MASS SPECTROMETRY

Product Overview

Bruker Daltonics

Innovation with Integrity

Driving innovation in proteomics, metabolomics, pharma/biopharma and other fields of life sciences and applied markets

Bruker is enabling scientists to make breakthrough post-genomic discoveries and develop new applications that improve the quality of human life. Bruker's high performance scientific instruments and high value analytical and diagnostic solutions enable scientists to explore life and materials at molecular, cellular, and microscopic levels. In close cooperation with our customers, Bruker is enabling innovation, improved productivity, and customer success in post-genomic life science molecular and cell biology research, in applied and pharma applications, in microscopy and nanoanalysis, as well as in industrial applications. Bruker offers differentiated, high-value life science and diagnostics systems and solutions in preclinical imaging, clinical phenomics research, proteomics and multiomics, molecular interactions, spatial and single-cell biology, functional structural and condensate biology, as well as in clinical microbiology and molecular diagnostics.

Premier provider of high-performance scientific instruments and life science research and diagnostic solutions

- Since 1960 track record of technological pioneering
- Culture of disciplined entrepreneurship
- Extensive collaborations with renowned science labs
- Deep chemistry, biology and physics applications expertise

Market leader in high-performance scientific instruments

+9700
Employees

+100
Countries worldwide

+1750
Employees dedicated to R&D

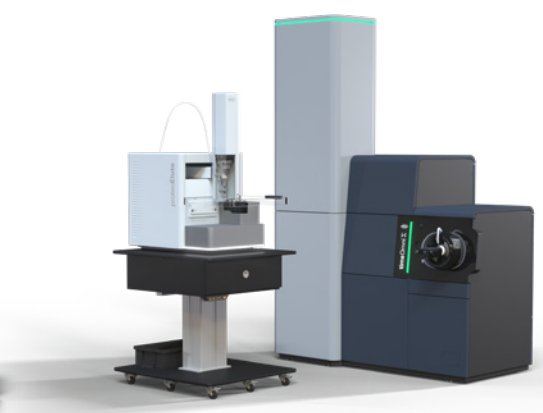
+4000
Patents pending or granted

Bruker holds **#1** or **#2** market positions in 70% of our portfolio.

Trapped Ion Mobility Mass Spectrometry

timsTOF – The next generation ion mobility separation

Bruker's timsTOF instruments revolutionized mass spectrometry by unlocking an additional dimension of separation with high sensitivity and speed. Trapped ion mobility increases peak capacity and confidence in compound characterization. Whether you need a reliable workhorse, a high-throughput powerhouse, a single-cell specialist, an ultra-sensitive flagship instrument, or a MALDI-guided SpatialOMx® expert there is the right timsTOF for your research needs. PASEF® (Parallel Accumulation Serial Fragmentation) is a powerful new technique that enables faster and more accurate identification, characterization, and quantification of proteins, peptides, lipids and other molecules providing significant benefits in their analysis. PASEF is an innovative feature incorporated into our timsTOF mass spectrometers that revolutionizes MS/MS sequencing.



	timsOmni	timsOmni Σ
resolution:	60,000	
acquisition rate:	up to 300 Hz in dda-PASEF	
PASEF methods:	dda-PASEF, dia-PASEF, diagonal-PASEF (midia, synchro), prm-PASEF	
instrument specific methods:	PASEF-EXD, Omnidirectional MSn, cDDA	PASEF-EXD, Omnidirectional MSn
source:	NEOS, ESI, CaptiveSpray Ultra 2, VIP-HESI, GC-APCI	ESI, CaptiveSpray Ultra 2, VIP-HESI, GC-APCI
size [mm]:	1419 x 900 x 1997	

timsTOF Series

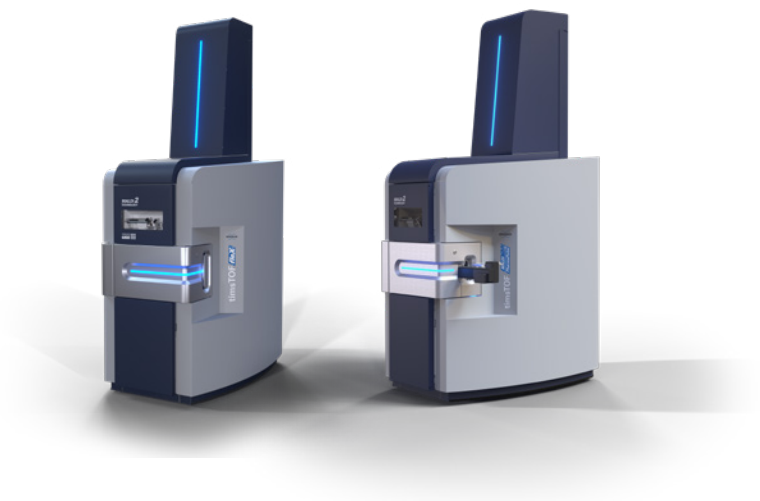
The timsTOF family offers unparalleled performance and versatility for a wide range of applications.

The timsOmni™ and timsOmni ∑ are the flagship instruments. Combining high sensitivity comparable to the timsUltra AIP while adding on top positive and negative fragmentation capabilities thanks to the integrated Omnitrap® technology. While the timsOmni was developed with a focus on high sensitivity intact protein structural analysis the timsOmni ∑ specializes in bottom-up, glycopeptides, PTM and small molecules structural identification using EXD capabilities.
The timsTOF Pro 2 delivers robust and comprehensive results for any challenge, while the timsTOF HT boosts the dynamic range and ion capacity to achieve maximum identification rates in proteomics experiments.
The timsUltra AIP, featuring the Athena ion processor (AIP) which allows controlled release of ions from the collision cell, sets new standards for single-cell and other very low input workflows, such as immunopeptidomics, reaching the highest sensitivity on the market.
The timsMetabo™ is developed specifically to deliver unprecedented sensitivity, separation power and annotation confidence for lipids and small molecules. This is made possible using the Mobility Range Enhanced 4D-Metabolomics (MoRE) workflow.

	timsUltra AIP	timsTOF HT	timsMetabo	timsTOF Pro 2
resolution:	60,000			
acquisition rate:	up to 300 Hz in dda-PASEF			up to 120 Hz in dda-PASEF
PASEF methods:	dda-PASEF, dia-PASEF, diagonal-PASEF (midia, synchro), prm-PASEF			
instrument specific methods:	-	-	Mobility Range Enhanced 4D-Metabolomics (MoRE)	-
source:	ESI, CaptiveSpray Ultra 2, VIP-HESI, GC-APCI	ESI, CaptiveSpray 2, VIP-HESI, GC-APCI	ESI, CaptiveSpray 2, VIP-HESI, GC-APCI, DART	ESI, CaptiveSpray 2, VIP-HESI, GC-APCI, DART
size [mm]:	1274 x 789 x 1997	980 x 1400 x 2752	1274 x 789 x 1997	980 x 1400 x 2752

timsTOF fleX Series

The timsTOF fleX combines trapped ion mobility with Bruker's powerful MALDI technology, adding a high resolution spatial dimension and enabling SpatialOMx® as an essential innovation for molecular imaging on one platform. The timsTOF MALDI PharmaPulse® (MPP) adds a label-free high throughput solution (HTS) with extreme speed and robustness to the timsTOF fleX portfolio. The options MALDI-2 and microGRID provide unprecedented sensitivity and high spatial resolution for imaging experiments down to cell size resolution in SpatialOMx® workflows.



	timsTOF fleX	timsTOF MALDI Pharma Pulse®
resolution:	60,000	
acquisition rate:	up to 300 Hz in dda-PASEF	
PASEF methods:	dda-PASEF, dia-PASEF, diagonal-PASEF (midia, synchro), prm-PASEF, iprm-PASEF	
source / laser:	ESI, CaptiveSpray 2, VIP-HESI, GC-APCI; MALDI (smartbeam 3D), MALDI-2 (MALDI-2 laser)	
size [mm]:	825 x 1920 x 750	
optional:	microGRID, MALDI-2	

timsTOF fleX Solutions

MALDI-2 Technology — Bringing enhanced depth and sensitivity
The MALDI-2 post-ionization boosts sensitivity by up to 2-3 orders of magnitude compared to traditional MALDI, depending on sample, matrix and analyte. This technique enables access to a wider range of chemical classes by reducing ion suppression effects. MALDI-2 is fully integrated in Bruker's software solutions and switching between ESI, MALDI and MALDI-2 is only one click away.

microGRID — A powerful MALDI stage technology for accurate and robust high resolution imaging
Bruker's microGRID technology combines MALDI stage and smartbeam 3D laser beam positioning to facilitate high quality imaging down to 5 µm spatial resolution during SpatialOMx® imaging. microGRID eliminates data striping, fading or oversampling effects in high resolution imaging data. The technology seamlessly integrates in Bruker's fully automated SCiLS autopilot workflow, making it attractive not only for experts but also for novelists as well as routine applications.

MALDI Sample Preparation Solution

superlimator — Automated, high-resolution sample preparation
Sample preparation is critical to MALDI Imaging success. The superlimator automates matrix sublimation using validated protocols, ensuring uniform coatings within 5-10 min. Its solvent-free approach prevents analyte delocalization, preserving spatial integrity for small molecules, while optional recrystallization enhances sensitivity. Designed for IntelliSlides®, it integrates seamlessly into the SCiLS™ autopilot workflow without method development. Cross-site studies demonstrate robust reproducibility, with matrix transfer efficiencies of 70-90% (DHAP, DHB, CHCA) and <5% standard deviation. Superlimator is independent of instrument, operator, or location.

MALDI-TOF and TOF/TOF Mass Spectrometry

Bruker's flagship FLEX series is the global leader for MALDI applications

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.

neofleX series

Discover the neofleX™ MALDI-TOF/TOF, a high-performance benchtop mass spectrometer designed for speed and flexibility. With smartbeam 3D laser, it supports multiomics, offering robust imaging and analysis.

rapifleX series

The rapifleX® MALDI-TOF/TOF system features a 10 kHz smartbeam 3D laser, adaptable ion optics, and advanced informatics for high-throughput screening and detailed protein characterization.

smartfleX

The smartfleX MALDI-TOF system offers seamless polarity switching, smartbeam laser tech, and IR laser-based source cleaning for minimal downtime, providing access to the full MALDI analyte space.

	neofleX [TOF and TOF/TOF]	rapifleX [TOF and TOF/TOF]	smartfleX
resolution:	30,000	43,000	2,000
mass range:	up to 500,000 m/z	up to 500,000	up to 500,000 m/z
mass accuracy:	1.5 (int. calib.) [ppm]	1 (int. calib.) [ppm]	≤ 150 (int. calib.) [ppm]
laser:	smartbeam™ 3D	smartbeam™ 3D	smartbeam™
laser frequency [Hz]:	10,000 (MS) / 5,000 (TOF/TOF)	10,000 (MS) / 10.000 (TOF/TOF)	200
size [mm]:	1570 × 710 × 730 mm	950 x 800 x 2750	500 × 710 × 1070 mm
optional:	-	autoloader	-
Fields of Application:	Imaging, Pharma QC workflows	Imaging, Pharma QC workflows, UHT screening	Intact protein verification, Profiling, QC

MALDI Solutions

rapifleX MALDI PhamaPulse

The rapifleX MALDI PharmaPulse (MPP) enhances label-free HTS, combining the mass detection of enzymes, substrates and products with the required speed to comb through compound libraries containing millions of substances. The use of mass spectrometry allows the measurement of unmodified substrates in primary screens, greatly reducing false positive rates, and minimizes compounds sent to confirmation screens. The system is designed for automatic handling of 1536 well sample plates to screen more than a million compounds in a week in support of drug discovery.

microflex

The microflex® LRF MALDI-TOF MS offers 15k resolution, PAN pulsed ion extraction, and a gridless reflector for unmatched sensitivity. Ideal for QC, biomarker discovery, and analysis across various applications.

autoflex maX series

The autoflex® maX MALDI-TOF MS features a 2 kHz smartbeam-II laser, enhanced dynamic range, and intuitive Compass software for rapid, high-quality data across diverse application fields.

	microflex LRF	autoflex maX [LIN, LRF and TOF/TOF]
resolution:	15,000	26,000
mass range:	up to 300,000	up to 500,000
mass accuracy:	15 (int. calib.) [ppm]	2 (int. calib.) [ppm]
laser:	Nitrogen	smartbeam II
laser frequency [Hz]:	60 (MS)	2,000 (MS) / 200 (TOF/TOF)
size [mm]:	530 x 680 x 1350	825 x 1920 x 750
optional:	-	-
Fields of Application:	Peptide & Protein QC Applications	Imaging, intact biomolecules

Magnetic Resonance Mass Spectrometry

Untangle complexity: Discern and identify with confidence

The analytical fields of MALDI Imaging, intact biomolecules, metabolomics as well as analysis of biofuels, petroleum, and battery materials for energy research, share the requirement for confident compound identification.
Magnetic Resonance Mass Spectrometry (MRMS) is ideally suited to tackle such challenging applications as it provides unrivaled mass accuracy and mass resolving power in the m/z domain.
This is facilitated for timsMRMS by TIMS (Trapped Ion Mobility Spectrometry) which employs gas-phase fractionation, based on ion mobility, prior to MRMS detection. The combination of TIMS and MRMS delivers unmatched depth and accuracy for complex chemical mixture analysis.

timsMRMS

timsMRMS is the next generation MRMS that combines the added specificity and selectivity of TIMS with the unparalleled eXtreme Resolution and mass accuracy of MRMS for ultimate depth of analysis. Versatility powered by a broad choice of ion sources, fragmentation options for flexible experiment design, automatic detector optimization & Maxwell magnet technology making the timsMRMS approachable and powerful.

scimaX® MRMS

Maxwell magnet technology is the basis of the smaller footprint scimaX MRMS system and removes the requirement of liquid cryogen fills or quench ducts. The instrument comes standard with 2xR and Absorption Mode Processing (AMP) technology which means you have performance rivaling high field MRMS at your fingertips.

solariX MRMS

This legacy platform for also high-field MRMS work (12T and 15T) is useful for ultra-complex mixture analysis requiring larger field strengths, such as analysis of intact biomolecules. These instruments feature long liquid cryogen (LHe) hold time with 1 year fill intervals as regular maintenance.

	7T timsMRMS	scimaX	solariX
maximum resolution:	> 20,000,000	> 20,000,000	> 10,000,000
mass accuracy (internal):	600 ppb[1]	600 ppb	600 ppb[1,2]
Magnet system	7T Maxwell[3]	7T Maxwell	7T US/R[4]
2xR detection	Yes	Yes	Optional
API source	ESI, optional APPI, APCI	ESI, optional APPI, APCI	ESI, optional APPI, APCI
MALDI	Smartbeam 3D & microGRID[5]	Smartbeam II	Smartbeam II

[1] Further improved mass accuracy can be achieved with optional high field magnets
[2] With 2xR detection option
[3] High field magnets are optionally available on request: 12T US/R, 15T US/R, 18T USR
[4] Optional high field magnets available: 12T US/R, 15T US/R
[5] 10 µm imaging

MALDI Consumables

Imaging workflows made easy

Bruker's MALDI consumables take analysis capabilities to the next level by simplifying lab workflows and ensuring highest preparation quality. Complementary consumables and accesoires streamline sample preparation and increase productivity during your daily lab routine. Exceptional purity of our products removes potential sources of contamination and improves uptime of your instruments.

IntelliSlides® – Maximize information content per pixel with intelligence

Bruker's IntelliSlides® are the perfect tool for SpatialOMx®. They simplify your MALDI Imaging workflows by enabling automated setup of each measurement. IntelliSlides incorporate permanent inscriptions on the conductive slide surface that indicates optimal placement of samples and pre-inscribed fiducials (teach marks) for Imaging. Additional unique serial numbers and barcodes fully automate sample registration and software tracking. Automated image acquisition is available on Bruker's timsTOF fleX and rapifleX instruments with the SCiLS autopilot included in flexImaging 6.0 and above.

fleXmatrix® – The key to success in MALDI MS analyses

fleXmatrix® kits enable easy and convenient preparation of matrix solutions for MALDI Imaging. Pre-portioned and packaged in convenient tubes, fleXmatrix® is stable and easy to handle to simplify sample preparation, particularly for standard spraying or sublimation methods. Different fleXmatrix® kits are dedicated to the imaging of proteins, peptides, and lipids, and a specialized matrix for MALDI-2 post-ionization analysis. fleXmatrix® is perfectly suited for the use with Bruker's IntelliSlides® and can be measured on all Bruker MALDI mass spectrometry imaging platforms.

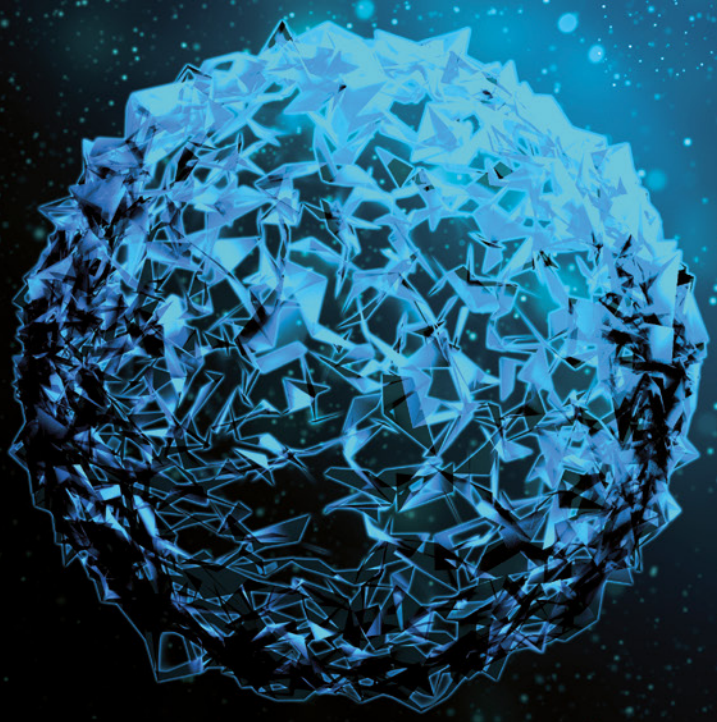
MALDI PharmaPulse® HTS accessories – A complete HTS solution

Brukers MALDI PharmaPulse® HTS accessories are an integrated solution specifically developed to improve the effiency of your HTS and uHTS daily lab workflows. The disposible Plain HTS MALDI Plates 1.0 mm are designed for automated MALDI preparations by high-performance liquid handlers in any format ranging from 96 to 1536 and beyond. These plates fit perfectly in Brukers lightweight HTS MALDI Plate Adapter 1.0 mm which is specifically designed for safe and efficient sample handling by lab robotics.

High Resolution QTOF Mass Spectrometry

Outstanding accurate mass capabilities

Obtaining the most complete and true picture of a sample set is a consistent goal. Complex sample matrices demand ever higher levels of sensitivity and speed to truly advance scientific knowledge. However, there are everyday practical realities that are required to be routinely overcome. The outstanding dynamic range, high mass accuracy, and MS/MS performance enable Bruker's high resolution QTOF MS systems to deliver confident, reliable results for both targeted analytical testing and broader discovery research applications.

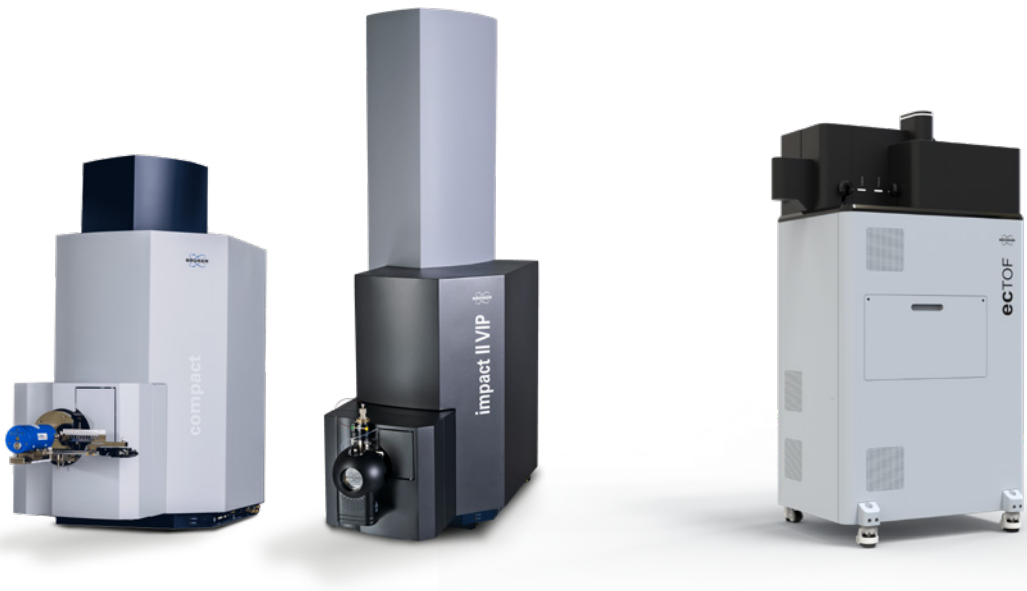


QTOF

Our QTOF mass spectrometers are the showcase instrument platform for life science research, drug discovery, and screening applications involving the analysis of both targeted and unknown compounds in complex matrices. The systems provide cutting edge performance in one-shot analysis for identification and quantitation from small molecules up to intact proteins, and the dynamic source configuration offers significant analytical versatility.

ecTOF

The ecTOF is the world's first GC-HRMS system capable of simultaneously acquiring EI (Electron Ionization) and CI (Chemical Ionization) data in a single injection. While EI remains the gold standard for GC/MS ionization, the ecTOF uniquely incorporates a parallel CI source. This innovation enables the instrument to deliver precisely aligned structural information from EI alongside accurate molecular ion data from CI – all within one GC run.



	compact	impact II VIP
resolution:	30,000	60,000
scan speed:	1-50 Hz (MS & MS/MS)	1-60 Hz (MS & MS/MS)
fragmentation:	CID	CID
source:	VIP-HESI, ESI, DART, APCI II, APPI II, Captive Spray II, GC-APCI, Direct Probe	
size [mm]:	624 x 510 x 1240	1200 x 800 x 1980

	ecTOF
resolution:	10,000 (CI), 8,000 (EI)
scan speed:	/
fragmentation:	/
source:	HRP (medium pressure, plasma based CI)/ Starbeam (EI)
size [mm]:	736 x 960 x 1661

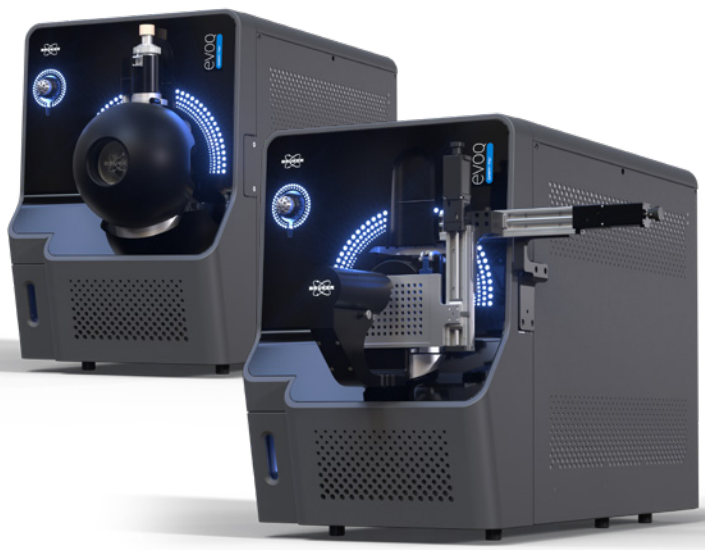
Triple Quadrupole Mass Spectrometry Systems

Bruker's EVOQ® TQ systems set a new standard of performance

Triple quadrupole MS systems are the backbone of many routine analytical and contract research laboratories. Successful, sensitive screening and quantitation for diverse compounds across a broad range of applications, including the screening of foodstuffs, environmental hazards, and forensic toxicology studies, require high performance instrumentation. Bruker's EVOQ TQ systems are designed and built to provide reliable, versatile, easy-to-use power on any laboratory benchtop. And now with chromatography-free workflows using Direct Analysis in Real Time (DART), sample analysis is easier, faster, more cost effective, and greener than traditional triple quadrupole LCMS.

EVOQ DART-TQ+ Triple Quadrupole Mass Spectrometry

EVOQ DART-TQ+ MS systems provide analysts with an MS platform designed for a singular purpose – to reliably quantify thousands of target analytes from real samples in the fastest sample-to-report time possible. These systems deliver exceptional sensitivity, precision, accuracy, and linearity over a wide dynamic range for your multiple reaction monitoring (MRM) assays. Innovations in software and atmospheric pressure ionization (API) technology make it a game changer for routine high-sensitivity, quantitative analysis. At Bruker today, we are leading the migration of technology from research to commercial laboratories. The EVOQ DART-TQ+ systems reflect this design philosophy and solve the hardware and software challenges faced by the quantitative analysis community.



EVOQ DART-TQ+	
mass range:	10-1,250
size [mm]:	580 x 400 x 860 DART plus motor rail: 580 x 610 x 980
sources:	VIP-HESI, APCI, integrated DART
MRM per second:	1,000
scan rate:	Up to 30,000 Da/sec

EVOQ Gas Chromatography – Triple Quadrupole Mass Spectrometry

EVOQ GC-TQ Speed MS systems set a new industry standard for GC-MS/MS performance and productivity. With their unique 'lens free' elliptical ion path design and novel high-speed electronics, the EVOQ GC-TQ Speed systems deliver incredible sensitivity and high stability along with reduced chemical noise and unprecedented speed. This analytical power is simple to use and comes complete in a spacesaving package that makes upgrading to new levels of robust and reliable performance straightforward and cost-effective.

EVOQ GC-TQ SPEED	
mass range:	10-1,200
size [mm]:	450 x 280 x 570
MRM per second:	1,000
scan rate:	Up to 30,000 Da/sec

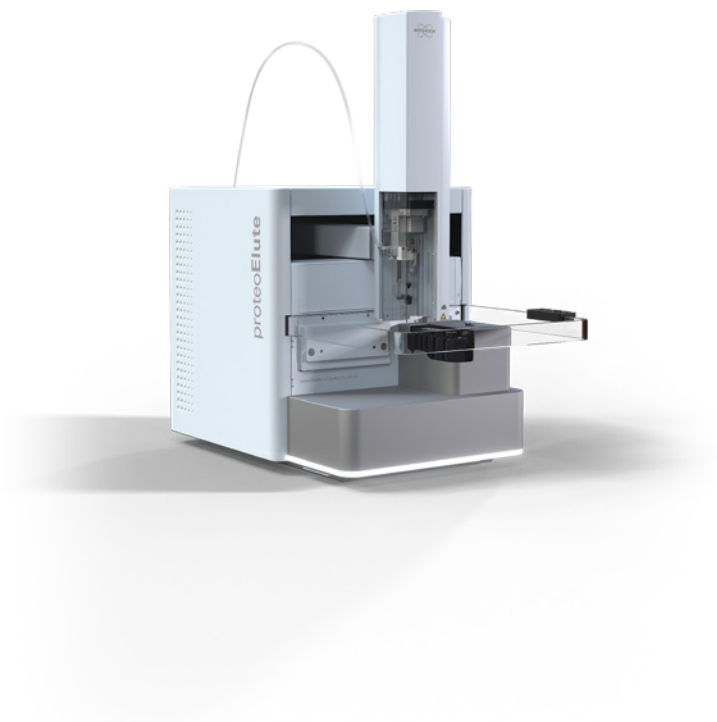
Liquid Chromatography

Access to the widest variety of HPLC systems

Chromatographic separation is critical in many sample analysis workflows, and its value, analytical depth, and versatility are amplified dramatically when coupled to MS systems. Bruker's Compass HyStar is a state-of-the-art software solution for configuring and controlling hardware for these hyphenated techniques. Compatible with HPLC systems from many vendors, HyStar fully integrates LC-MS data collection. Subsequent data processing and report generation can be specific to a given workflow, including necessary quantitation, target identification, and screening tasks.

ProteoElute – Designed to deliver piece of mind

The proteoElute optimizes nanoflow workflows for high throughput and ultra-sensitive multiomics experiments. With innovative TwinScape technology continuously monitoring key instrument parameters in real-time, the proteoElute™ is designed to deliver peace of mind when analyzing precious samples. It integrates seamlessly with your TIMS-enabled mass spectrometers, optimizing nanoflow workflows for high throughput and ultra-sensitive multiomics experiments. The system's robustness is achieved through biocompatible ceramic valve technology and strategically integrated porous metal filters across the pressurized solvent lines. The environmentally friendly design helps minimize hazardous waste, making it ideal for sustainable research practices.



	ProteoElute
flow range:	50 - 3,000 nL
pressure limit:	1,000 bar
connections:	UHPLC finger-tight connections; reusable torque limiting bottom sealing capillaries
size [mm]:	830 × 460 × 900
additional information:	Trouble-free operation, ease-of-use along with top performance
gradient delay volume	< 0.4 µL
Fields of Application	single cell to high throughput routine proteomics

Elute⁺ LC Series – Simply more for your MS analysis

Elute⁺ LC systems are built around binary gradient UHPLC pump with intelligent flow control algorithms to deliver robust and precise gradients regardless of solvent compressibility, pressure, and flow rates. Elute binary pump module incorporates self priming and self purging capabilities through the built in pump, offering a simple and fast exchange of mobile phases and avoiding any leaks associated with manual operations. Additionally, the selection of the LC autosampler, column oven and PFAS-free options across the Elute⁺ LC portfolio allows to choose the optimal solution for various applications and use scenarios.

The new Elute⁺ SL UHPLC System ensures exceptional injection accuracy and reproducibility, along with the ability to inject down to the last few microliters of precious sample in the most demanding analytical workflows. The system's horizontal column oven supports multi-column configurations while maintaining the smallest LC stack footprints in the industry.

For the laboratories demanding maximal throughput and sample capacity Elute⁺ HT System with industry-standard PAL RSI autosampler offers a fully flexible and scalable solution addressing the most challenging high throughput LC MS workflows, including large volume injections, fast cycle times, and possible integration of additional sample preparation steps - allowing laboratories to scale from routine high throughput screening to fully automated, unattended LC MS operations.

Elute⁺ LC Series

	SL	HT
flow range:	1 - 5,000 µL	1 - 5,000 µL
pressure limit:	1,300 bar	1,300 bar
sample capacity:	Up to 132 x 2 mL vials or 2 well plats	From 324 x 2 mL vials or 6 well plates
size [mm]:	715 × 330 × 545	550 × 1,180 × 500
additional information:	Fast and high resolution separations combined with ultimate precision and space saving footprint	UHPLC combined with PAL autosampler for high sample throughput and complex workflows

PepSep Consumables

More samples. Less time. Better reproducibility

Achieve precise separation of peptides and proteins with our cutting-edge reversed-phase HPLC columns. Experience deeper sequence coverage, higher sample throughput, and robustness, meeting the demands of even the most challenging samples. Tested at ultra fast PASEF® speeds, PepSep columns are robust, easy to use, and provide consistent results making it the perfect choice for your proteomics applications.

What we offer:

- **PepSep Advanced**
  Advanced columns delivering superior sensitivity and resolution for cutting-edge proteomics.
- **PepSep Classics**
  Reliable and versatile columns designed for routine proteomic analyses.
- **PepSep Emitter**
  Ready to use fused silica emitter.
  Simple plug and play design.

	Columns		Emitters
	PepSep Classics	**PepSep Advanced**	**CaptiveSpray 2 Emitter**
Size	Various dimensions	25 cm x 75 µm x 1.5 µm	10 µm or 20 µm
Features	Combines speed, durability, and versatility for all proteomics workflows - featuring a cost-effective design with separated emitters to maximize productivity and performance.	Delivers high-sensitivity protein and peptide analysis with minimal clogging and back pressure - engineered for performance and reliability as a smart alternative to traditional pulled-tip columns.	Save time with pre-assembled static tips and ZDV union - ready to use out of the box and fully compatible with all CaptiveSpray sources. Sold as a pack of two.

BeatBox® – Cell Lysis and Tissue Homogenization Simplified

For cells and tissue an efficient homogenization is a crucial part of sample preparation. Reproducibility, cross-contamination and scalability, but also usability and space requirements are challenges to be faced.
Enter the BeatBox by PreOmics. A fast and easy to use instrument for up to 96 samples, which completes the homogenization in as little as 10 minutes without sample cross contamination and minimal heat induction. BeatBox has a surprisingly small footprint and quiet operation in comparison to traditional tissue processing. With the BeatBox, tissue homogenization (fresh, frozen & FFPE) and cell lysis be integrated into the PreOmics® iST sample prep workflows.

- Unique GYUTO bead technology for best homogenization results and reproducibility
- Seamlessly compatible with iST workflows for even greater efficiency
- Fast and easy to use: Maximum protein release in 10 minutes by the push of a button
- Versatile: Compatible with multiple tissue (1-50 mg) and cell (up to 10^7) types; compatible with FFPE samples
- Safe: Minimized heat induction and no cross contamination
- Flexible throughput and parallelization: 96 well or 24 single tube formats

BeatBox consumables –
kits for cell and tissue homogenization

	BeatBox Tissue Kit 24x	BeatBox Tissue Kit 96x
P.O.	00128	00121
Size	24-sample kit	96-sample kit
Features	Homogenization of up to 24 samples with 5-50 mg	Homogenization of up to 96 samples with 1 - 5 mg

BeatBox accessories –
tools for better workflow compatibility

BeatBox Bead Remover	BeatBox Bead Remover Foils
00001	00027
	10 pieces
Removal of GYUTO beads from the BeatBox Tissue Kit 96x	Separation foils for BeatBox bead remover

Ion Sources

Dynamic source configuration

Bruker's LC-MS systems support a wide range of source options from both Bruker and from third-party vendors.

Source Type		Description
	NEOS-source	The NEOS-Source is Bruker's advanced offline nanoESI solution, optimized for top-down proteomics and structural biology. It supports a wide range of emitter types and integrates dual cameras for precise, stable spray control. Designed for compatibility with timsOmni systems, it delivers high sensitivity and reproducibility in demanding workflows.
	CaptiveSpray Ultra 2	The CaptiveSpray Ultra 2 combines nano-flow sensitivity with ease of use, thanks to its "on-off" design and zero-adjustment positioning. It ensures the highest signal-to-noise ratio and clearer data for advanced proteomics research. Optimized for the timsTOF Ultra 2.
	CaptiveSpray 2	The next generation of the CaptiveSpray ion source builds on the exceptional nano-flow performance of its predecessor while introducing unparalleled ease of use into proteomics workflows.
	VIP-HESI dual source	This VIP-HESI source is compatible with Bruker's timsTOF and QTOF systems and generates a higher sensitivity for a broad range of components. The vacuum insulated probe enhances ionization efficiency whilst minimizing thermal degradation of analytes. Matrix is rapidly and efficiently removed from the source via an active exhaust maximizing system robustness.
	APCI	Atmospheric Pressure Chemical Ionization is used in metabolomics, as well as for drug or pesticide screening for less polar molecules where ESI fails to deliver reasonable quantities of ions.

Source Type		Description
	APPI	Atmospheric Pressure Photo Ionization is used for less polar or non-polar molecules that cannot be ionized by ESI or APCI.
	DIP	The DirectProbe add-on for the Bruker APCI II and APPI II ion sources allows for direct analysis of liquid and solid samples without tedious sample preparation.
	GC-APCI II	The GC-APCI II source with a unique flexible heated transfer line and calibrant delivery enables GC coupling to any Bruker TOF, QTOF, or MRMS system originally designed for LC coupling.
	DART source	The Direct Analysis in Real Time (DART) source is a rapid and efficient ionization for mass spectrometry for measuring a wide range of analytes - solids, liquid and gases - in their native form, including many that don't ionize well with other methods. Add it to an existing mass spectrometry system to ramp up versatility and throughput or invest in a fully integrated DART-MS solution.

Power Up Your Skills and Share Your Knowledge

Trainings on Bruker instrumentation, software packages and solutions are provided by very experienced application experts. Various courses are available covering the range from absolute beginners to experienced users.

- Training
- Improvement
- Practice
- Focus
- Intelligence
- Lesson
- Motivation
- Success

General remarks and information for training courses

Registration
For registration, please access the online registration at www.bruker.com or contact hb@bruker.com.

Registration
After submission of your registration, you will get a summary of the submitted information automatically. This is not a confirmation. The registrations will be taken into consideration on a first come, first served basis.

Confirmation
After receiving your registration, we will confirm your participation. If the selected training course is already fully booked, we will inform you immediately.

Training costs
Training costs include the course fees as well as lunch and beverages during the training. Travel and accommodation are excluded. Please contact your local Bruker Training Center to get a list of recommended hotels located nearby.

Course language
All courses will be held in English unless otherwise agreed with the customer.

Cancellation
Bruker Daltonics GmbH & Co. KG reserves the right to cancel the training if the minimum number of participants is not achieved one month prior to the training date. Customers may cancel in writing not later than one month prior to the training date at a full refund of the training price. If customers cancel later than two weeks before the training, the full training fee will be charged. Customers may substitute a participant without extra charge or payment in this case. Bruker needs to be informed to register the new participant beforehand.

Training material
Training material will be provided by the trainer. Any recordings of training or parts of training are prohibited. Bruker general terms and conditions of supply and service apply.

Learn more and visit:
https://www.bruker.com/de/services/training/mass-spectrometry.html

Service Agreements

Choose one of the following LabScape Maintenance Service Agreements available for selected MS, LC, GC, and SPR instruments:

LabScape Connect – Affordable remote service model. A basic package with unlimited remote access with experienced factory-trained service engineers.

LabScape Essential – Ensure peak performance. A combination of remote support and regular annual maintenance helps you operate your instrument under its optimal conditions.

LabScape Access – A cost-effective solution for unforeseen instrument breakdowns in low throughput laboratories with unlimited on-site repair visits including spare parts.

LabScape Complete – All support you need. A comprehensive solution providing complete service coverage including spare and wear and tear parts which helps you avoid instrument failures, costly repairs and down time.

LabScape Complete 48 – All the support you need within 48 hours. A VIP package including guaranteed on-site response within 2 business days to resolve the problem before it affects your business.

	LabScape Connect	LabScape Essential	LabScape Access	LabScape Complete	LabScape Complete 48
Remote Services					
Remote Monitoring*	✓	✓	✓	✓	✓
Unlimited Priority Remote Support	✓	✓	✓	✓	✓
Software services					
Compass & Data Analysis SW Upgrades	✓	✓	✓	✓	✓
Postprocessing SW Licenses & Upgrades**		discount	discount	premium discount	premium discount
Upgrade of Postprocessing Software**				1 Voucher p.a	1 Voucher p.a
Regular Maintenance					
Regular Maintenance Work and Parts		✓	✓	✓	✓
On-site Repair Services and Parts					
Unlimited Repair Visits incl. Spare Parts			✓	✓	✓
Wear and Tear Part Replacement	discount	discount	discount	✓	✓
Loaner Equipment*					✓
Compliance Services					
Operational Qualification / Perform. Validation					included
On-site Response Service Level					
On-site Response			3-5 business days	3-5 business days	2nd business day
Additional benefits					
Consumable Parts	discount	discount	discount	premium discount	premium discount
Operation Training or Applications Training	discount	discount	discount	premium discount	premium discount

* if applicable to the respective MS or Biosensors Products
** SCiLS Pro, MetaboScape, TASQ, Biopharma Compass

Software Solutions

Compass and bioinformatics

Bruker Daltonics software solutions provide maximum information via streamlined, easy to use processes

BioPharma Compass® Field of Application: BioPharma	BioPharma Compass provides integrated workflows for biopharmaceutical industry supporting 21 CFR Part 11 requirements. Workflows comprise all aspects from data acquisition to report generation, characterization and comparative quantitative assessments in multiple attribute monitoring (MAM) analyses. MAM peptide analysis as well as host cell protein (HCP) analyses can benefit from the use of CCS-enabled data analysis in terms of sequence coverage and dynamic range. Multi-Target-Screening workflows enable batchwise processing multiple samples. OligoQuest™ enables oligonucleotide sequence analysis using LC-UV-MS/MS including side product quantitation and identification or targeted analysis.
OmniScape™ Field of Application: Top-Down protein sequencing	OmniScape™ offers unparalleled access to Top-Down mass spectrometry data of proteins. The OmniWave™ algorithm excels at detecting even low-abundance, highly charged fragment ion isotope patterns, seamlessly integrating them into further analysis workflows. Unknown proteins can be de novo sequenced and identified through homology-based database searches. Protein sequences, including their various proteoforms, can be confirmed and screened for PTMs. All results are validated peak by peak within an intuitive software interface. Multiple datasets from different experimental conditions can be combined to achieve significantly larger sequence coverage and higher certainty in proteoform assessment. OmniScape™ supports data import from all Bruker instruments and third-party instruments via a generic profile data text format. The software is user-friendly and quick to learn, with algorithms that handle complex computational challenges at high speed.
Bruker ProteoScape™ Field of Application: Proteomics	Run & Done with Bruker ProteoScape! A hardware and software solution, enabling integrated real-time CCS-enabled analysis of dda-PASEF, dia-PASEF and diagonal-PASEF data. Bruker ProteoScape (BPS) removes the data analysis bottleneck introduced by large sample cohorts allowing for greater throughput and more identifications seconds after a measurement is complete. BPS is smart, allowing for user-defined qualifications/parameters to seamlessly guide the progression of your sample queue, while checking suitability and saving precious samples, expensive consumables, and instrument time. Utilizing workflows integrated with powerful algorithms such as TIMSrescore, TIMS DIA-NN, Spectronaut and BPS Novor, Bruker ProteoScape streamlines your labs analysis pipeline from data to results as quickly as possible.

TwinScape

Field of Application:
Proteomics,
Metabolomics

TwinScape™ is a cutting-edge software solution designed for proteomics and metabolomics laboratories utilizing hyphenated liquid chromatography-mass spectrometry (LC-MS). Its key functionality lies in continuously monitoring instrument performance, leveraging advanced AI algorithms to identify and notify users of any deviations in readback values or quality control (QC) outcomes. This ensures the highest levels of precision and reliability throughout the data analysis process.
As a central platform for quality control data, TwinScape seamlessly integrates with the Biognosys iRT™ kit and Bruker ProteoScape™ software as well as Bruker QSee™ quality control (QC) , providing streamlined data management. Its seamless remote monitoring capabilities, along with longitudinal data tracking, enable researchers to detect trends early and ensure the ongoing health of their instruments, greatly simplifying the management of data quality. By guaranteeing accuracy, reproducibility, and operational efficiency, TwinScape plays a vital role in improving research outcomes, making it an indispensable asset for today's proteomics and metabolomics laboratories.

Spectronaut®

Field of Application:
Proteomics

Spectronaut® is Biognosys' flagship data analysis software for data-independent acquisition (DIA) mass spectrometry (MS) based proteomics.
The software employs advanced search with Pulsar and Kuiper search engines, and artificial intelligence (AI) algorithms to translate data into actionable insights for life science research. Spectronaut enables reproducible and precise quantification of thousands of proteins in a single experiment and provides multi-dimensional insights into protein expression, function, and structure across all major biological species and sample types.
The software fully supports library free analysis with a proprietary workflow directDIA®
With scalable, high-performance computing or cloud environment deployment, Spectronaut enables high-speed, high-throughput parallelized DIA data analysis, eliminating data processing bottlenecks.

SpectroMine™

Field of Application:
Proteomics

SpectroMine™ is Biognosys' data analysis software for data-dependent acquisition (DDA) mass spectrometry (MS) based proteomics.
The software powered by the Pulsar and Kuiper search engines offers fast and comprehensive proteomics and peptidomics workflows.
SpectroMine's intuitive interface and automated workflows streamline DDA proteomics analysis of label-free, isobarically- and isotopically-labelled approaches with minimal set up. The software enables classical FASTA based spectrum centric analysis but also DDA library based, peptide centric analysis, which benefits low input workflows.

SpectroDive™

Field of Application:
Targeted Proteomics

SpectroDive™ is Biognosys' software providing a fast, robust, and seamless targeted proteomics solution for an effortless experience and maximum productivity.
The software provides complete and seamless support for a multitude of targeted workflows, from calibration curves generation to absolute quantification with broad reporting and deep visualizations.
With SpectroDive, custom panels can easily be generated from spectral libraries, FASTA files or peptide sequences. Powerful automatic peak picking algorithms allow for the streamlined parallel quantification of hundreds of proteins across large datasets with automatic FDR control.

BRUKER MetaboScape®	**MetaboScape®** Field of Application: Metabolomics and Lipidomics	MetaboScape is the software for 4D-Metabolomics™ and 4D-Lipidomics™ to pinpoint and identify compounds that change because of perturbation or disease. T-ReX® 4D processing unlocks CCS values as additional criterion for the Annotation Quality Scoring (exact mass, retention time, isotopic pattern, MS/MS spectrum, CCS). MetaboScape supports spectral libraries like MetaboBASE®, HMDB, MetaboBASE Plant, as well as custom libraries, *in-silico* fragmentation and CCS-Predict Pro. A range of interactive tools for quality control, and data exploration help to bring analysis results into biological context. Using its REST-API, MetaboScape and many of its functions can also be integrated into custom bioinformatics pipelines.
BRUKER TASQ®	**TASQ®** Field of Application: Screening and Quantitation	TASQ (Target Analysis for Screening and Quantitation) is Bruker's solution for screening, confirmation and quantitation of large sample batches, including hundreds of compounds per analysis. The CCS-enabled TASQ solution allows exploiting the ion mobility separation on timsTOF instruments for further confidence. TASQ takes advantage of both nominal and high resolution, accurate-mass data generated by Bruker's triple quadrupole and QTOF mass spectrometers. Multiple quantitation modes are supported including in-batch quantitation, usage of calibration functions from previous batches, surrogate quantitation and standard addition procedure. Additionally UV-VIS and GC data can be used for quantiation. TargetScreener HR – driven by TASQ – allows report generation from 'vial to report' in seven clicks. TASQ includes support of Audit Trail, User Action Rights and User Access Control.
SCiLS	**SCiLS™ Lab** Field of Application: Imaging	SCiLS Lab is the worldwide leading software for analysis of mass spectrometry imaging data from all major MS vendors, including Bruker's FLEX series and MRMS, as well as data in the open imzML format. For timsTOF fleX ion mobility data, SCiLS Lab displays and analyzes mass-mobility ion images allowing CCS-enabled data interpretation. Comparative analysis of multiple samples can be visualized in both 2D and 3D, enabling a multitude of applications in pharmaceutical drug development, tissue-resolved biomarker discovery, and translational pathology research. SCiLS Lab supports intuitive workflows for quantitation of target molecules directly from tissue and for interpreting MS/MS imaging data generated using iprm-PASEF. It integrates with MetaboScape for confident molecular annotations and enables easy integration of MALDI Imaging-based spatial multiomics data. For integration with histology, it provides an interface to the powerful open-source software QuPath widely used in digital pathology. The SCiLS Lab application programming interface (API) lets you directly interact with your data in Python or R and use your own code to perform custom processing and reporting or to create unique visualizations based on your SCiLS Lab data.

SCiLS	**SCiLS™ Scope** Field of Application: Imaging	SCiLS™ Scope lowers the barriers for sharing and viewing MALDI HiPLEX-IHC and MALDI Imaging data. With the easy-to-use, lightweight interface and data in the open OME-TIFF format, it is ideal for sharing data between collaborators who want to focus on examining images. Intuitive review of images within a pathological context provides more insight per pixel.
BRUKER MALDI PharmaPulse®	**MALDI PharmaPulse®** Field of Application: High-Throughput Screening (HTS)	MALDI PharmaPulse allows data acquisition and analysis of high-throughput screening data acquired on the timsTOF MALDI PharmaPulse (with and without MALDI-2). The Screening software workflow module provides the tools required for seamless setup, execution and result visualization of HTS screens. The Synthesis Screening workflow allows flexible screening of many different target compounds per individual well. Data in timsON and timsOFF, MS and MS/MS and optionally MALDI-2 mode are supported.
BRUKER GlycoScape™	**GlycoScape™** Field of Application: Glyco-proteomics	Run & Done for glycopeptide analysis! GlycoScape is included with the Bruker ProteoScape package and extends the capabilities to include real-time glycopeptide analysis for glycobiologist. Powered by the Myriad workflow which effectively deconvolutes glycopeptide fragmentation spectra into peptide and glycan moiety spectra using common N-glycan fragments. Each moiety is then identified by a specialized real-time algorithm after which the glycopeptide is "reassembled". A significant advantage of the Myriad workflow is that it does not require any glycan database(s), enabling the identification of glycans not in the database(s) and minimizing false negatives.
	Other solutions	Bruker's data formats are open to everyone, including third-party software vendors, and SDKs can be downloaded from our website. This reflects Bruker's commitment to fostering a collaborative and innovative software ecosystem for our mass spectrometry instrumentation. Moreover, Bruker actively supports various commercial partners and academic groups, contributes to open source software projects, promoting a thriving community.

Working Towards a More Sustainable Future

Innovation with Integrity

As a forward-thinking, innovative company, Bruker has a rich legacy of protecting the environment, treating others with dignity and respect, and following the highest standards of ethical compliance and governance. These principles more recently characterized as Environmental, Social, Governance (ESG), have been an integral part of our DNA for over 60 years.

Bruker's innovative technologies and solutions support scientists and businesses around the world to explore, understand, and improve the world in which we live. Our innovative spirit drives solutions intended to address environmental challenges, improve recycling, advance research discovery, identify hazardous and harmful materials in the environment, and keep our foods and environment safe. We are proud to support a more sustainable future.

As a global innovation leader in developing and marketing advanced analytical technologies and solutions, our scientists and engineers support businesses and scientists around the world to better understand environmental hazards, protect our essential food supply, research clean, sustainable energy, and search for new ways to improve the quality of life.

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