



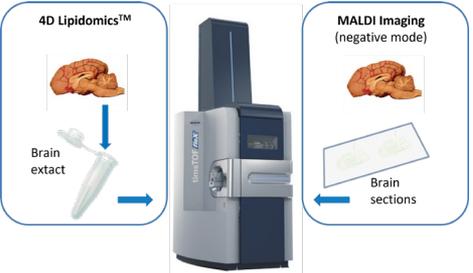
# CCS-enabled SpatialOMx<sup>®</sup> for automatic annotation of lipids in MALDI Images based on 4D-Lipidomics<sup>™</sup> data

Janina Oetjen<sup>1</sup>, Sven Meyer<sup>1</sup>, Christian Marsching<sup>1</sup>, Corinna Henkel<sup>1</sup>, Annika Nyhuis<sup>1</sup>, Ansgar Korf<sup>1</sup>, Nikolas Kessler<sup>1</sup>, Wiebke Timm<sup>1</sup>, Aiko Barsch<sup>1</sup>, Jan Hendrik Kobarg<sup>1</sup>, Heiko Neuweger<sup>1</sup>, Carsten Hopf<sup>2</sup>  
<sup>1</sup>Bruker Daltonics GmbH & Co. KG, Bremen, Germany. <sup>2</sup>Center for Mass Spectrometry and Optical Spectroscopy (CeMOS), Technical University, Mannheim, Germany

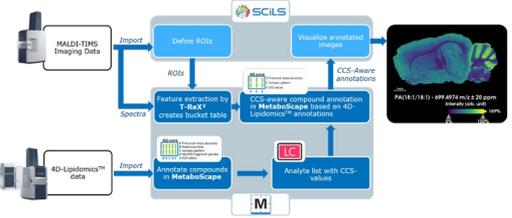
## Introduction

The CCS-enabled SpatialOMx workflow opens new dimensions by combining the molecular and spatial information measured by MALDI-TIMS Imaging with highly confident 4D-Omics annotations. MetaboScape<sup>®</sup> 2021b and SciLS<sup>™</sup> Lab 2021b provide the interface to match data from both ionization techniques and enable automatic and CCS-enabled annotations of MALDI Imaging data. The CCS-value is a key component of this workflow.

## Methods

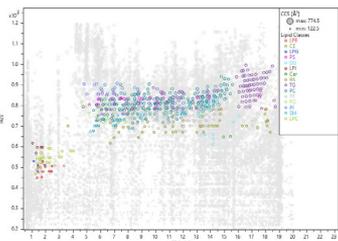


Mouse brain lipids were annotated after LC-ESI PASEF using a brain homogenate. Annotations were based on exact mass, retention time, MS/MS spectra and CCS-value. The resulting list was used to annotate lipids after MALDI Imaging of sections from the same brain sample. In addition to the exact mass, the mobility information (CCS-value) adds an additional confirmation criterion for reliable annotations.

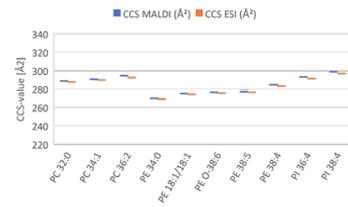


Computational pipeline using SciLS<sup>™</sup> Lab 2021b and MetaboScape<sup>®</sup> 2021b for CCS-enabled annotation of MALDI Imaging data.

## Results



Annotated lipids from the 4D-Lipidomics<sup>™</sup> (LC-ESI PASEF) experiment. 292 unique lipids were annotated in negative mode and 295 in positive mode using the rule-based lipid annotation tool of MetaboScape.

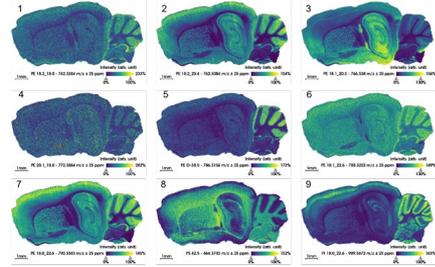


Reproducibility of CCS-values across ESI- and MALDI-ionization for different lipids.

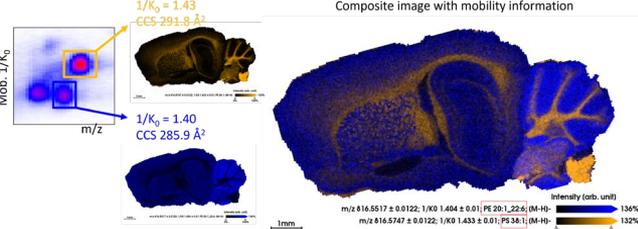
Extract of feature table listing the selected lipids shown below<sup>1</sup>.

Rank	m/z (exact)	MS (exact)	Isom	Name	Δm/z (ppm)	ΔCCS (%)	Molecular For.	Annotations	ΔQ
1	742.53843	742.54866	+	PE 18:2_18:0	-1.079	0.0	C <sub>36</sub> H <sub>70</sub> N <sub>2</sub> O <sub>6</sub> P	CCS, ESI, MALDI	1.1
2	762.50055	763.51533	+	PE 30:6	0.162	0.0	C <sub>40</sub> H <sub>78</sub> N <sub>2</sub> O <sub>6</sub> P	CCS, ESI, MALDI	1.1
3	766.53053	767.54580	+	PE 18:3_20:3	-1.559	0.2	C <sub>38</sub> H <sub>74</sub> N <sub>2</sub> O <sub>6</sub> P	CCS, ESI, MALDI	1.1
4	772.56837	773.58595	+	PE 20:1_18:0	2.842	0.2	C <sub>38</sub> H <sub>74</sub> N <sub>2</sub> O <sub>6</sub> P	CCS, ESI, MALDI	1.1
5	786.52753	787.53297	+	PS 18:1/18:1	-2.175	0.0	C <sub>36</sub> H <sub>70</sub> N <sub>2</sub> O <sub>7</sub> P	CCS, ESI, MALDI	1.1
6	788.52289	789.53597	+	PE 18:1_22:6	-1.620	0.0	C <sub>38</sub> H <sub>74</sub> N <sub>2</sub> O <sub>6</sub> P	CCS, ESI, MALDI	1.1
7	790.53831	791.54539	+	PE 18:2_22:6	-1.199	0.1	C <sub>38</sub> H <sub>74</sub> N <sub>2</sub> O <sub>6</sub> P	CCS, ESI, MALDI	1.1
8	864.57427	865.58135	+	PS 4:3	-2.010	0.0	C <sub>16</sub> H <sub>30</sub> N <sub>2</sub> O <sub>7</sub> P	CCS, ESI, MALDI	1.1
9	909.54725	910.55432	+	PI 18:0_22:6	-2.865	0.4	C <sub>36</sub> H <sub>70</sub> O <sub>10</sub> P	CCS, ESI, MALDI	1.1

Visualization of annotated lipids in SciLS<sup>™</sup> Lab 2021b.



<sup>1</sup>Missing ΔCCS indicates that a different adduct was detected with ESI.



Visualization of MALDI-TIMS Imaging data in SciLS<sup>™</sup> Lab 2021b.

## Conclusions

- Mobility enhanced MALDI-TIMS Imaging enables the separation of isobaric or even isomeric compounds and thereby delivers unprecedented imaging results, especially for spatial lipidomics.
- The novel CCS-enabled SpatialOMx<sup>®</sup> workflow increases the confidence in lipid annotations for MALDI images through the acquisition of CCS-tagged data.
- The CCS-enabled SpatialOMx<sup>®</sup> workflow is facilitated by a seamless communication between MetaboScape<sup>®</sup> 2021b and SciLS<sup>™</sup> Lab 2021b.