

Benchtop MALDI-TOF

neofleX MALDI-TOF

More insight per pixel

Groundbreaking 116 protein panel at 30 μm imaging in 7 hours

Innovation with Integrity

If you could simultaneously image >100 proteins on a tissue section, how would you ask questions differently?

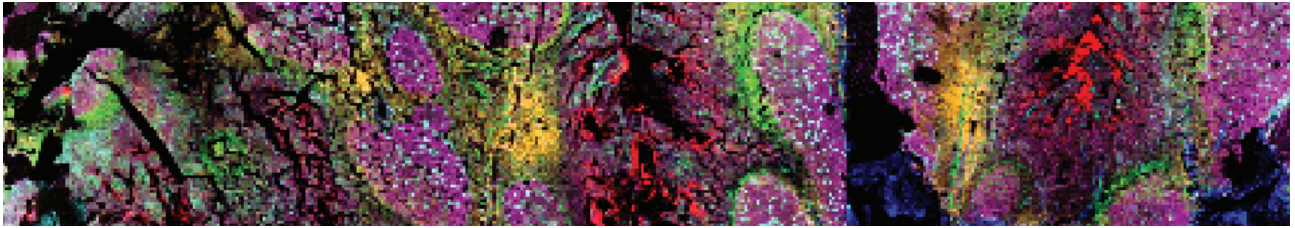
Methods that track targeted protein expression on tissue surfaces have significantly changed the understanding of biology and disease. The ability to connect data from single cell, or bulk experiments to specific locations within the tissue microarchitecture informs deep insight on how cellular neighborhoods interact to drive biological processes and disease states.

Understanding complex cellular landscapes that exist for certain disease pathologies, such as the tumor microenvironment, is a known challenge with a lack of complete characterization and contextualization.

Of the powerful tools available to researchers, most are heavily focused on biological discovery creating the need for a platform with the flexibility and efficiency to influence hypothesis testing in real-time.



See the Roberts' lab
and neofleX in action!



Inspired innovation for spatial biology

Automated Acquisition

The advanced technology built into neofleX™ is accessible to anyone utilizing pre-run automation, powered by SCiLS™ autopilot, which automatically optimizes the instrument prior to each acquisition to ensure peak performance for each tissue section or tissue microarray (TMA).

Flexible Acquisition

You choose how you want to acquire data based on the question at hand. Want to quickly process a stack of sections to evaluate expression patterns across a tissue regardless of plex level? The integrated Smartbeam 3D laser system will “zoom out” for the run and process your samples in minutes instead of days to help you decide what comes next.

Flexible Region of Interest

Having trouble deciding on an ROI? neofleX is not limited to small areas and can image entire slides, with higher plex levels having no impact on acquisition speed.

Flexible Targeting

neofleX leverages the advanced MALDI HiPLEX-IHC workflow for spatial biology that uses unique peptide reporters for each probe, meaning you retain the familiarity and ease of IHC with the flexibility of mixing and matching any validated probes and panels without modifications.

Sample Integrity

Tissue samples are not degraded during the measurement and can be used for additional studies after mapping with neofleX.

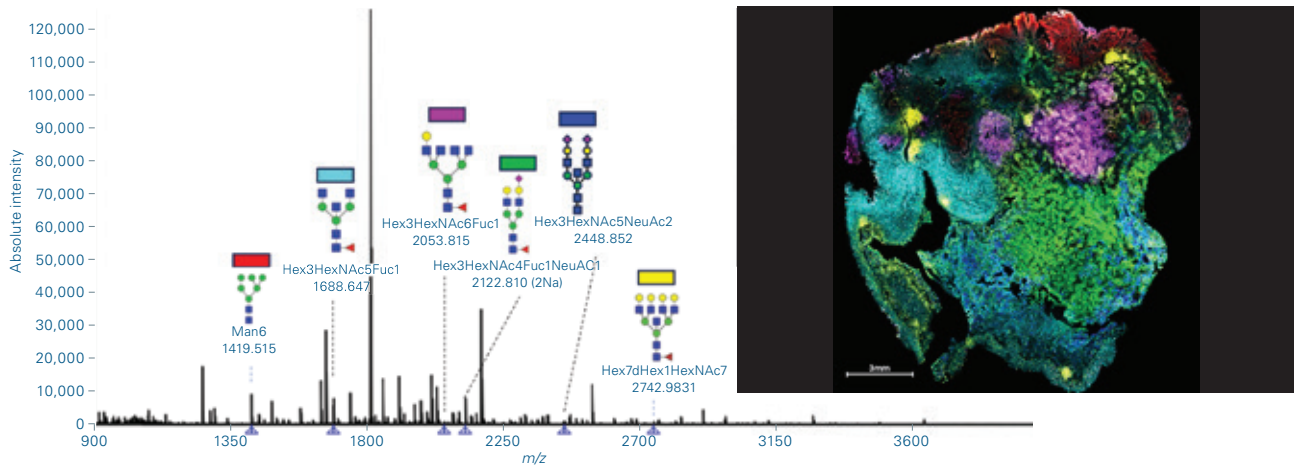
Building the cellular neighborhood with neofleX:

- What are the cell types and states present?
- Determine expression patterns.
- Define the spatial structure (e.g. is the tumor infiltrated?).



Bring OMICS context to cancer research

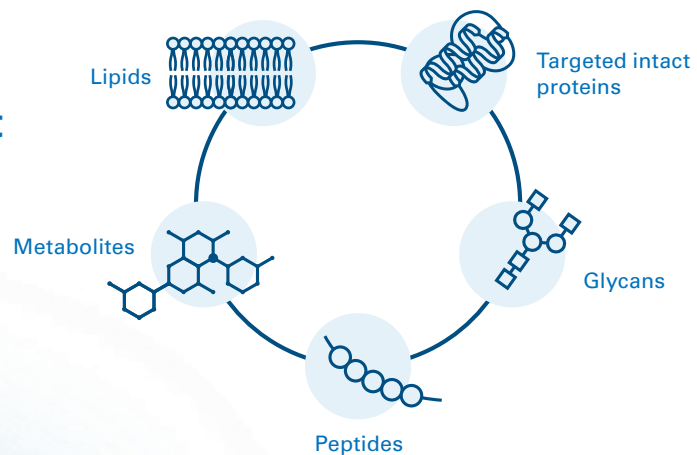
Integrating neofleX into your spatial biology workflow allows you to know both where your proteins **are and what they are doing**. Multiomics goes beyond RNA and protein expression to redefine important inputs by spatially co-localizing selected proteins with glycans, targeted metabolites and lipids to expression targets within the tissue or tumor microenvironments.



Mean spectrum of the entire N-glycan MALDI Imaging dataset from a colorectal cancer section and multichannel ion image showing the distribution of the indicated peaks (blue triangles under the x-axis).

Putative structures of the N-glycans are given above each peak. The colors used for false-color coding of the ion image are given above each glycan structure. Sample courtesy of A. Tannapfel and Jens Christmann, Institute of Pathology, University of Bochum, Germany.

Use neofleX multiomics to add biological context beyond expression



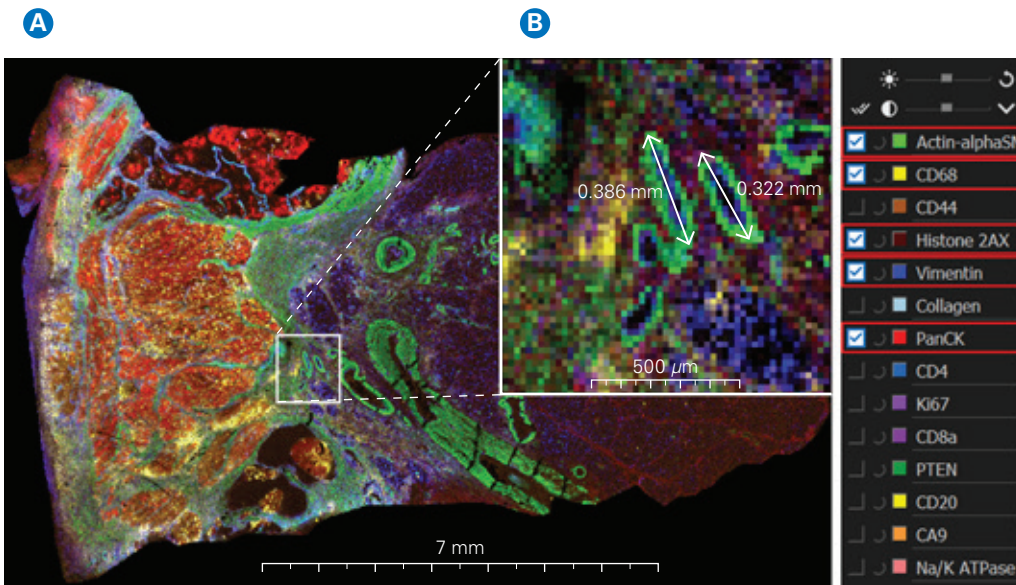
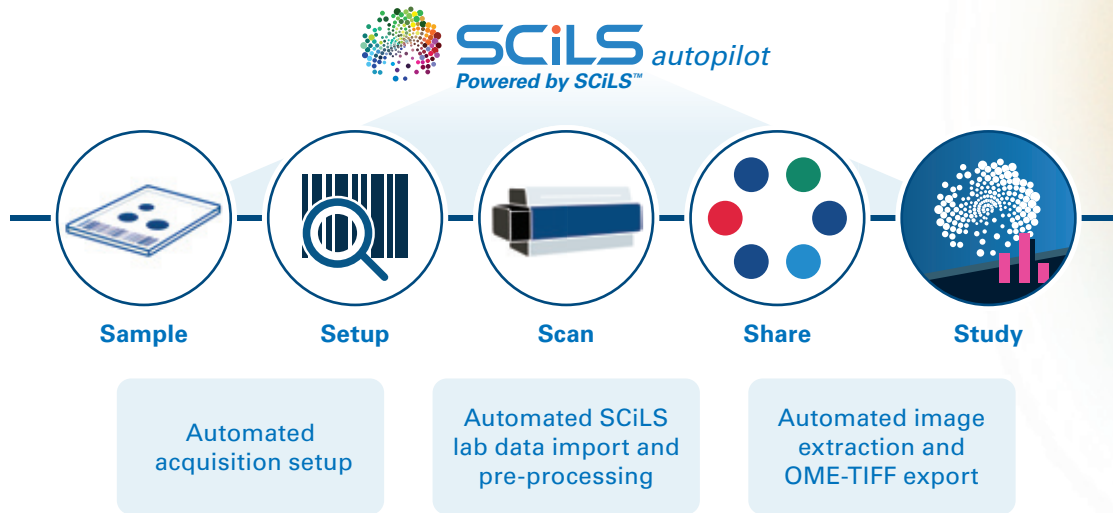
» Peggi Angel, Ph.D.

Associate Professor at Medical University of South Carolina

From the perspective of a lab heavily invested in cellular signalling processes involved with cancer, MALDI HiPLEX-IHC is a game changer allowing integration of mass spectrometry imaging with cell biology.



A complete workflow



SCiLS Scope visualization of MALDI HiPLEX-IHC data from a colorectal cancer sample.

Various cancer-, immune-, and microenvironment-specific markers were activated, and the distribution of the proteins is shown **(A)**. In the zoomed window **(B)** the distance measure was applied to highlight blood vessel diameter.



Prof. Dr. Carsten Hopf

Hochschule Mannheim – Center for Mass Spectrometry and Optical Spectroscopy

neofleX presents an incredibly versatile opportunity in ease-of-use for entry-level researchers wanting to expand their biomedical applications.



World class MALDI lineup

The leading expert in MALDI



← Translation

Discovery →

neofleX™
Multiomic
translational



rapifleX®
Targeted
throughput



MALDI-TOF MS: Powerful analysis, fast results

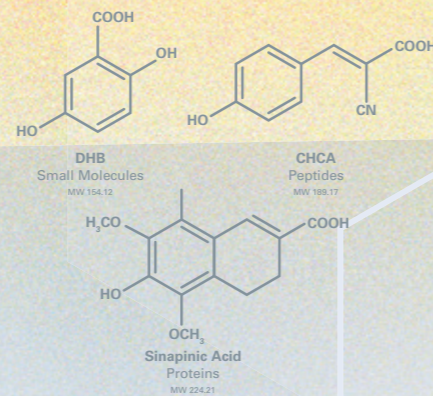
For over 30 years, matrix assisted laser desorption ionization (MALDI) TOF MS has proven its analytical capability. Offering unparalleled speed (time to results) and flexibility, MALDI-TOF MS stands out for its low sample volume requirements and ability to handle a broad range of sample content, including salts and buffers.

With continued innovation, intuitive software and seamless automation enhance the depth of MALDI analyses while ensuring high throughput solutions.

timsTOF fleX
Flexible
discovery



scimaX®
Toughest
problems



Time of flight principle

Kinetic energy of an ion acceleration by voltage U:

$$E_{kin} = \frac{1}{2} mv^2 = zeU$$

Velocity of an ion in a field free region:

$$v = \frac{L}{t}$$

Substitution of v in (1):

$$E_{kin} = \frac{1}{2} m \left(\frac{L}{t} \right)^2 = zeU$$

$$m/z \sim t^2$$

- m = ion mass
- v = velocity of the ion after acceleration
- z = charge number
- e = elementary charge
- U = acceleration voltage
- t = time of flight in seconds
- L = traveled (AE) distance

Common MALDI matrices

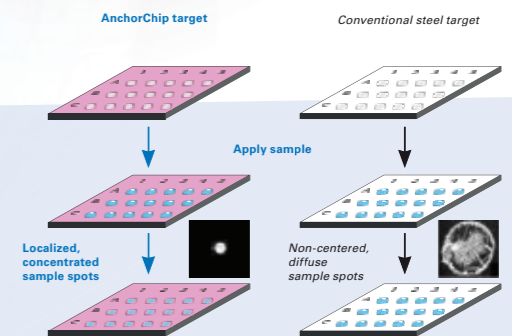
fleXmatrix® – The key to success in MALDI MS analyses
fleXmatrix pre-portioned vials simplify matrix solution preparation for MALDI Imaging, especially for standard spraying or sublimation methods. This ensures consistency and saves time in your workflow.



Smart consumables

IntelliSlides® – Maximize information content per pixel with intelligence

IntelliSlides are the perfect tool for SpatialOMx®. They simplify your MALDI Imaging workflows by enabling automated setup of each measurement and via barcoding and permanent inscriptions on the conductive slide surface for optimal placement of samples and registration marks (teach marks) for imaging.



Analytical advantages

AnchorChip Target Technology – Simplify sample preparation and improve reproducibility
Sample positions on patented AnchorChip targets contain "anchors" – hydrophilic patches surrounded by a hydrophobic ring. The "anchor" localizes droplets and ensures that every single laser shot fired throughout an automatic run will hit a sample spot.

Online information
bruker.com



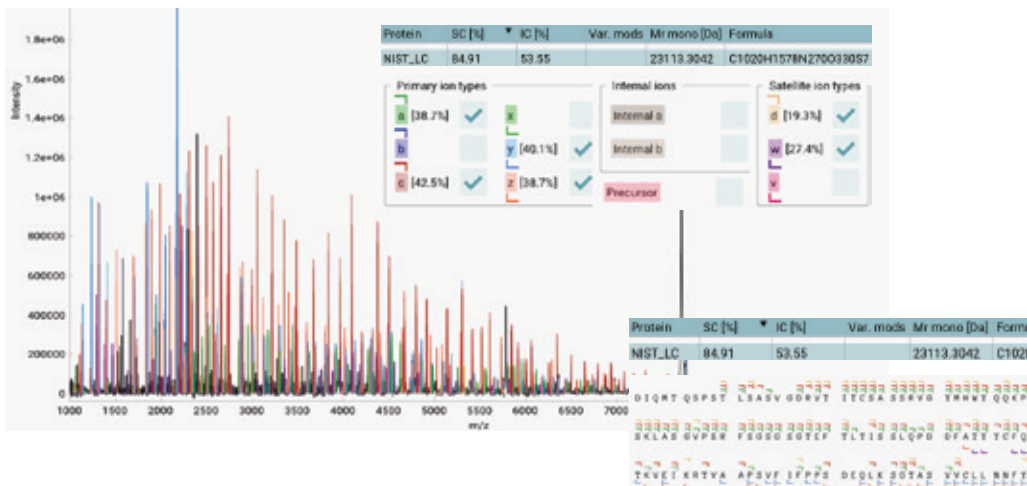
Protein sequence validation in seconds

A protein primary sequence is a critical attribute directly impacting its structure and function. As such it is an essential parameter to verify, whether working on affinity-based reagents for biological assays or a biological drug.

The neofleX brings high performance MALDI top-down sequencing (MALDI-TDS) to benchtop instruments for the first time, enabling users with a powerful sequence validation tool for purified proteins that minimizes the time to results.

MALDI-TDS measurements can be carried out in less than a second and produce singly charged spectra which can easily be analyzed with Bruker's OmniScape™ software. The neofleX resolving power affords high confidence verification of recombinant proteins such as mAb subunits, with MS/MS T3 sequencing to increase confidence. Beyond time savings, minimal sample inputs are required (1 pmol) which make this technique applicable to precious reagents or research-grade quantities.

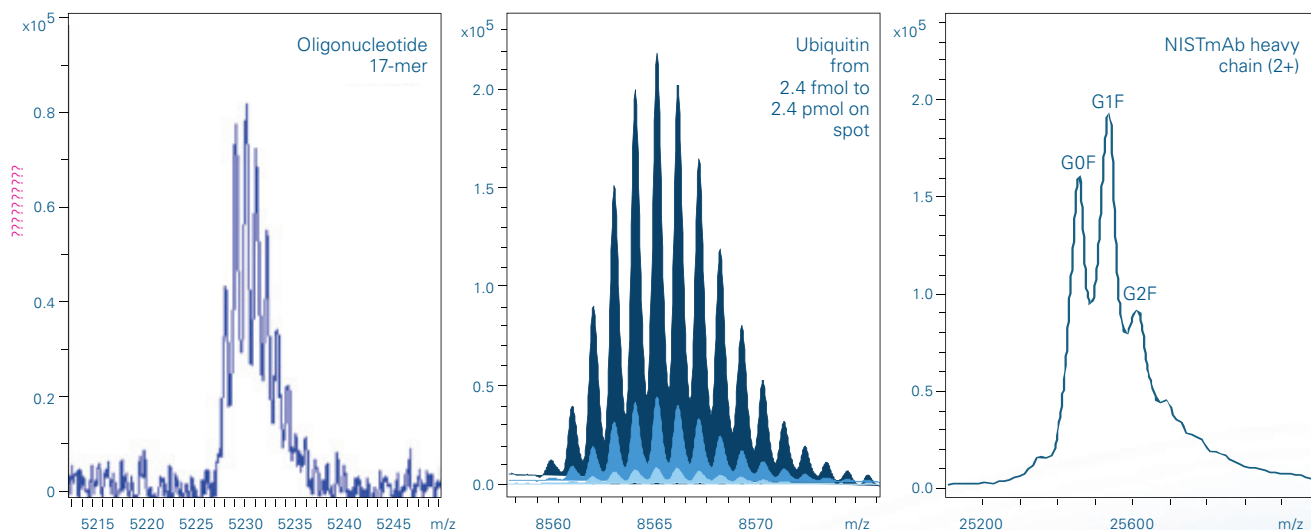
Comprehensive sequence verification with OmniScape processing (NISTmAb LC)



Sequence verification of NIST mAb light chain by MALDI top-down sequencing (MALDI-TDS). Simple and robust sequence readout that does not require charge deconvolution. Matching MALDI-TDS data against a target protein sequence using Bruker OmniScape software requires only few mouseclicks. Confident sequence confirmation with a short time to result enables instant decision making.

- Results in less than 5 seconds
- < 1 pmol sample input
- Easy data interpretation

Comprehensive toolbox for biologics characterization



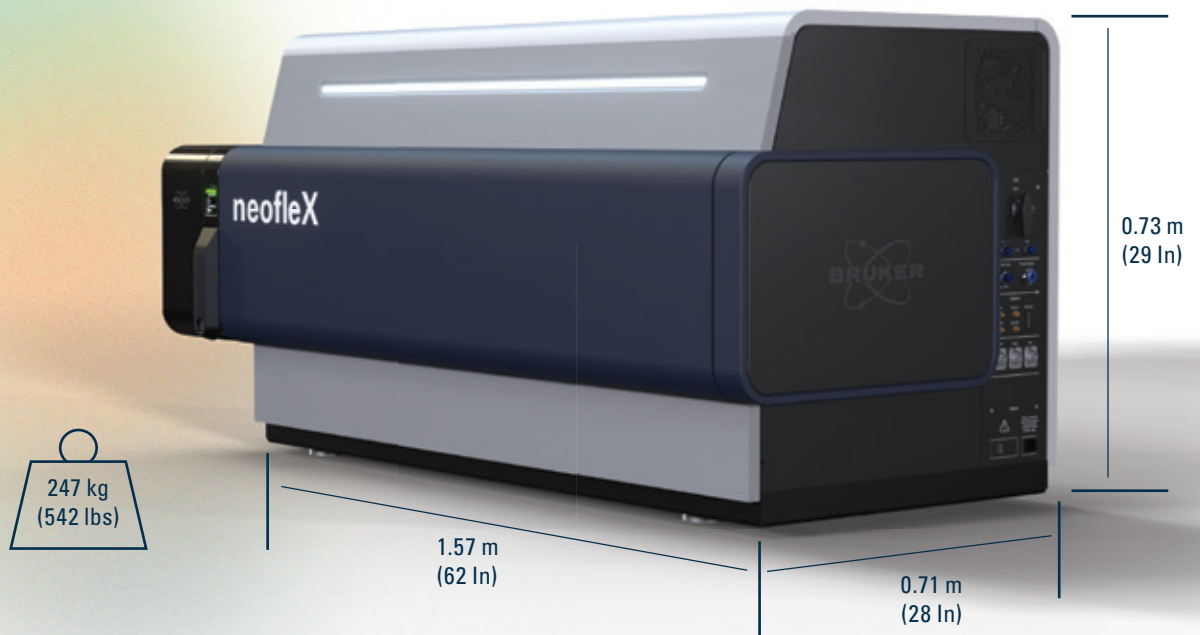
High sensitivity and resolution across a wide m/z range provide essential data for biologics projects

MALDI offers the unique capability of measuring biopolymers across a wide molecular weight range with high speed, sensitivity and non-overlapping charge states (1+ dominated spectra). This provides the foundation for a large range of workflows.

The simple output and rapid analysis make MALDI attractive for applications such as clone screening or enzyme activity assays. The ease of use, matrix tolerance, sample diluent flexibility and easy data review are ideal characteristics for identity verification workflows at the intact or digested level.

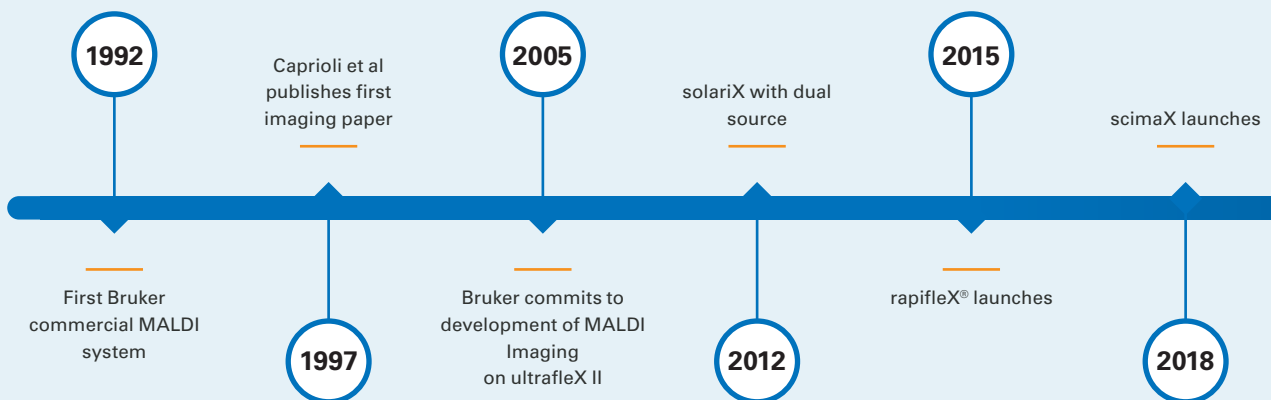
With the neoflex, users are empowered with research-grade performance in a benchtop instrument equipped to support R&D projects requiring the analysis of biologics of high hydrophobicity, heterogeneity (e.g. conjugation) or with high speed. Together with BioPharma Compass® data processing, neoflex offers the next-generation toolbox for your research.

High confidence protein
characterization



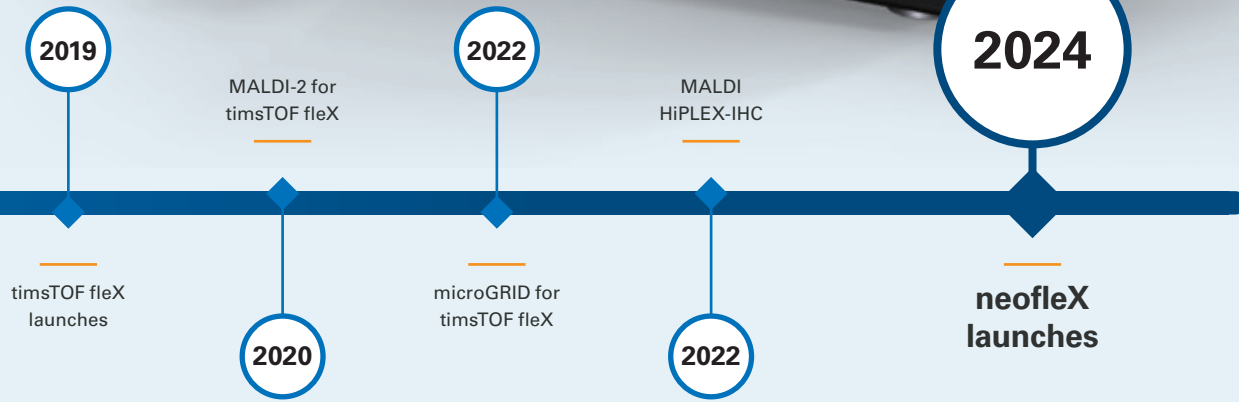
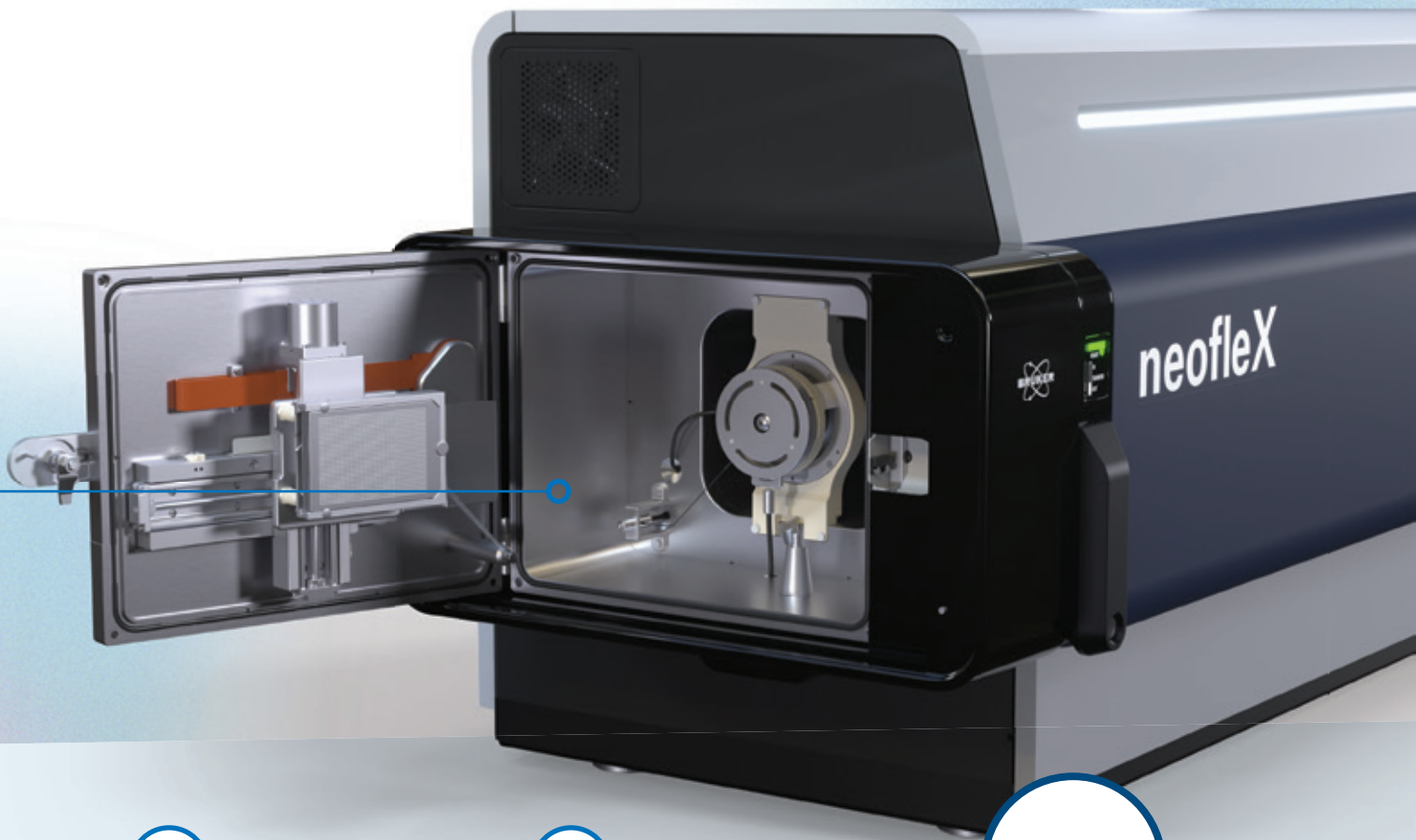
EASY to

- access
- clean
- operate



Use neofleX multiomics to add biological context beyond expression including:

- Energy bioavailability
- Metabolic output
- Function
- Structural components
- Protein activity



The neoflex seamlessly complements Bruker's existing MALDI Imaging portfolio including the rapiflex, the timsTOF flex and the scimaX.

Unparalleled performance

- **True pixel imaging:** Patented smartbeam 3D technology delivers industry-standard 20 µm spatial resolution for detailed analysis.
- **Enhanced imaging detectors:** Capture high-quality data for accurate results.
- **Sweeping MS/MS capabilities (LID, CID, ISD):** More insight into structural details. Seamless top-down and bottom-up sequencing of proteins.

Powerful tools, seamless integration

- **IntelliSlides®:** Maximize insight per pixel with intelligent slide technology.
- **SCiLS autopilot:** SCiLS™ Lab and open-source OME-TIFF files directly after measurement for seamless data analysis.
- **SCiLS Scope:** Quickly and easily visualize images of interest.
- **OmniScope:** Get the most out of your top-down sequencing data
- **BioPharma Compass®:** Accommodate large amounts of MS and MS/MS data in structured projects for enhanced efficiency in data analysis

Technical specification

Spatial resolution	20 µm
Max speed	20 px/s
Resolution (FWHM)	30,000
Mass accuracy (Int)	≤ 1.5 ppm
Effective flight length	124 cm linear mode 260 cm reflector mode
Benchtop size (LxWxH)	157 cm × 71 cm × 73 cm 62 in × 28 in × 29 in
Weight - TOF - TOF/TOF	247 kg (542 lbs) 270 kg (595 lbs)

Trusted comprehensive analysis

Advanced visualization and statistical evaluation with SCiLS Lab

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

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