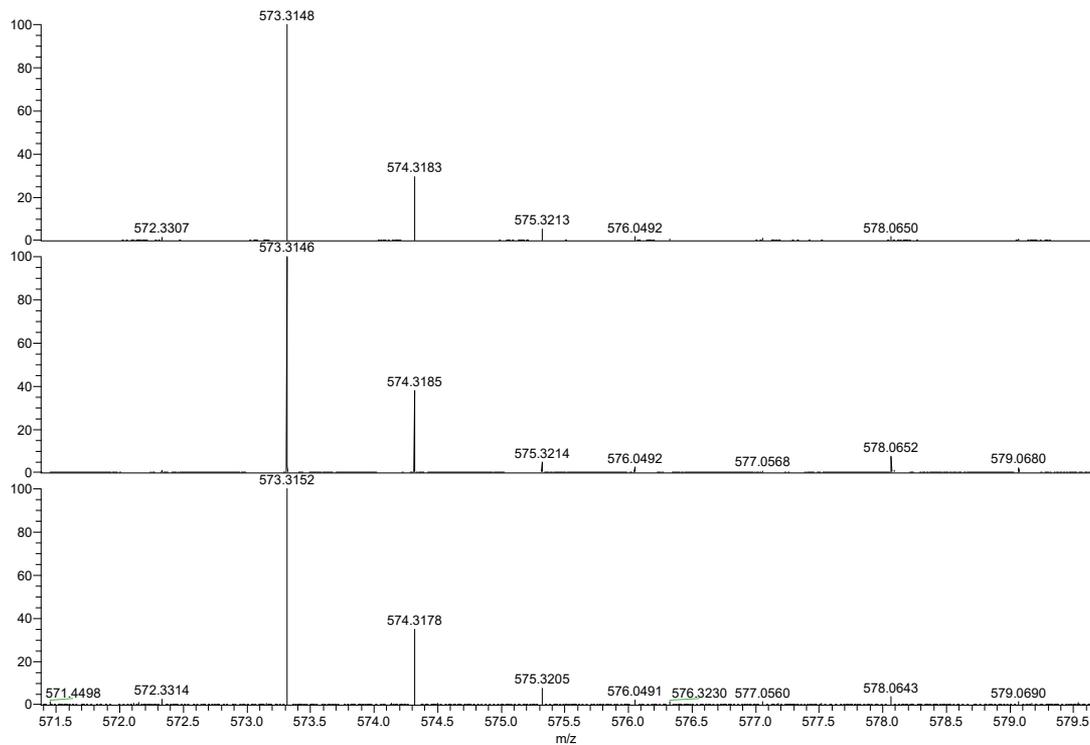
OT 480k
(Elapsed scan time = 1.03 s)

NL: 7.73E4
20250218_test_mix5_e1_3kHz_ast
al-agg1000#41-238 RT: 0.07-0.34
AV: 198 T: +c ESI Full ms2
1360.0000@hcd1.00
[500.0000-2000.0000]

ASTRAL
(Elapsed scan time < 35ms)

PEPTIDE MIX5

Average MS / E1%@3kHz



NL: 1.27E6
20250218_Test_Mix5_E1_3kHz_12
0kOT-isd50_20250218105640#31-
48 RT: 0.18-0.26 AV: 18 T: FTMS +
c ESI sid=50.00 Full ms
[500.0000-2000.0000]

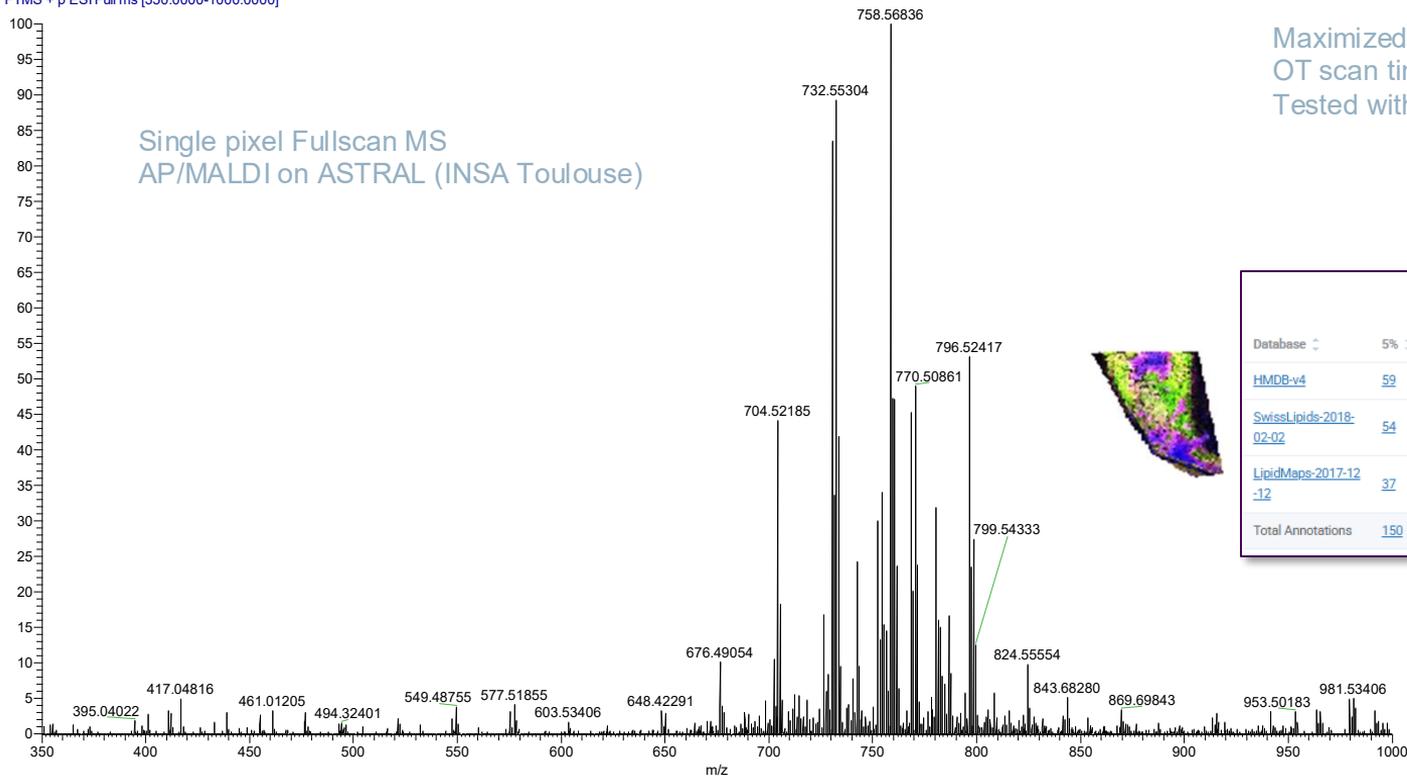
NL: 2.07E5
20250218_test_mix5_e1_3kHz_480k
ot-profile#34-51 RT: 0.57-0.86 AV:
18 T: FTMS + p ESI Full ms
[500.0000-2000.0000]

NL: 1.12E4
20250218_test_mix5_e1_3kHz_astra
l-agc1000#41-238 RT: 0.07-0.34
AV: 198 T: + c ESI Full ms2
1360.0000@hcd1.00
[500.0000-2000.0000]

EXAMPLE OF FULL SCAN IMAGING (MS1-ONLY)

(Drosophila, R=240k, 10 $\mu\text{m}/\text{pixel}$)

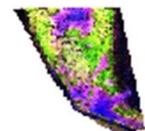
20250220 droso FS-FTonly 63min 10um-E3-350-1000-1kHz3 #3714 RT: 31.96 AV: 1 NL: 3.98E4
T: FTMS + p ESI Full ms [350.0000-1000.0000]



Maximized sensitivity
OT scan time = 512ms \rightarrow **Max IT = 490ms**
Tested with AGC ON (target 1E6)

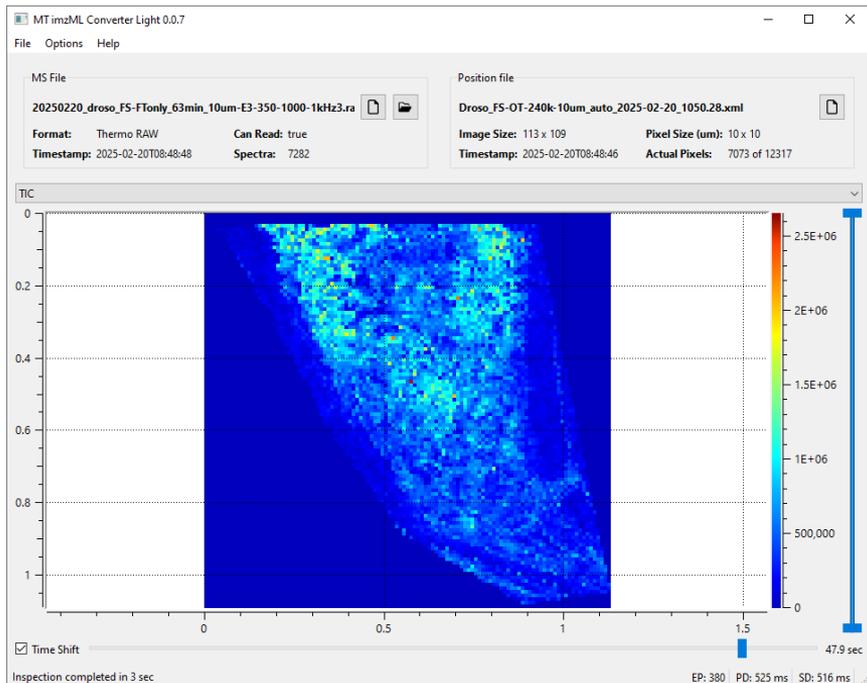


	# of annotations with FDR% <=			
Database	5%	10%	20%	50%
HMDB-v4	59	159	295	1235
SwissLipids-2018-02-02	54	117	288	1849
LipidMaps-2017-12-12	37	83	280	1425
Total Annotations	150	359	863	4509



CONVERSION & ANNOTATIONS

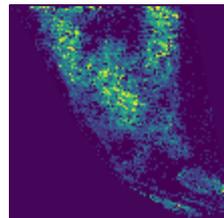
New MT imzML converter



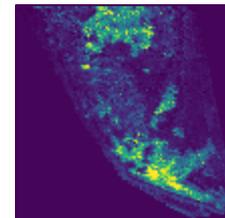
→ ROI_1.raw



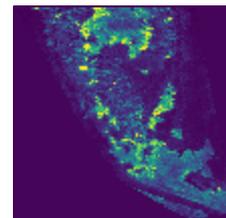
→ ROI_1.xml



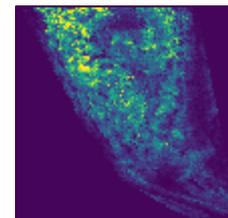
[C42H82NO11P + H]⁺
808.5698
PI-Cer(d20:1/16:0)



[C49H92O6 + Na]⁺
799.6786
TG(14:0/14:0/18:1(9Z))[iso3]



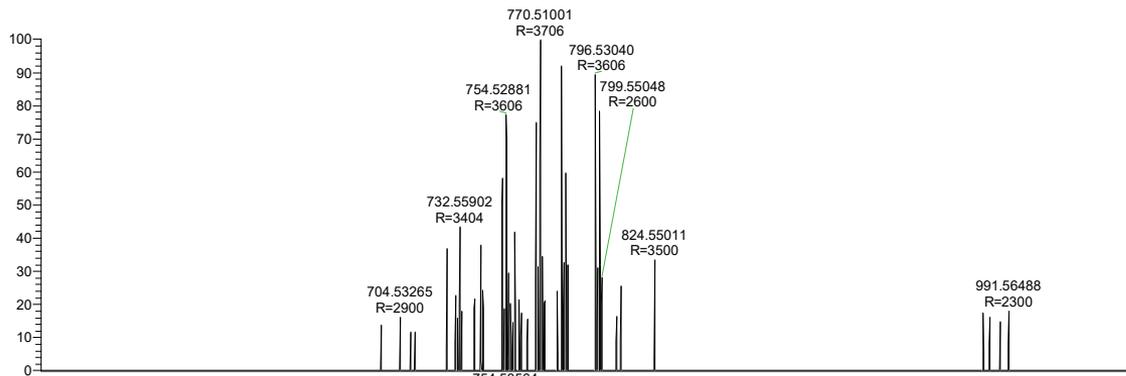
[C37H68O4 + H]⁺
577.5190



[C39H76NO8P + K]⁺
756.4940
PE(15:0/19:1(9Z))

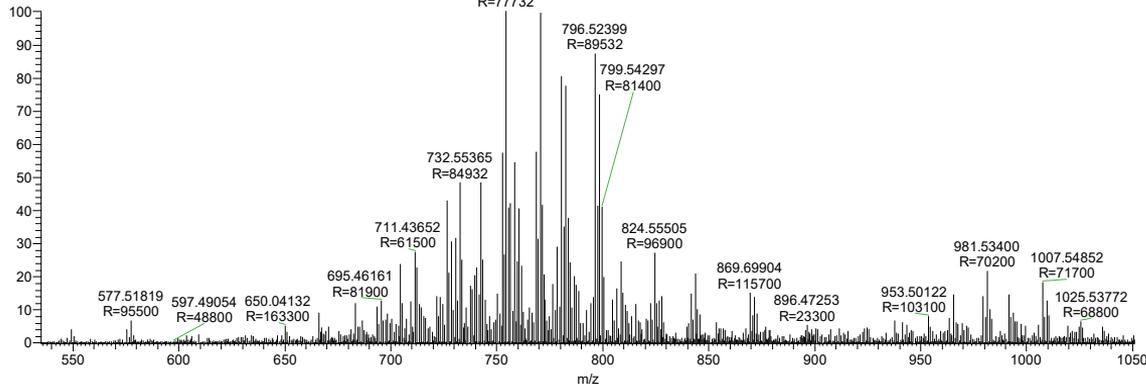
PSEUDO FS IN ASTRAL

HCD@1%NCE, XXL isolation window



NL: 2.39E5
20250219_test_Droso_Verre_pseud
oFS_8min_ExList2_20um-E5-
1kHzZ#6339 RT: 3.72 AV: 1 T:
FTMS + p ESI Fullms
[450.0000-2000.0000]

**1 Single pixel Fullscan MS
AP/MALDI in Exploris @R=7,500
IT=5ms (trigger only)
Number of peaks = 50**

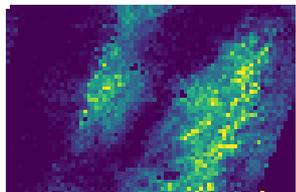


NL: 4.49E4
20250219_test_Droso_Verre_pseud
oFS_8min_ExList2_20um-E5-
1kHzZ#6338 RT: 3.72 AV: 1 T: + c
ESI Fullms2 1250.0000@hcd1.00
[450.0000-2000.0000]

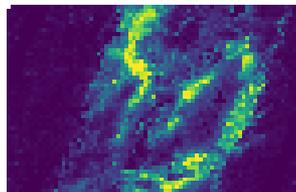
**1 Single pixel Fullscan MS
AP/MALDI in Astral @R=75,000
IT=16ms (AGC On @1E6)
Number of peaks = 8599**

FAST IMAGING MODE (DROSOPHILIA)

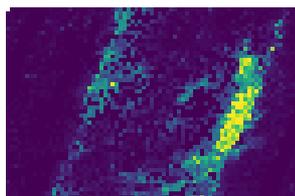
15 pixel / second, (6minutes) @ R=75k in ASTRAL (pseudo Full Scan)



[C51H96O6 + K]⁺
843.6838 m/z



[C42H82NO8P + K]⁺
798.5410 m/z



[C40H78NO8P + Na]⁺
754.5357



Database	5%	10%	20%	50%
HMDB-v4	30	95	214	1028
SwissLipids-2018-02-02	39	99	185	1416
LipidMaps-2017-12-12	18	67	137	1018
Total Annotations	87	261	536	3462

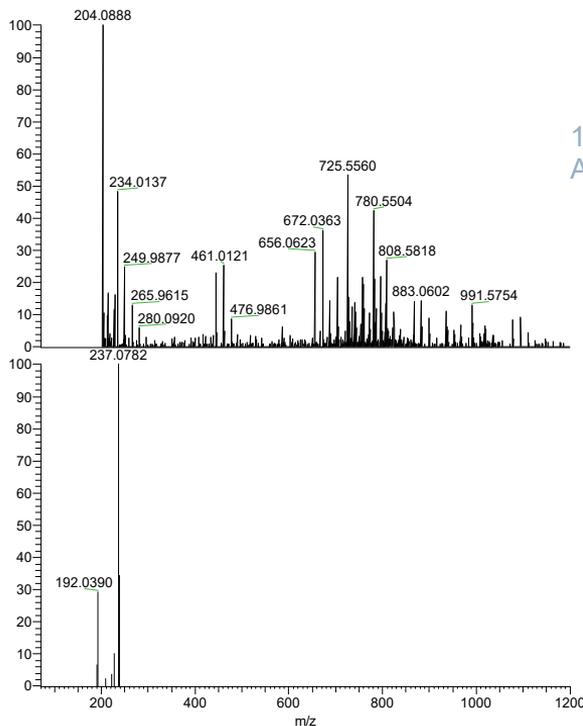
Exploris detection only :

15 pixel/s = 7.5k → x10 mass resolution in Astral

75k at m/z700 = 3.7 pixel/s@120k setting → x4 scan rate in Astral

EXAMPLE OF MULTI SCAN EVENT IMAGING (MS1 + TMS2 + DDA)

(SKIN, R=240k, 10 $\mu\text{m}/\text{pixel}$, 40 minutes)



NL: 2.30E4
20250220_Skin_FS240+IMS2+
ddA_2min_E3-1kHz_10um#32376
RT: 35.39 AV: 1 T: FTMS + p ESI Full
ms [203.0000-1200.0000]

1 Single pixel Fullscan MS
AP/MALDI on ASTRAL

NL: 3.15E2
20250220_Skin_FS240+IMS2+
ddA_2min_E3-1kHz_10um#32503
RT: 35.54 AV: 1 SB: 69 21.01-21.98
T: + c ESI Full ms2
237.1114@hcd30.00
[70.0000-250.0000]

1 Single pixel tMS2
AP/MALDI on ASTRAL

Balanced sensitivity & IDs
FS/OT scan time = 512ms \rightarrow **Max IT = 200ms**
Tested with AGC ON (target 1E6)

\rightarrow Remaining IT is reserved for tMS2 + DDA
 \rightarrow Max IT=50ms

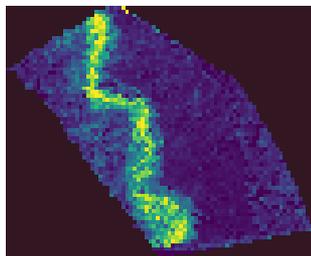
\rightarrow **1 cycle = 1 FS + 4 tMS2 + 12 DDA within
882 milliseconds/pixel**



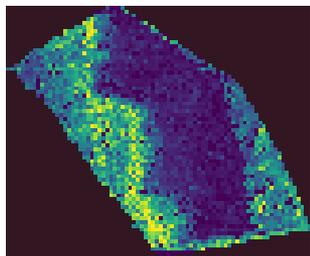
20250220_Skin_FS240+tMS2+ddA_2min_E3-1kHz_10um-cen...
Homo sapiens (human), skin (wildtype)
APMALDI + Orbitrap, positive mode, RP 240k @ 200
Submitted 3 minutes ago by Gilles Frache
[110 annotations](#) @ FDR 10% (SwissLipids - 2018-02-02)

SKIN

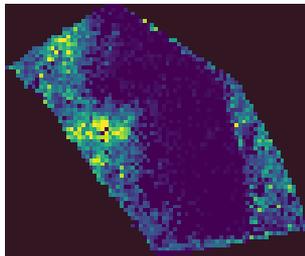
Full scan (balanced sensitivity)



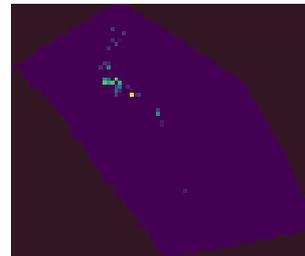
[C₄₂H₈₀NO₈P + Na]⁺
780.5514
PC(34:2)
Norm/TIC



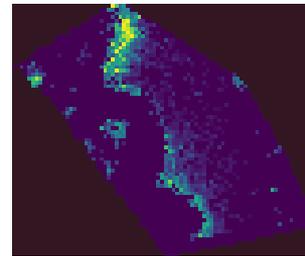
[C₄₃H₇₆NO₇P + Na]⁺
772.5252
PE(38:5)
Norm/TIC



[C₄₇H₉₃N₂O₆P + H]⁺
813.6844
SM(42:2)
Norm/TIC



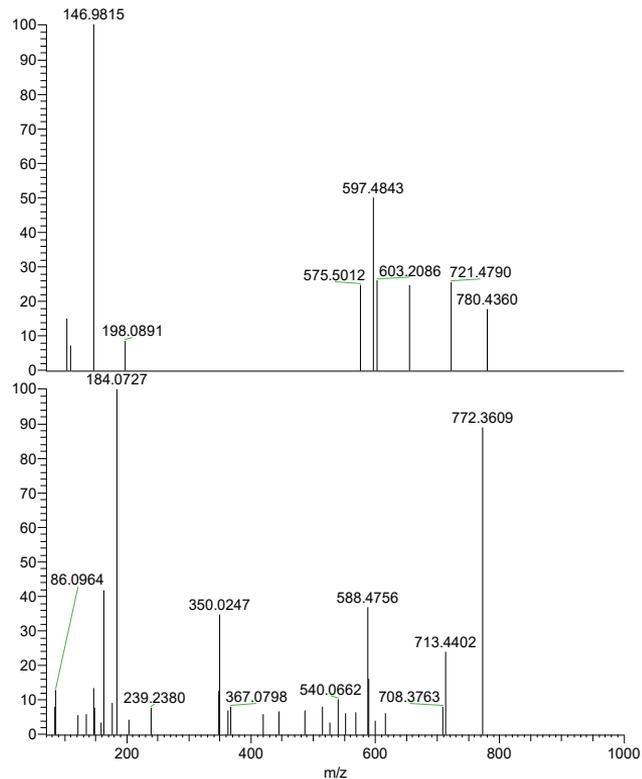
[C₄₄H₈₉NO₅ + H]⁺
712.6814
Cer(t18:0/26:0(2OH))
Norm/TIC



[C₅₇H₉₈O₆ + H]⁺
879.7436
TG(44:6)
Norm/TIC

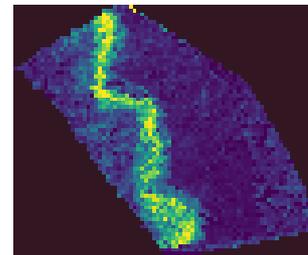
IN-PIXEL MS/MS

From DDA scans

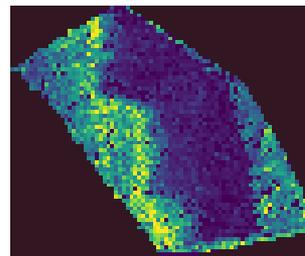


NL: 1.13E2
20250220_Skin_FS240+MS2+
ddA_2min_E3-1kHz_10um#27009
RT: 29.50 AV: 1 T: + c ESI d Full ms2
780.5505@hcd30.00
[70.0000-1000.0000]

NL: 4.31E1
20250220_Skin_FS240+MS2+
ddA_2min_E3-1kHz_10um#29104-
31375 RT: 31.98-34.08 AV: 6 T: + c
ESI d Full ms2 772.5247@hcd30.00
[70.0000-1000.0000]



[C42H80NO8P + Na]⁺
780.5514
PC(34:2)
Norm/TIC



[C43H76NO7P + Na]⁺
772.5252
PE(38:5)
Norm/TIC

AP/MALDI ON THE ORBITRAP ASTRAL

After 2.5 days of tests

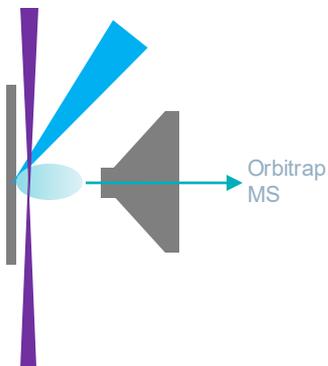
- **Benefits of the Exploris 480**
 - Mass resolution, mass accuracy, stability over acquisition
- **Coupling with Astral, Astral Zoom or Excedion Pro**
 - Increases the performances +/- by x10
 - 4-10x number of scan/second at 75k,
 - or 10x more MS/MS scans per pixel,
 - or 10x more Mass resolution at high speed
- **Efficient data conversion for complex methods (FS + tMS2 + DDA in each pixel)**
- **New challenge for AP/MALDI : to keep the 2 analysers busy!**

AP/MALDI Development “AP/MALDI-2”

AP/MALDI-2

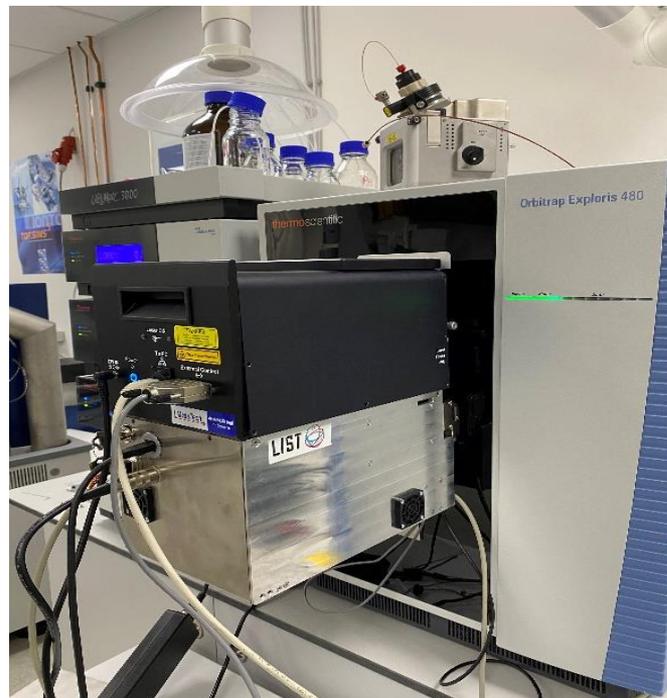
AP/MALDI with laser post-ionization

- ESI / AP/MALDI-2 swap within 1 minute
- Fully integrated design
- Laser desorption/ionization (355nm) + post-ionization (266nm)
- Synchronization of 2 lasers



Masstech
AP/MALDI
source

AP/MALDI-2
Add-on
(patent LU505964)

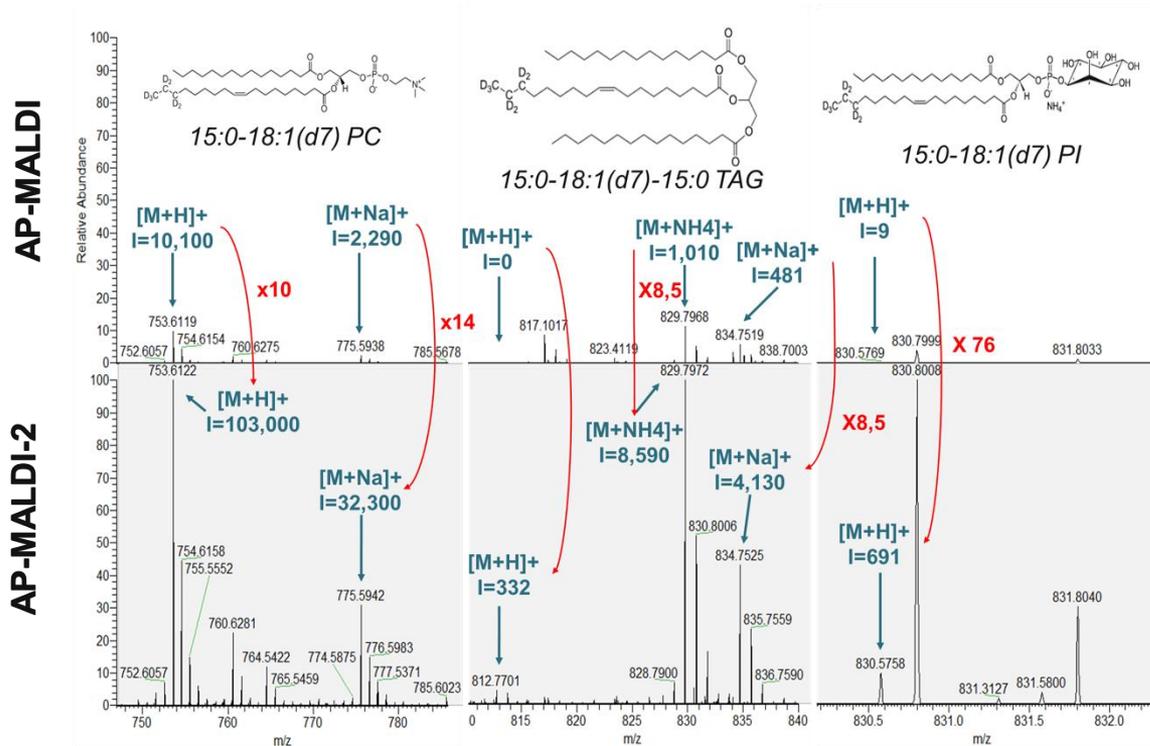


Exploris 480 ThermoFisher
Orbitrap high resolution
mass spectrometer

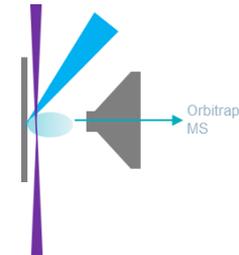
*** R&D prototype, class IV laser ***

AP/MALDI-2

Increased sensitivity for lipids (Equisplash deuterated lipid mixture)

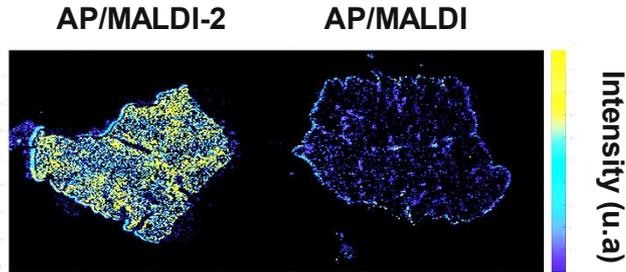


- substantial enhancement in lipid detection with the AP/MALDI-2 prototype.
- Detection of triacylglycerols (TAG), not achieved with conventional AP/MALDI sources under the tested conditions.

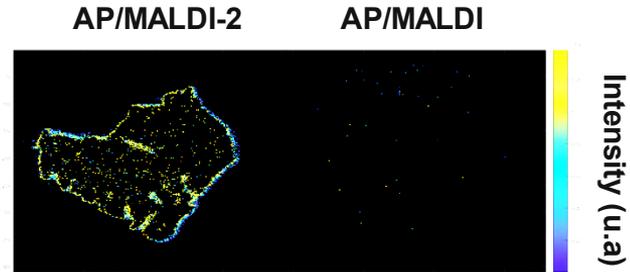


AP/MALDI-2 IMAGING

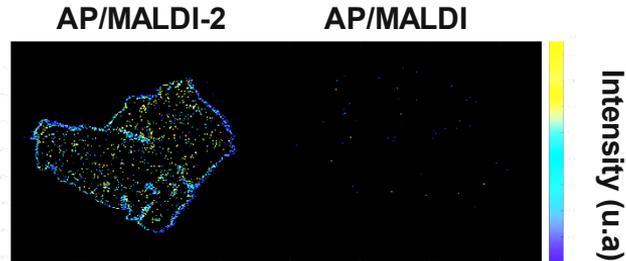
Liver section



PE 38:6 $m/z=764.522$



PI(40:0) $m/z=943.6254$



TG(57:12)
 $m/z=947.6530$

→ Sensitivity increase by up to two orders of magnitude in lipid imaging applications using AP/MALDI-2

→ New detected molecules (different ionization mechanisms)

CONCLUSIONS

AP/MALDI coupled to all Orbitraps

- 1 Flexibility of AP-MALDI**
→ easy swap between ESI/AP-MALDI, and between Orbitraps and allows for full MS calibration
- 2 Compatible with Astral Zoom and Excedion Pro**
→ Enhanced dynamic range and higher scan rate
- 3 Coupling with AP/MALDI with Astral opens new perspectives for MS/MS imaging**
- 4 New prototypes such as AP/MALDI-2 were developed at LIST in collaboration with Masstech**

Thank you for your attention

MASSTECH 



*European Application
& demo lab for
MassTech AP/MALDI*

Sue Kennerley
sue@kranalytical.co.uk

AP/MALDI
European distributor

ThermoFisher
SCIENTIFIC

 **METABOHUB** Infrastructure nationale
en métabolomique et fluxomique

FNRF

Luxembourg
National
Research Fund



LE GOUVERNEMENT
DU GRAND-DUCHÉ DE LUXEMBOURG
Ministère de l'Économie



Pierre Fabre
Dermo-Cosmétique

LUXEMBOURG
INSTITUTE OF SCIENCE
AND TECHNOLOGY

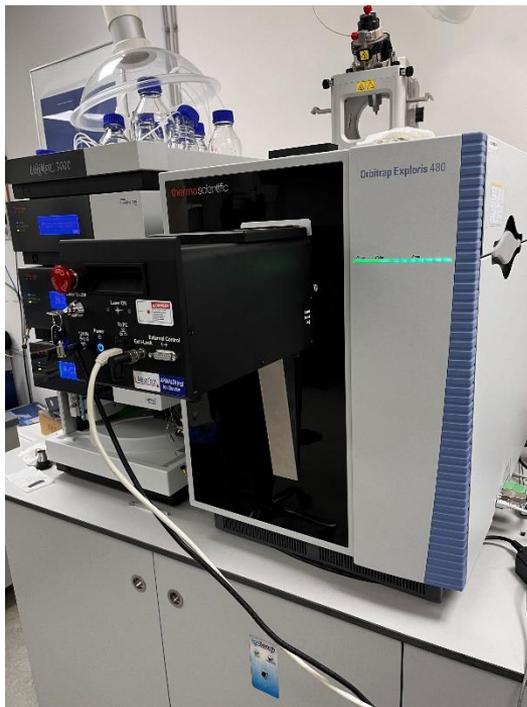




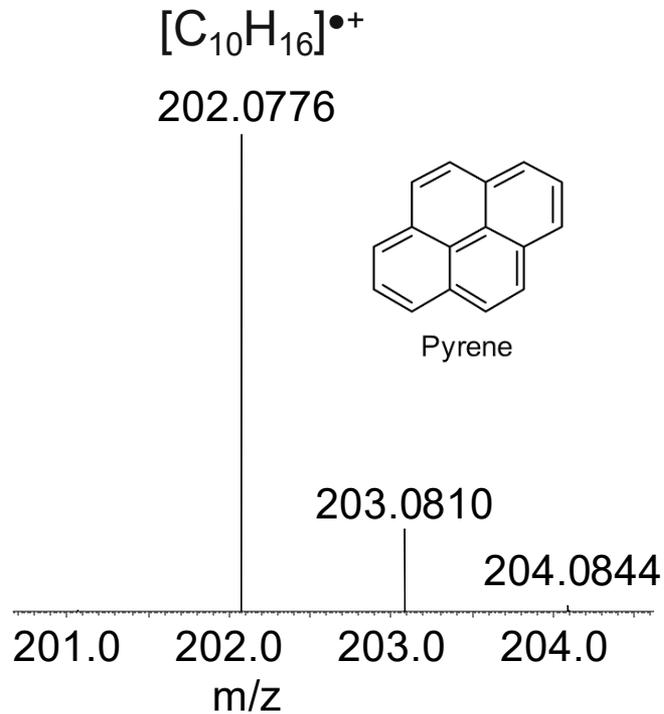
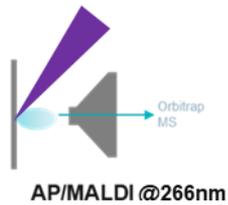
AP/MALDI Development “MT266”

APMALDI AT 266NM

REMPI MECHANISM

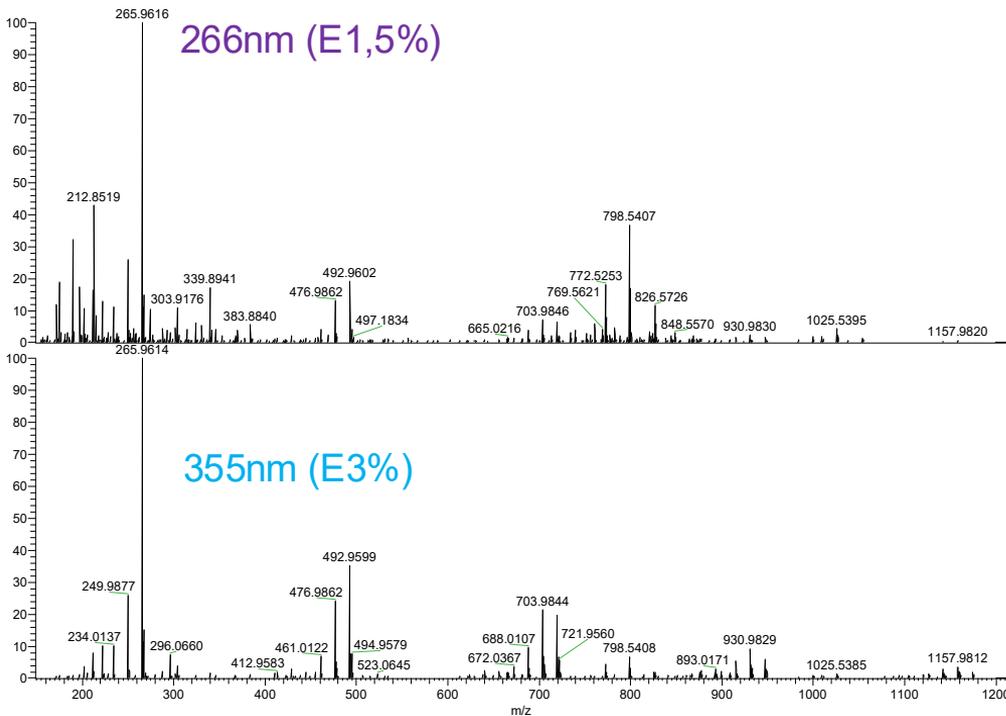


*** R&D prototype, class IV laser ***



WP1 APMALDI MSI - 355NM (E3%) VS 266NM (E1,5%)

Brain sections



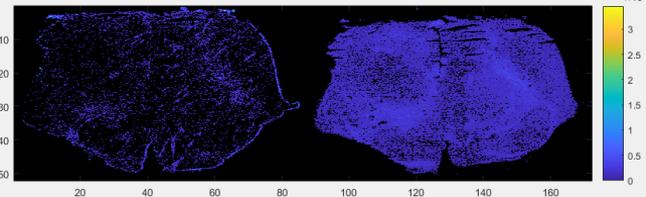
NL: 2.26E5
 20250424_Brain_MT266_120k_20um_E
 1k_HCCA_pos#64263-64639 RT:
 292.42-294.14 AV: 377 T: FTMS + p
 MALDI Full ms [150.0000-1200.0000]

NL: 1.26E6
 20250507_brain_355_120k_20um_e3_1
 hcca_pos: 20250507200610#66492-
 66892 RT: 292.52-294.28 AV: 401 SB:
 222 471.00-472.00 T: FTMS + p ESIFull
 ms [150.0000-1200.0000]

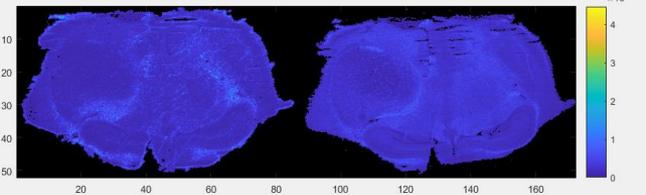
355nm (E3%)

266nm (E1,5%)

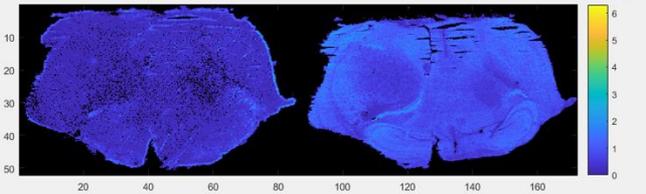
798.5407



826.5726



848.557

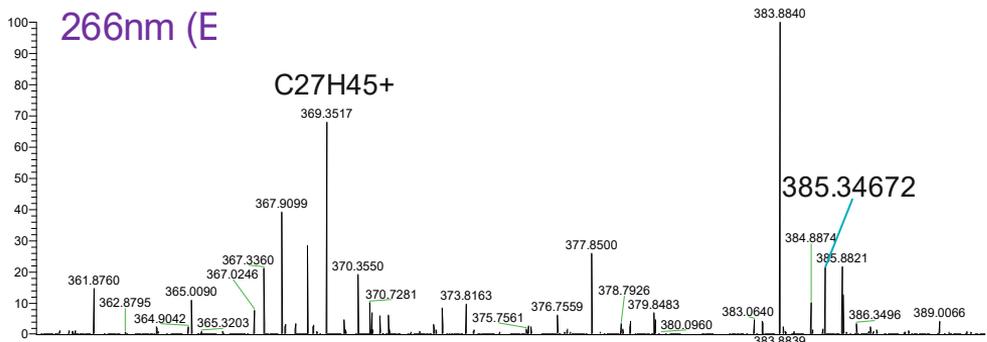


WP1 APMALDI MSI - 355NM (E3%) VS 266NM (E1,5%)

Brain sections

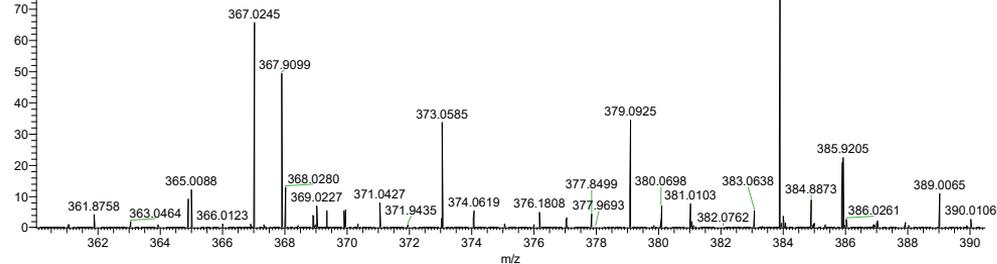
266nm (E

C27H45+



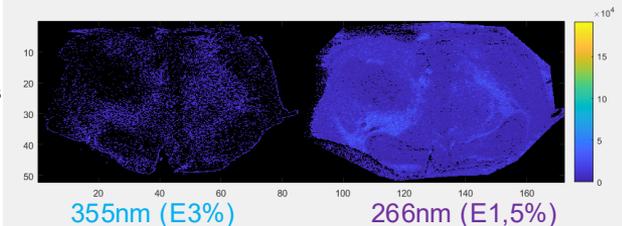
NL: 1.30E4
20250424_Brain_MT266_120k_20um_E1.5
_1k_HCCA_pos#64263-64639 RT:
292.42-294.14 AV: 377 T: FTMS + p
MALDI Full ms [150.0000-1200.0000]

355nm (E3%)

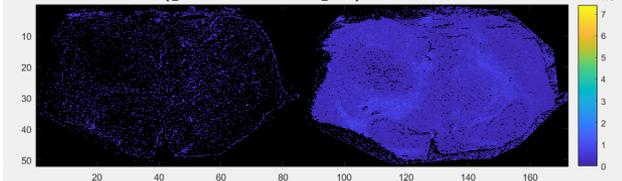


NL: 1.57E4
20250507_brain_355_120k_20um_e3_1k_
hcca_pos_20250507200610#66492-
66892 RT: 292.52-294.28 AV: 401 SB:
222 471.00-472.00 T: FTMS + p ESI Full
ms [150.0000-1200.0000]

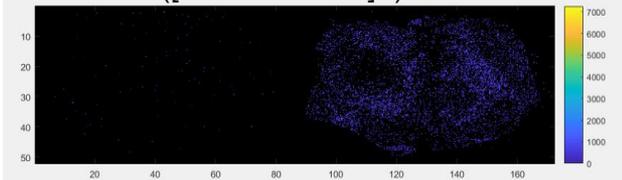
C27H45+ (cholesterol fragment -H2O)



385.34649 ([cholesterol]+)

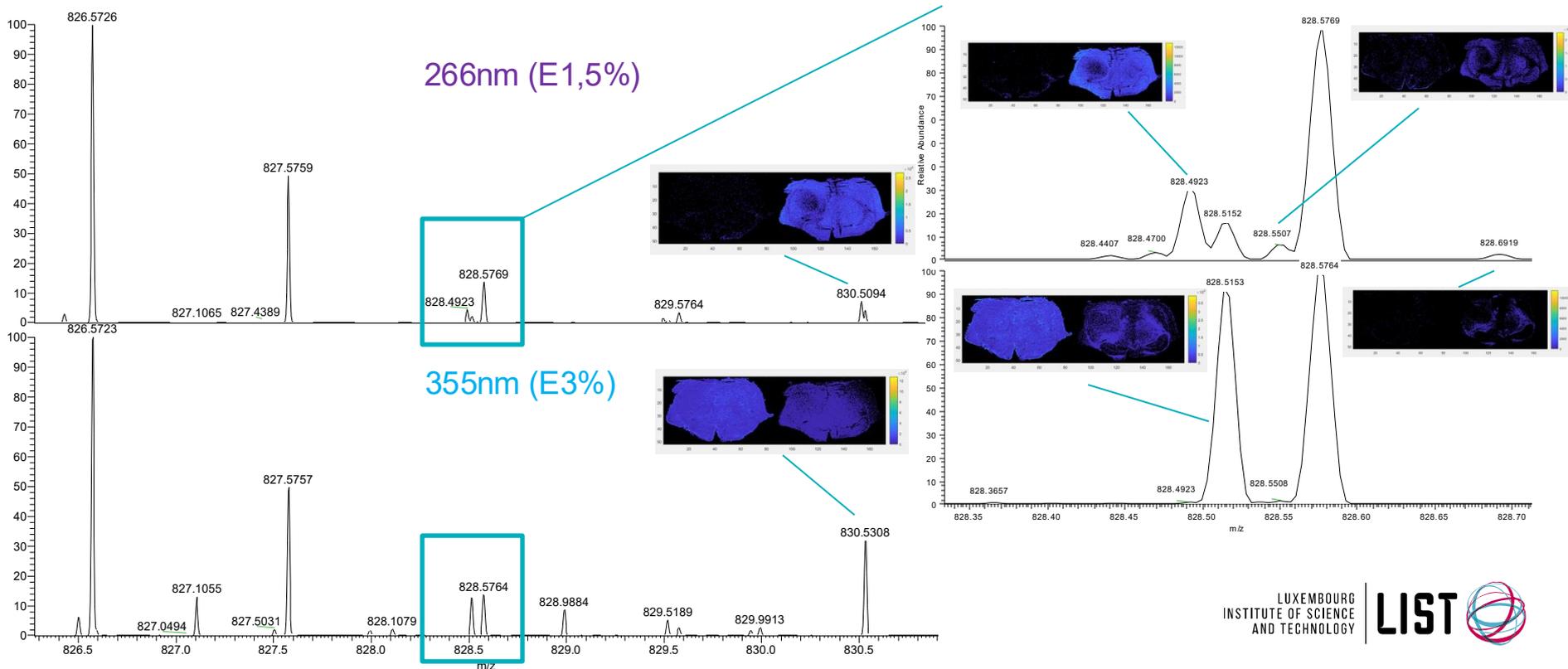


386.35432 ([cholesterol +H]+)



APMALDI AT 266NM VS 355NM

More to learn from this experiments...



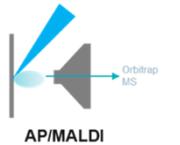
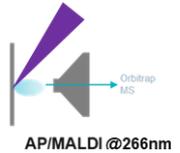
SAMPLES

(old) mouse brain sections



→ 1st half of the brain section AP-MALDI (266nm, CHCA matrix)

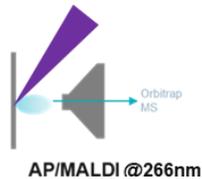
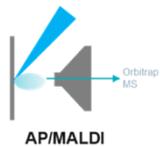
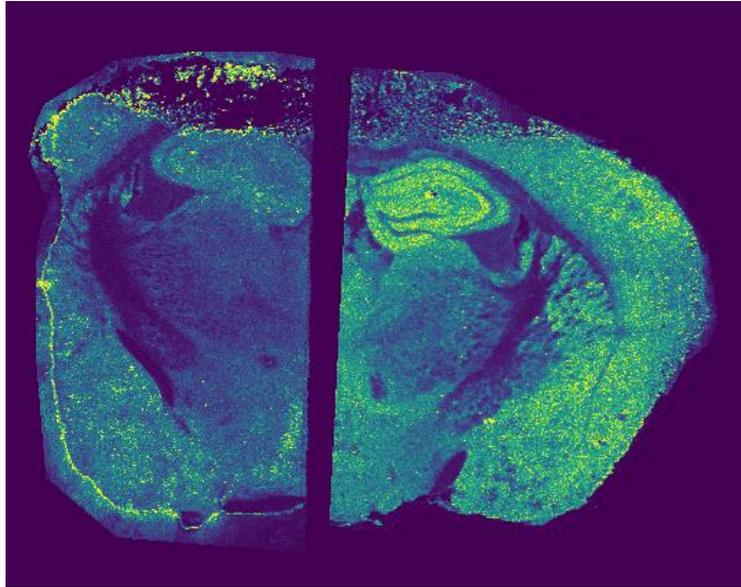
→ 2nd half of the brain section AP-MALDI (355nm, CHCA matrix)



NB: samples were old and degraded on the upper part

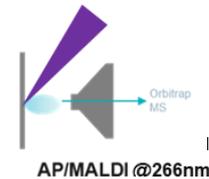
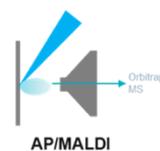
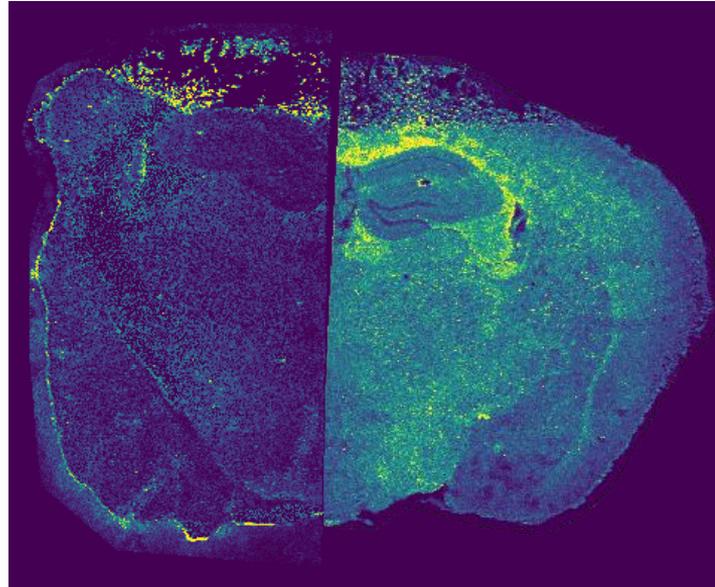
[PE(38:5)+NA]⁺

772.5254



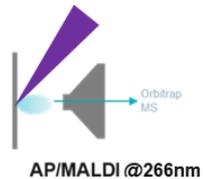
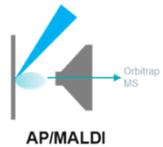
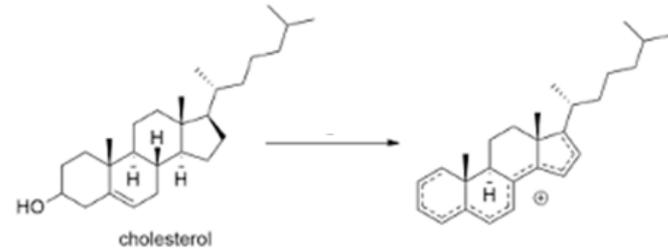
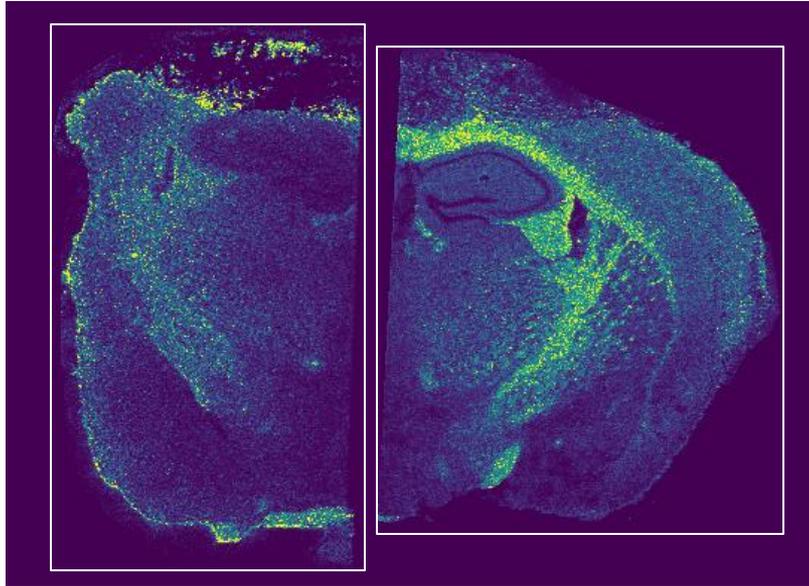
PI-CER(T18:0/18:0)

[C42H84NO12P + H]⁺, 826.5804m/z



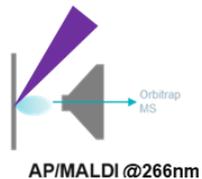
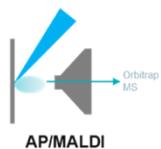
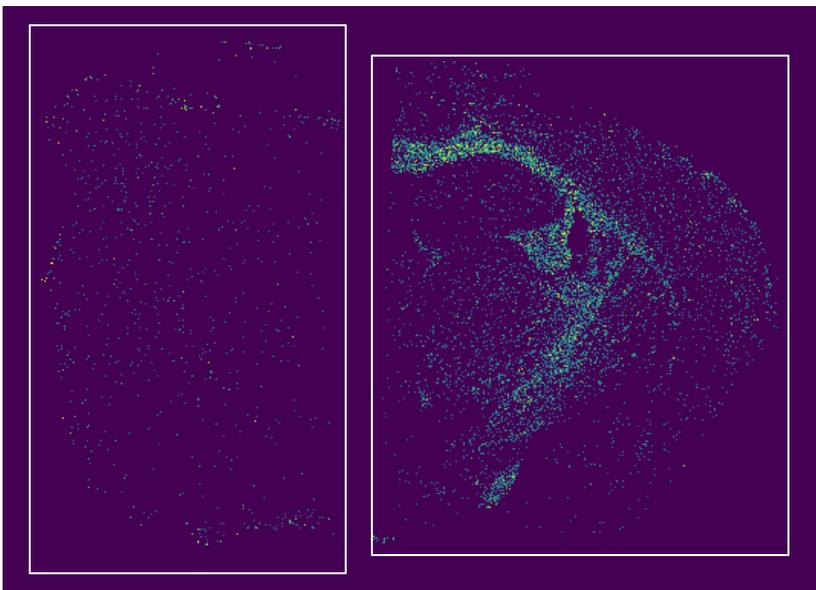
CHOLESTEROL FRAGMENT ([M+H-H2O]+)

369.3515 (same signal for Cholesterol or cholesteryl esters)



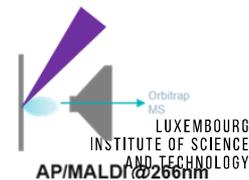
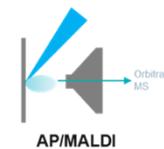
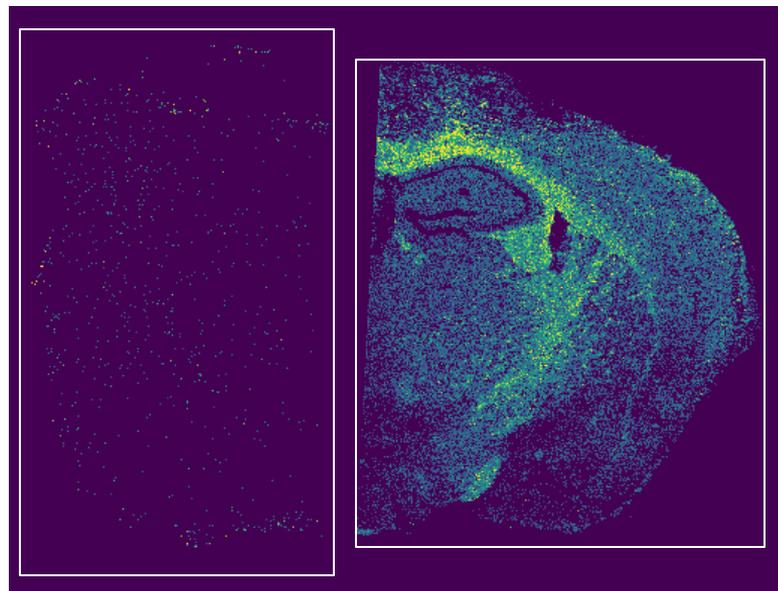
CHOLESTEROL INTACT ([M+H]⁺)

387.3621



CHOLESTEROL INTACT ([M[•]+])

386.3543



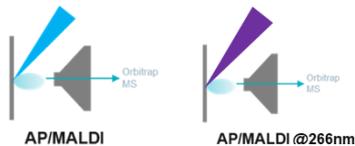
LUXEMBOURG
INSTITUTE OF SCIENCE
AND TECHNOLOGY



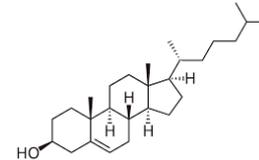
GLOBAL DATABASE MS1 SEARCH

Metaspace annotations FDR 20%

Database ⇅	20% ⇅	20% ⇅
HMDB-v4	130	94
SwissLipids-2018-02-02	10	4
LipidMaps-2017-12-12	14	6
Total Annotations	154	104



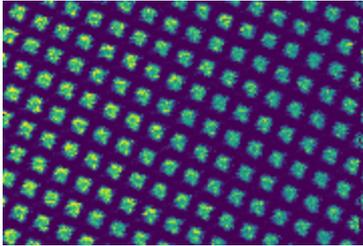
- More data mining is needed (threshold, specific vs. common lipids...)
- Label-free mass spectrometry imaging of intact cholesterol detected as $[M]^{\bullet+}$ and $[M+H]^+$ (No silver cationization, no OTCD with Girard reagent)



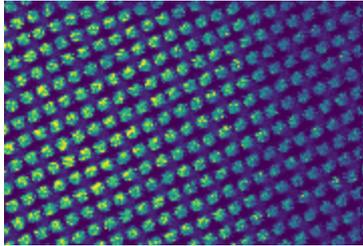
- APMALDI at 266nm to be tested with better suited matrix (Nicotinic acid): New experiments are planned on Friday December 13th

OLED

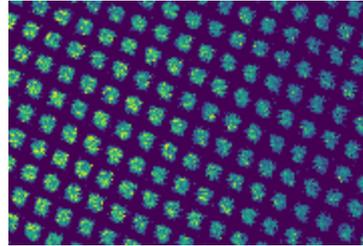
(266nm 5 $\mu\text{m}/\text{pixel}$)



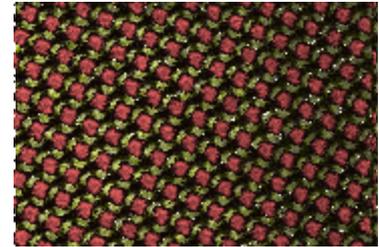
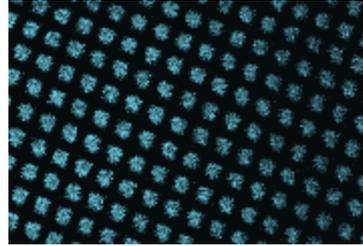
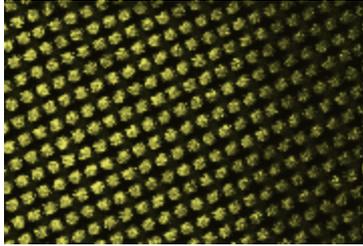
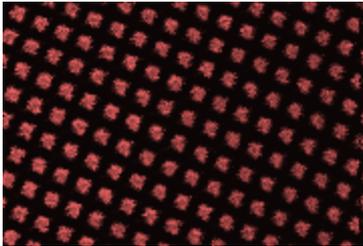
638.2719
m/z



636.2562
m/z



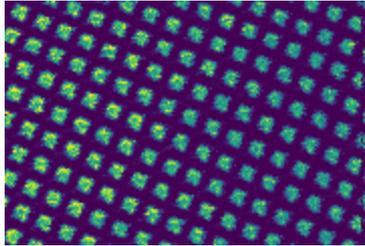
729.2668
m/z



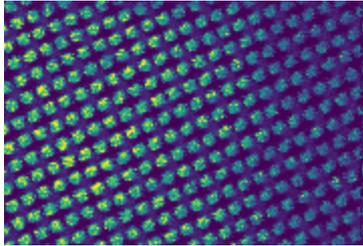
100 μm

OLED

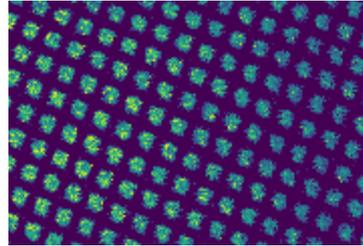
(266nm 5 $\mu\text{m}/\text{pixel}$)



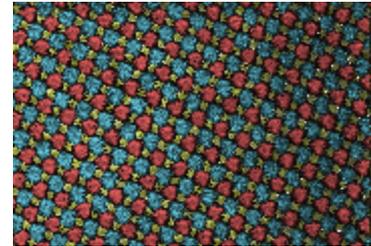
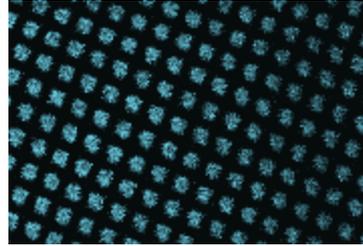
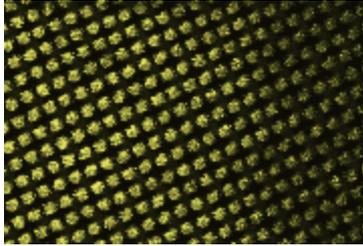
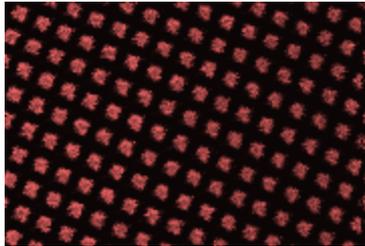
638.2719
m/z



636.2562
m/z



729.2668
m/z



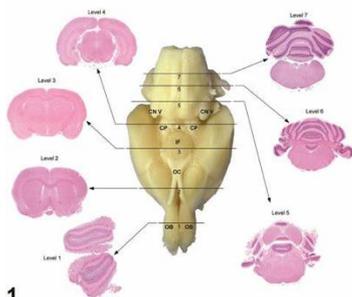
100 μm

BACKUP SLIDES

—

MALDI Imaging workflow

Prepare biological section
(cryo microtome)



Typically: Fresh Frozen organs
attached to the cryo-microtome with OCT,
or embedded with CMC/Gelatine
or other media
Sliced with 5-15 μm thickness
Thaw-mounted on ITO-coated glass slides
Stored at -80°C until analysis

AP/MALDI also works with FFPE tissue,
fresh plant tissue, materials...

Matrix sprayer
(+Internal standard)



SunChrom

Typically:

- Slices are placed 15 minutes
in a dessicator at room temperature
- Prepared sections are coated
with matrix (HCCA, DHB, NH, 9-AA...)
deposition using pneumatic sprayer,
a sublimation device or others

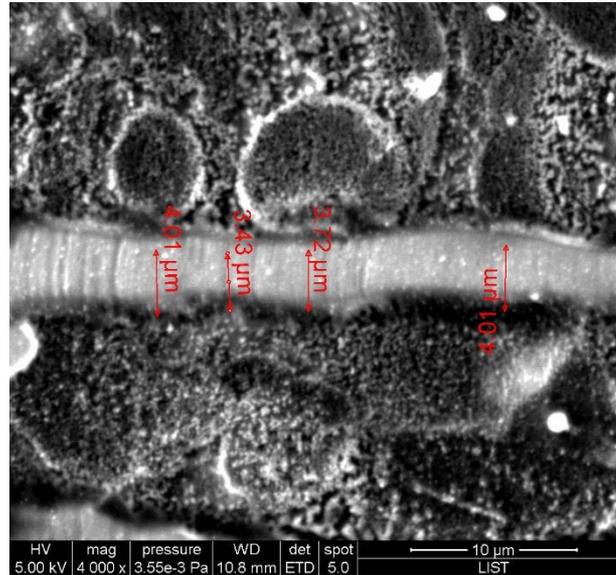
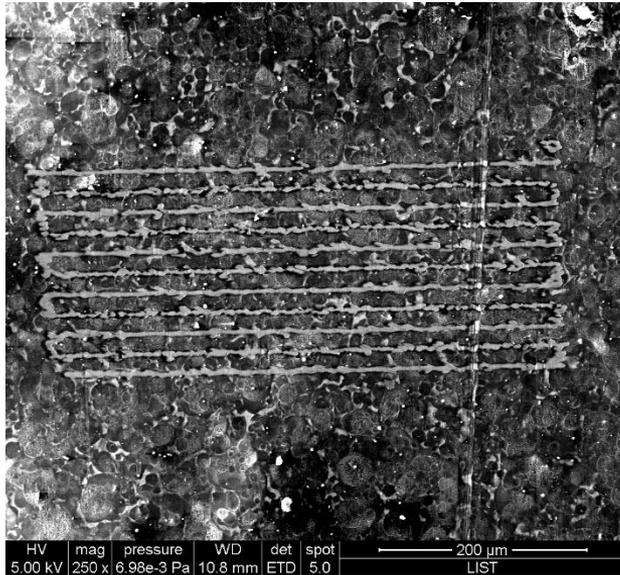


Typically:
Optical images are taken
from an optical microscope,
USB microscope
or a slide scanner

AP/MALDI IMAGING

(Exploris 480, 5 μ m/pixel)

Without oversampling



AP/MALDI on HCCA matrix layer (pneumatic sprayer)

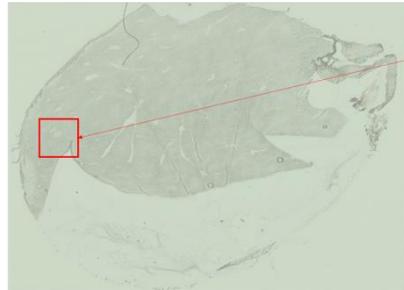
Raster motion 2 mm/min,
Energy = 0.5%, laser
repetition rate=1000Hz
Laser ablation traces
measured at 4 micrometer

APPLICATIONS TO CANCER RESEARCH

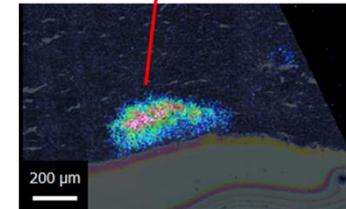
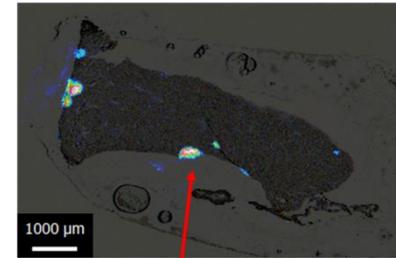
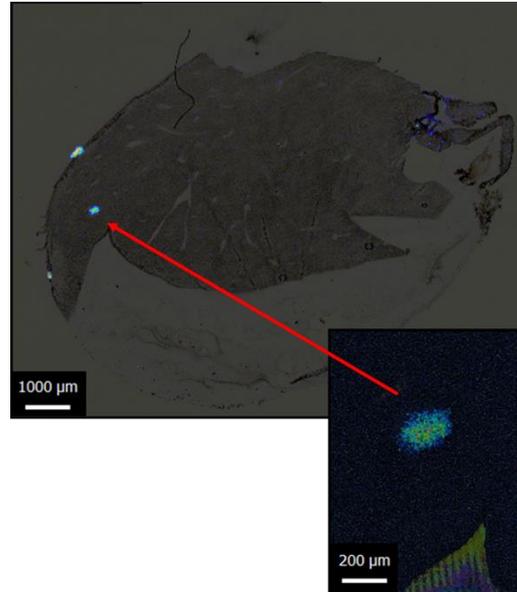
Visualize the invisible by AP/MALDI MSI !

Specific detection of metastases biomarkers in liver sections Not seen by biologists but detected by MSI

(Unpublished data)



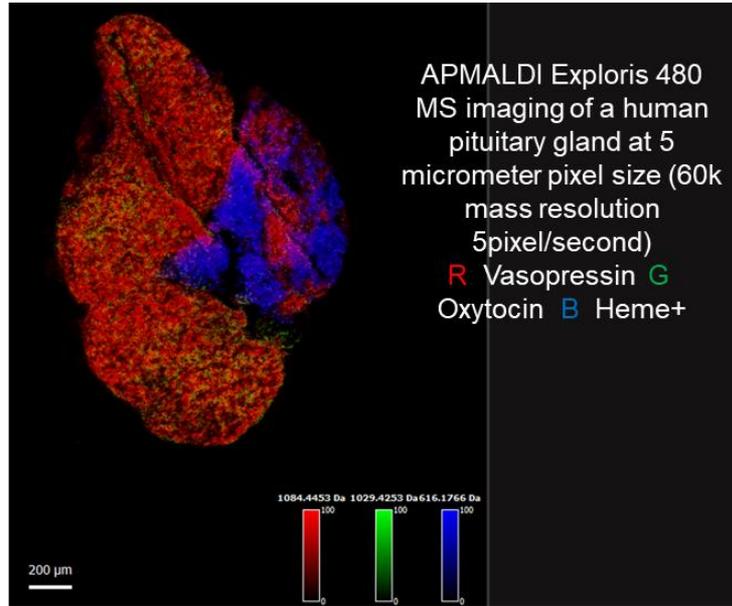
ROI
=
metastasis



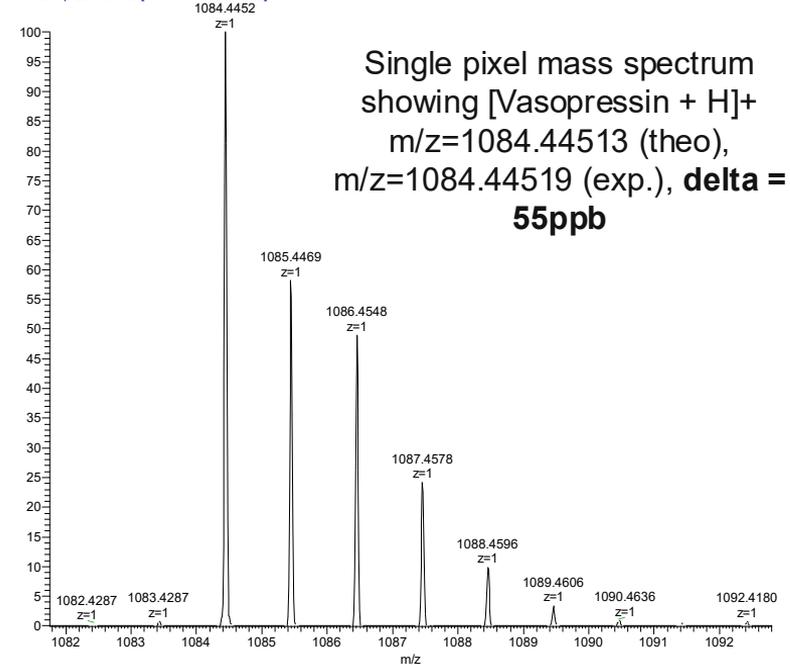
BEYOND LIPIDS IN FRESH FROZEN TISSUE SECTIONS



AP/MALDI on FFPE tissue (ProteoFormiX)



20220822_PFX_B-1809848-1-2#3_E20_100Hz_60k_200msIT_5micron#98637 RT: 353.92 AV: 1 NL: 1.59E5
T: FTMS +p ESI Full ms [400.0000-1500.0000]

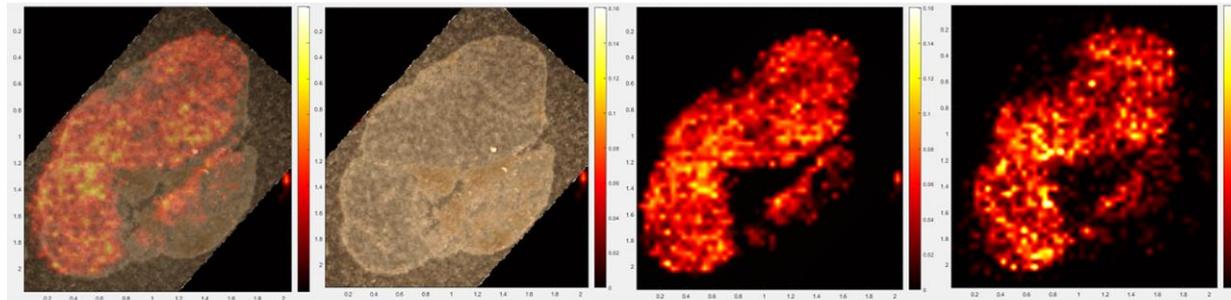


BEYOND LIPIDS IN FRESH FROZEN TISSUE SECTIONS



AP/MALDI MSMS imaging on FFPE tissue (ProteoFormiX)

- 40um pixel size, E8%@1000Hz
- 1st image : CSR, 1 MSMS scan per pixel, 1084/CID@35NCE, wideband activation, 680ms injection time.
- 2nd image : between CSR lines of 1st image, 1 Full scan per pixel, 600-1200 @15k, 600ms injection time
- Same CSR stage velocity for both images, duration <30 minutes per image



Optical
image+HRMS
image

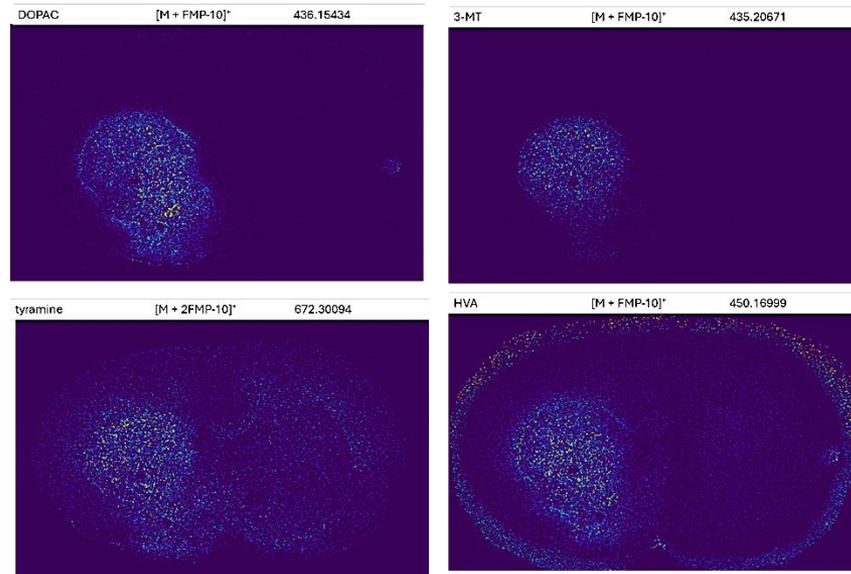
Optical image

HRMS Image
 $m/z=1084.4451$
 $\pm 15\text{ppm}$

MS/MS Image
 $m/z=757.3$
 $\pm 0.5\text{Th}$

BEYOND LIPIDS IN FRESH FROZEN TISSUE SECTIONS

On-tissue chemical derivatization of neurotransmitters (FMP-10, www.tag-ON.se)

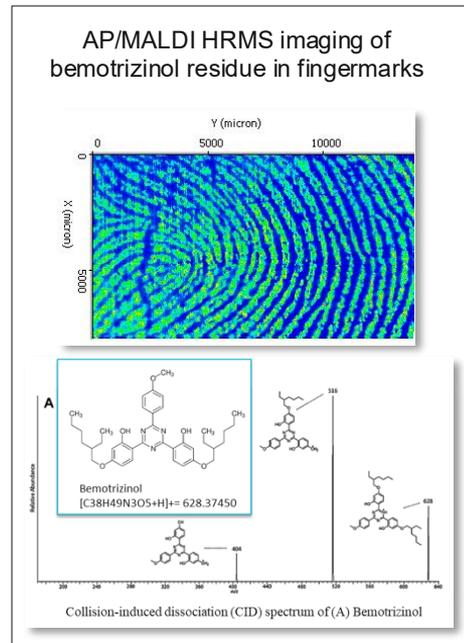
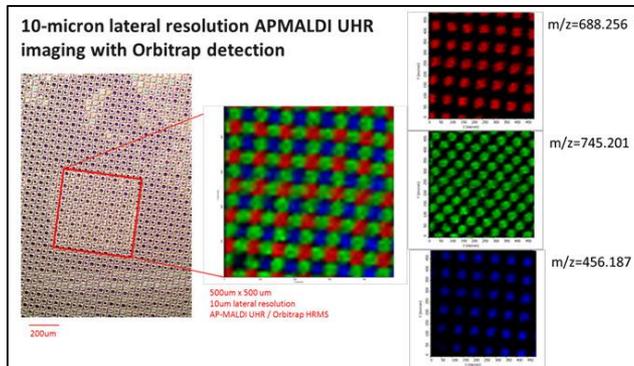
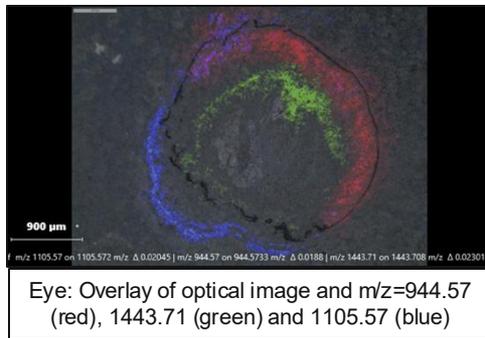


Data are acquired in a single experiment from a 6-OHDA unilaterally lesioned rat brain tissue section using AP/MALDI Exploris 480
(First experiment)

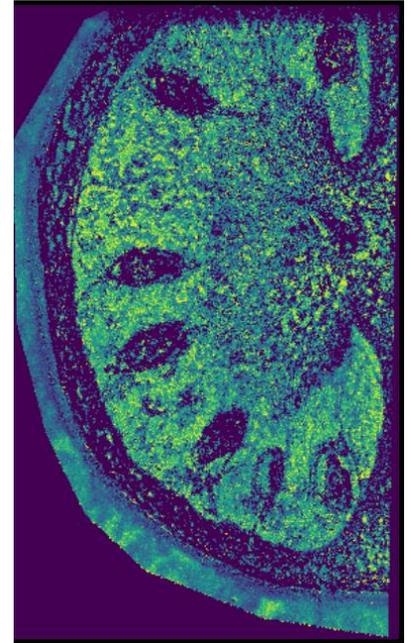
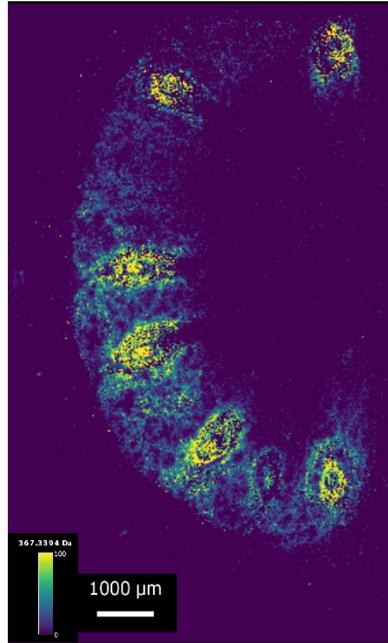
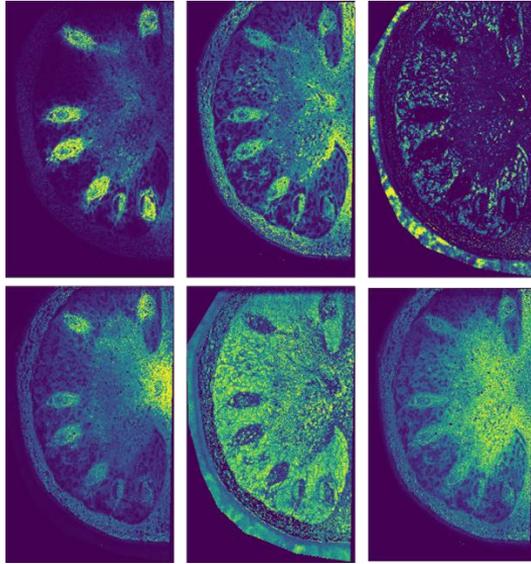


BEYOND BRAIN AND SKIN SAMPLES

- Liver, eyes, organoids, tumors
- Blood disease markers
- Fingerprints
- Materials (polymers, OLED displays)
- Plant materials (leaves, petals, roots, seeds, fruits)



APMALDI ORBITRAP IMAGING OF A TOMATO SECTION



Dr Gerhard Saalbach, The John Innes Centre, Norwich

