

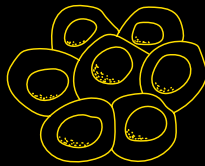
Mesenchymal
(Vimentin)



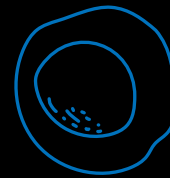
Macrophage/
Monocyte (CD68)



Epithelial/Tumor
(PanCK)



B-Cell (CD20)



T-Cell (CD3)



THE NEXT REVOLUTION IN MALDI IMAGING

MALDI HiPLEX-IHC

Transforming Multiomic Spatial Tissue
Imaging with MALDI Mass Spectrometry

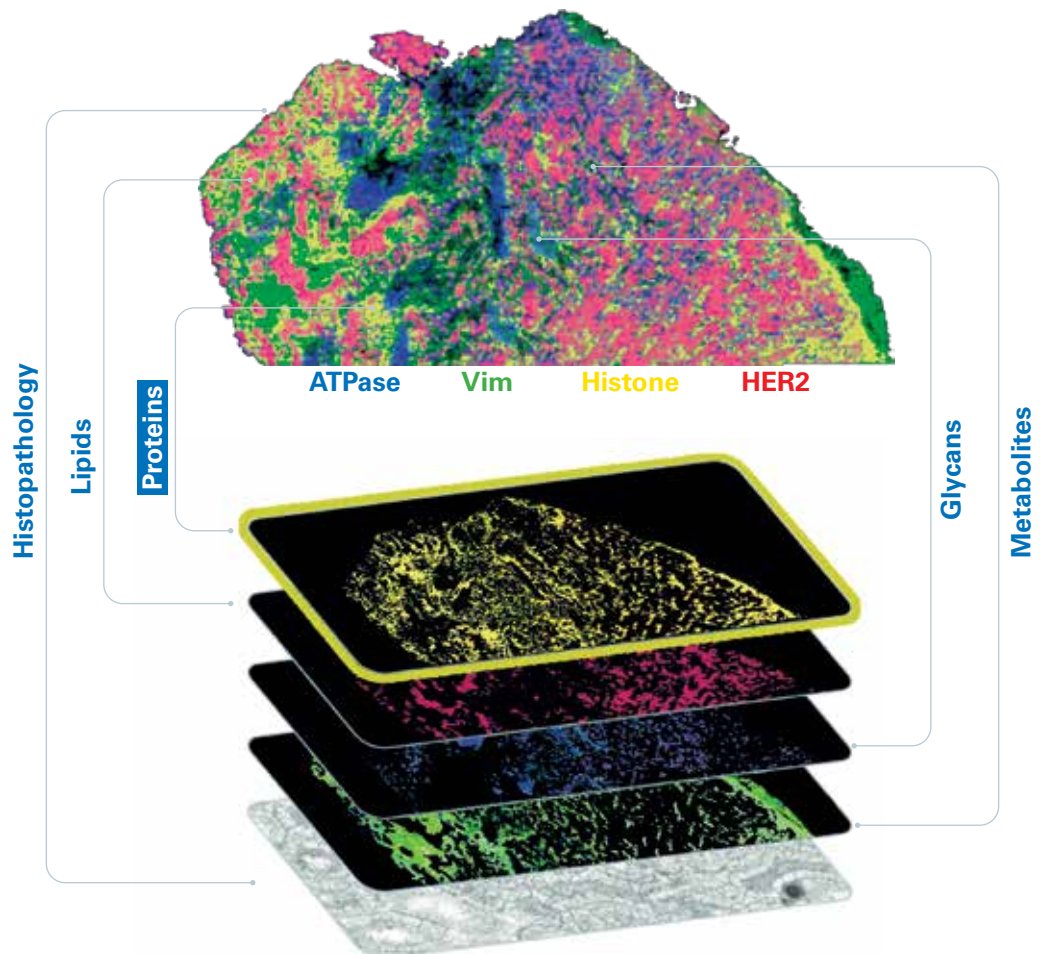
Innovation with Integrity

Differentiated biomarker imaging that exceeds your translational needs.

Maximize information from tissue micro-environments by tying together transcriptome relevant protein expression information with glycan and metabolite imaging from the same tissue section.

Redefine your spatial biology capabilities and tie your biomarkers to research breakthroughs in:

- Immunooncology
- Neuropathology
- Therapeutic response
- Toxicology and toxicity



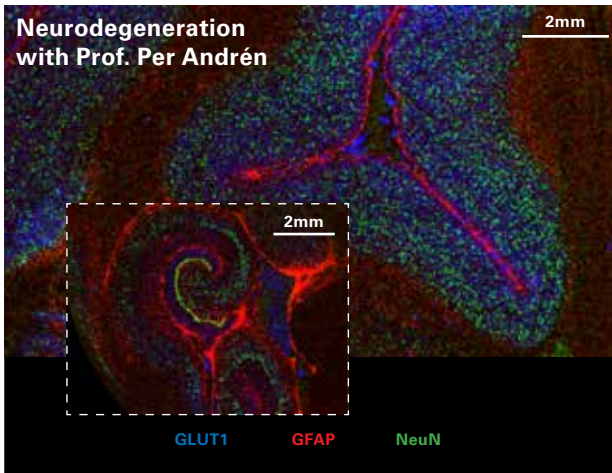
Elizabeth Neumann

University of California – Davis

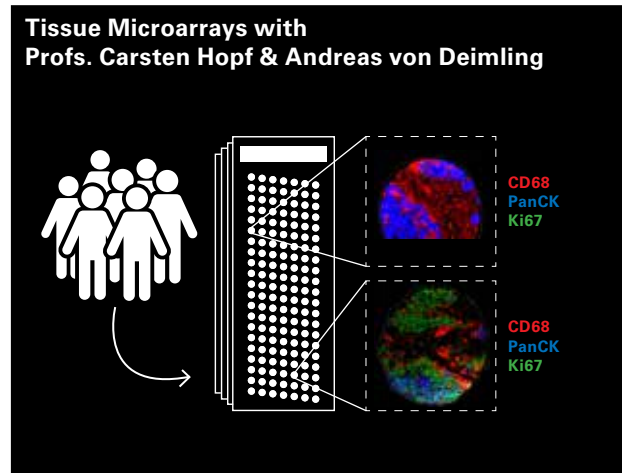
We are moving **beyond the microscope** to an all-in-one analytical system for multiomics approaches, which is the future of tissue interrogation and biological science. The ability to lean on well-established antibodies without having to cycle or bleach will enable more difficult/brittle systems to be analyzed.



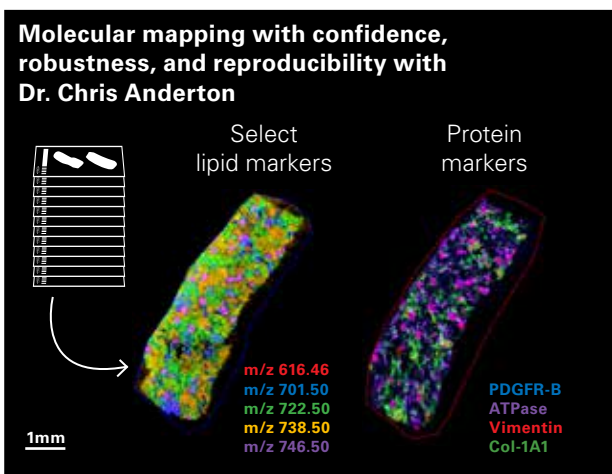
Extend the reach of your disease focused-research



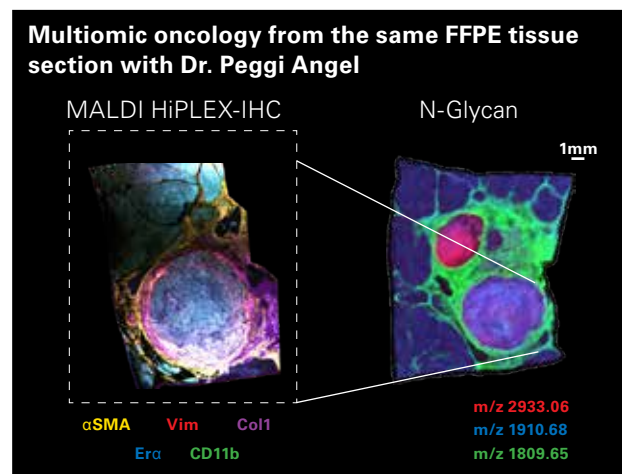
- Neurodegenerative disease visualization for key protein differentiators and structural disease pathology
- Combine direct MALDI Imaging of neurotransmitters and neuropeptides with targeted intact protein imaging on the same tissue section with the same platform
- MALDI HiPLEX-IHC is shown on an MPTP parkinsonian Macaca brain model system designed to study L-DOPA-induced dyskinesia



- Ultra high-dimensional imaging using MALDI HiPLEX-IHC on Tissue Microarrays (TMAs) of 100s of pathological specimens for high throughput statistically-robust clinical research
- Example cores are shown from a neuropathology TMA imaged by MALDI HiPLEX-IHC, with protein markers for understanding cell types in context



- Combined metabolomic/lipidomic and targeted protein imaging on the same slide with co-localization across molecular classes
- Sequential lipid imaging and MALDI HiPLEX-IHC imaging on the same fresh frozen human kidney section is shown

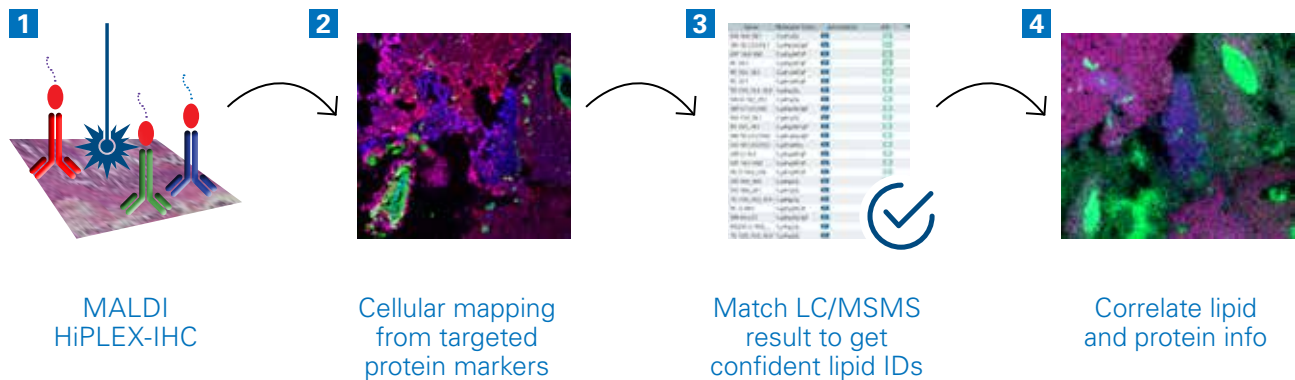


- Enable multiomic imaging on standard pathological FFPE biospecimens by combining MALDI HiPLEX-IHC for intact proteins with direct glycan detection
- Hepatocellular carcinoma imaging can reveal aberrant glycosylation and protein co-localization

Synergy of MALDI HiPLEX-IHC and SpatialOMx

Disease complexity requires a comprehensive understanding of biological system and includes analysis of intact proteins and their contextual interaction with other small molecules like metabolites, lipids or drugs.

The MALDI-HiPLEX IHC workflow, in combination with a SpatialOMx® approach, provides a basis for achieving this high information content imaging of tissue. The multiomic and multimodal workflow uncovers the interplay between metabolites and protein expression for basic research and clinical applications.



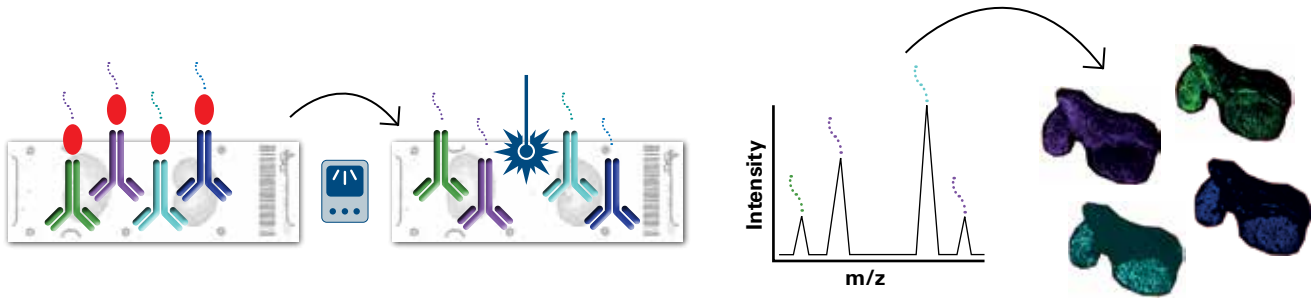
Prof. Dr. Oliver Schilling

Institute of Surgical Pathology, University Medical Center
Freiburg, Germany

MALDI imaging has huge potential to play an essential part in pathological diagnostics and research, especially with regard to characterising the spatial biology of lipids and metabolites. Moreover, MALDI Imaging of multiplexed immunostaining (HiPLEX) is emerging as an exciting novel approach. The timsTOF fleX enables innovative workflows to significantly advance this field and will play an essential role in our research portfolio.

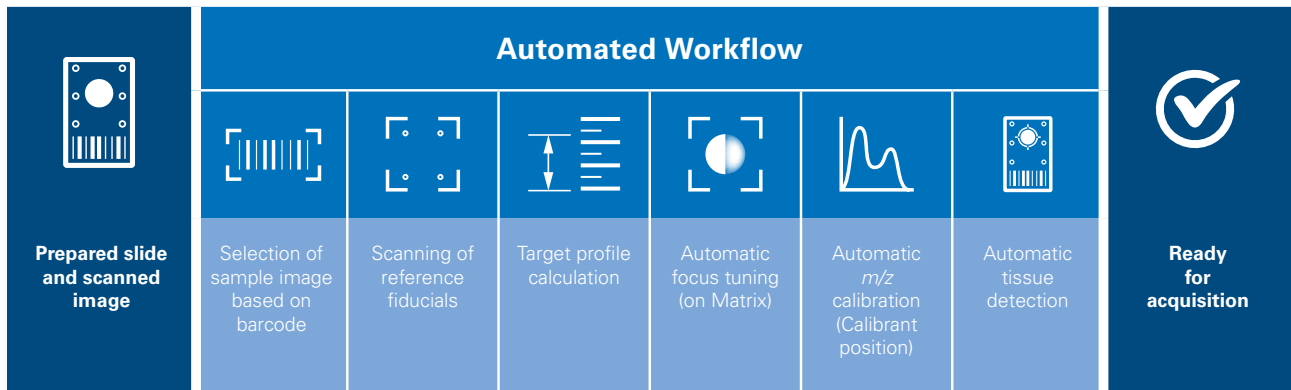


How it works

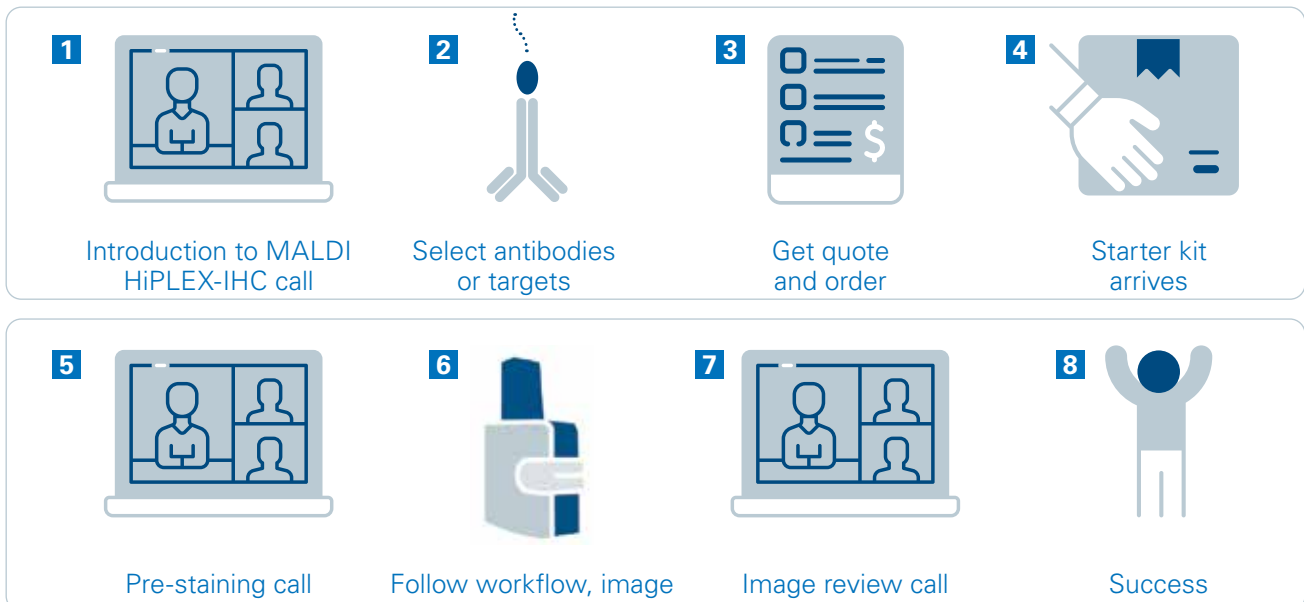


- 1 IHC staining
- 2 Photocleavage of mass tag
- 3 MALDI measurement & readout
- 4 Targeted images

No experts required



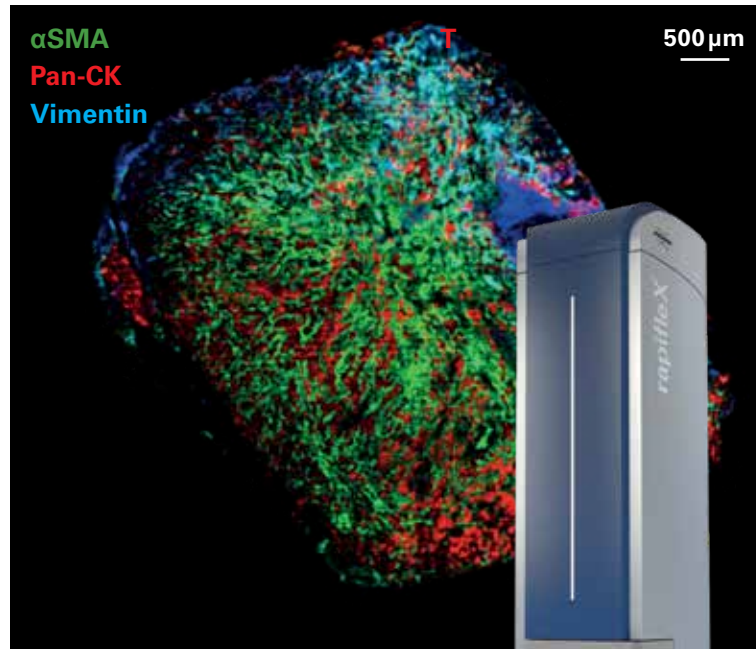
How you can get it



MALDI Imaging platforms for all applications

rapifleX – the fastest MALDI Imaging platform available

- New levels of multiplexing without increasing analysis time
- Simple operation, easy to use and maintain with automated setup features for reproducible and consistent analysis

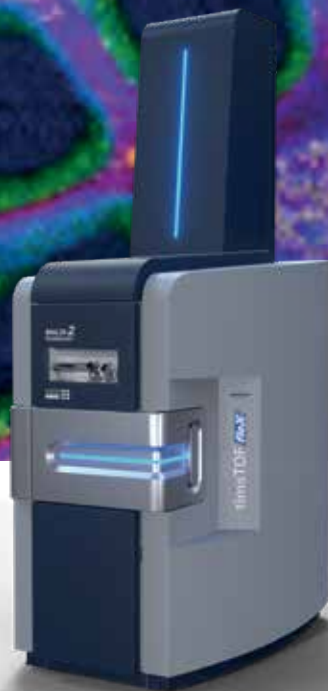


Ganglioside
Co-Localized
Anti-MBP/Sulfatide
Anti-Syn1
Anti-GLUT1
Anti-NeuN

200 μ m

timsTOF fleX – multiomics workhorse with spatial contextualization

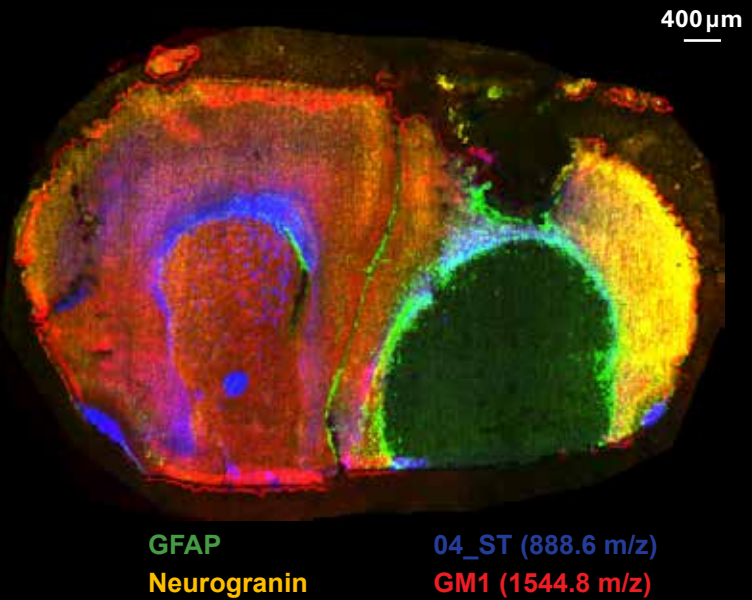
- Biomarker access from one platform: proteins, glycans, metabolites, lipids, and xenobiotics
- Uniquely ID non-targeted small molecules with CCS databases or link to LC-MS/MS
- MALDI-2 adds chemical dimensionality and improves sensitivity
- microGRID enables 5 μ m imaging



Turning data into knowledge

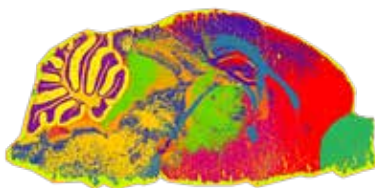
Multimomics studies using multiple acquisitions with different protocols from the same tissue sample reveal spatial correlations between the distribution patterns of, for example, proteins, lipids, and glycans.

SCiLS offers a unified software workflow for multimomics MALDI Imaging, state-of-the-art visualization tools and computational analysis algorithms.



The Application Programming Interface (API) enables integration, customization, scalability, and innovation

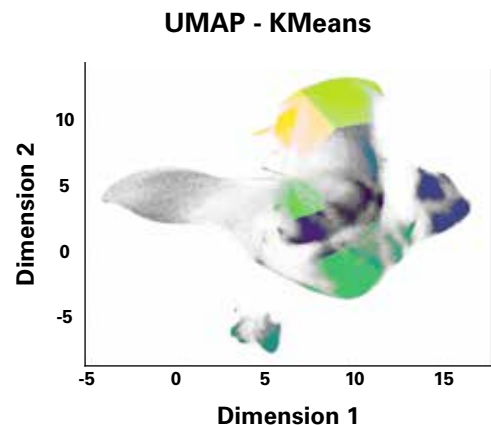
- SCiLS advanced 4D annotation to seamlessly evaluate within your own pipelines
- Generate dataframe with region attributes and spectral intensities for subsequent statistical analysis
- Find new meaningful connections from MALDI Imaging data, such as localized differences in enzyme metabolic activity or metabolic flux in healthy vs. diseased tissue



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MALDI HiPLEX-IHC is for:

- Researchers who need to contextualize systems biology from a functional perspective, especially for cancer and disease pathologies to compliment work performed in bulk Omics or single-cell work

Who want to:

- Visualize expression of known proteins in tissue structures or cellular compartments with important small molecule biological markers such as glycans, lipids, or metabolites

Bruker Provides:

- MALDI HiPLEX-IHC Workflow on the timsTOF fleX or rapifleX[®] for antibody probe-based protein imaging with SCiLS[™] Lab Software solutions for automated sample interrogation and analysis

That offers:

- Multiplexed and multimodal data visualization in the highest field-of-view without compromising protein multiplex level

Allowing you to:

- Gain maximum multiomic information for more thorough tissue imaging to better understand the relationship of cellular interactions to tissue homeostasis or disease pathology

Unanticipated benefit:

- Multiomics workflows all on the timsTOF fleX or fastest analysis on the rapifleX[®]

For Research Use Only. Not for use in clinical diagnostic procedures.

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