



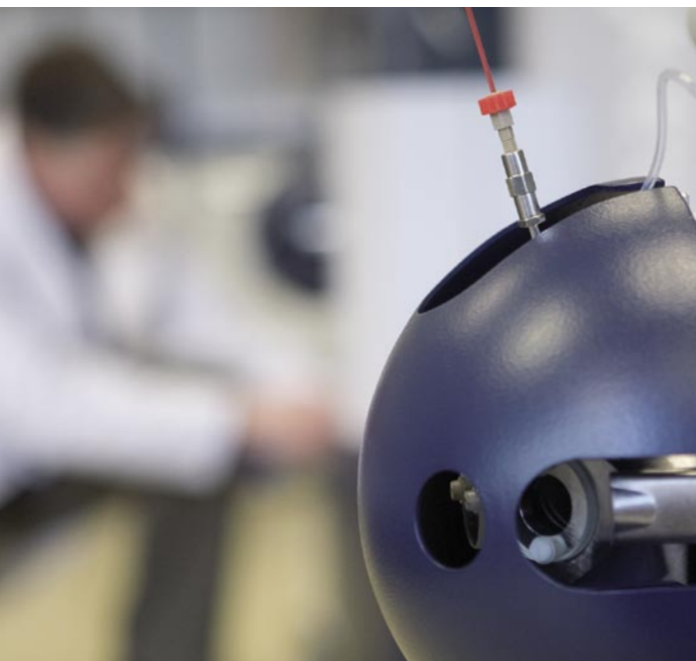
maxis

- Maximum Information@Maximum Speed

think forward

UHR-TOF

Now Highest Performance Mass Spectrometry Matches Ultrafast Chromatography...



maXis is a revolution in high-resolution tandem mass spectrometry offering a no-compromise solution for exceptional accurate mass, high resolution and high sensitivity analysis at a speed able to take full advantage of ultra-high performance chromatography.

The latest development from Bruker, the novel UHR-TOF ultra high resolution technology, again proves Bruker Daltonics leadership in the design of cutting-edge mass spectrometry to meet future requirements in applications like:

- Small molecule identifications
- Metabolomics
- Quantitative proteomics & biomarker discovery

Modern discovery applications demand definitive tandem MS results on ever more complex samples. maXis is the only mass spectrometer able to deliver the maximum MS performance specification at the very highest speeds delivered by modern Ultra Performance Liquid Chromatography and Capillary Electrophoresis.



...we call it maXis, Maximum MS Information at Maximum Speed

Transform your expectations

It's time to embrace a new concept of what is possible with a mass spectrometer. maXis UHR-TOF technology delivers a simultaneous combination of key mass spectrometry performance parameters impossible to obtain with any other technology.

Redefining high performance mass spectrometry

With resolution in excess of 40,000 FWHM and MS and MS/MS mass accuracy typically between 600 – 800 ppb at speeds of up to 20 full spectra per second simultaneously, no other mass spectrometer is better equipped to deliver definitive data on complex samples in proteomics, metabolomics and small molecule identification challenges.

- 20 Hz speed of acquisition at high resolution for high-speed chromatography
- High 40 k resolution in both MS and MS/MS mode
- High dynamic range of 5 orders of magnitude for trace detection in complex mixtures
- Sub-ppm mass accuracy in both MS and MS/MS mode for high confidence IDs
- Uncompromised sensitivity for discovery applications

Unsurpassed capabilities that evolved from Bruker's continuous time-of-flight innovations makes this instrument a revolutionary new mass spectrometer, the maXis UHR-TOF.



Speed, accuracy and sensitivity – fundamental for your applications

- Extract full quantitative information from ultra performance chromatography
- High resolution analysis for the evaluation of complex samples in metabolomics and biomarker discovery
- Selectivity from complex mixtures with high resolution extracted ion chromatograms (hrEICs) for quantitative studies
- Certainty in identification in combination with SmartFormula 3D™ – unequivocal formula generation with superb mass accuracy
- Novel IonCooler™ technology delivering full width MS/MS sensitivity

● Intelligent Small Molecule Analysis – Certainty Delivered by maXis Performance

Speed

The latest ultra high performance chromatography can only be fully utilized by the most agile mass spectrometer. Here, a complete gradient LC separation of typical drug molecules is achieved in under 30 seconds; maxis delivers 10 sub-ppm full-scan result datapoints over LC peaks only one second wide.

Confidence from mass accuracy

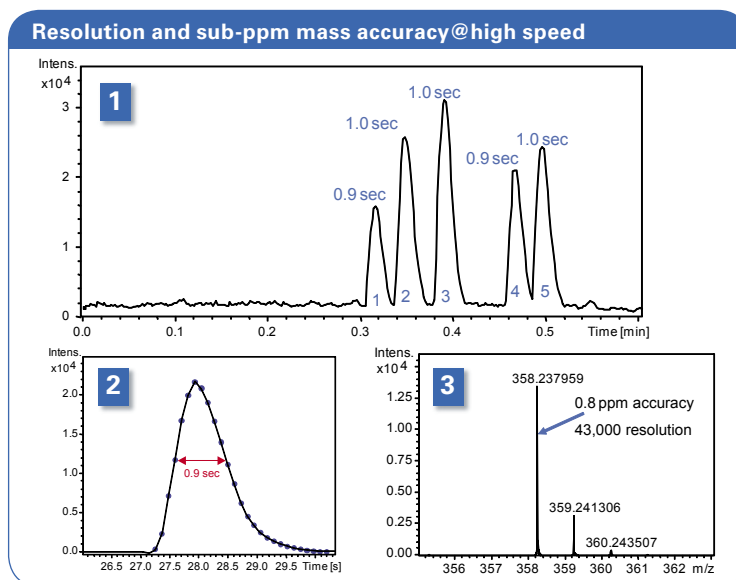
Accuracy of better than 1 ppm allows unequivocal answers in many identification problems.

Certainty from SmartFormula 3D

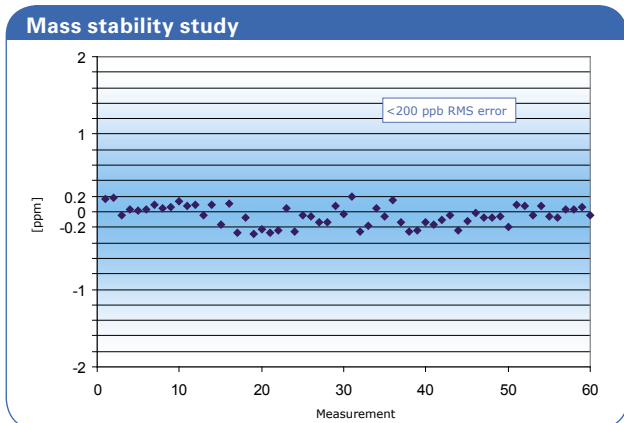
In complex molecular identification challenges such as pharmaceutical impurities, maXis MS/MS data quality in combination with Bruker's unique ab-initio formula discovery tool SmartFormula 3D™ rapidly identifies species using accurate mass and isotopic analysis of MS and MS/MS without assumptions or recourse to libraries.

Absolute stability

In the stability study below, under internal calibration, the maXis is showing an RMS error < 200 ppb over 60 consecutive measurements of the sample.



Base-peak chromatogram of the separation of five molecules performed in 30 seconds with chromatographic peak widths (FWHM) of one second or below. A hrEIC of peak 4 is shown in more detail in (2), with each single data point highlighted. (3) Averaged MS spectrum of peak 4. Both mass accuracy (0.8 ppm) and resolution (43,000) are maintained at the high acquisition rate of 10 Hz.

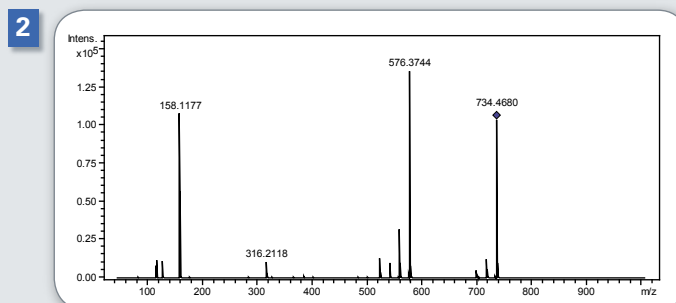


The maXis achieves a mass accuracy of < 200 ppb RMS error in MS mode using internal calibration.

SmartFormula 3D certainty

1

#	Meas. m/z	Formula	m/z	err [ppm]	N-Rule	e ⁻ Conf	mSigma
1	734.4683	C 34 H 60 N 11 O 7	734.4672	-1.6	ok	even	6.51
2	734.4683	C 37 H 68 N 0 13	734.4685	0.3	ok	even	8.19
3	734.4683	C 35 H 56 N 15 O 3	734.4685	0.2	ok	even	18.68



3

SumFormula	m/z calc	err[m...]	err[ppm]	mSigma	eConf	Com. ...	Com. ...	Com. ...
<input checked="" type="checkbox"/> C 37 H 68 N 0 13	734.4685	0.2	0.3	8.2	even	16.0	0.5	0.4

For erythromycin, a higher molecular weight compound at m/z 734, SmartFormula proposes 3 formulae within 2 ppm by comparing the isotopic pattern to candidates with appropriate elemental formulae limits and chemistry rules (1). SmartFormula 3D gives an extra dimension of information. Interpretation of the erythromycin MS/MS spectrum (2) considers the masses and isotopic patterns for all the fragment ions. Only one possible formula for the parent molecule fits to the proposed formulae for these fragment subunits (3).

Developed from an original concept by Don Richards, Pfizer.
Read more: Bruker Daltonics Technical Note TN-23.

High Performance@High Speed – a New Class of Proteomics Data

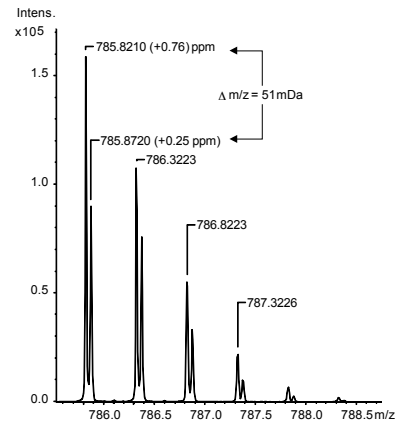
Resolution

Resolution of beyond 40,000 FWHM enables the discreet analysis of near isobaric species and allows the exploration of new depths of complexity in metabolomics and biomarker discovery applications. Peptides extremely close in mass are clearly separated even at relatively high mass.

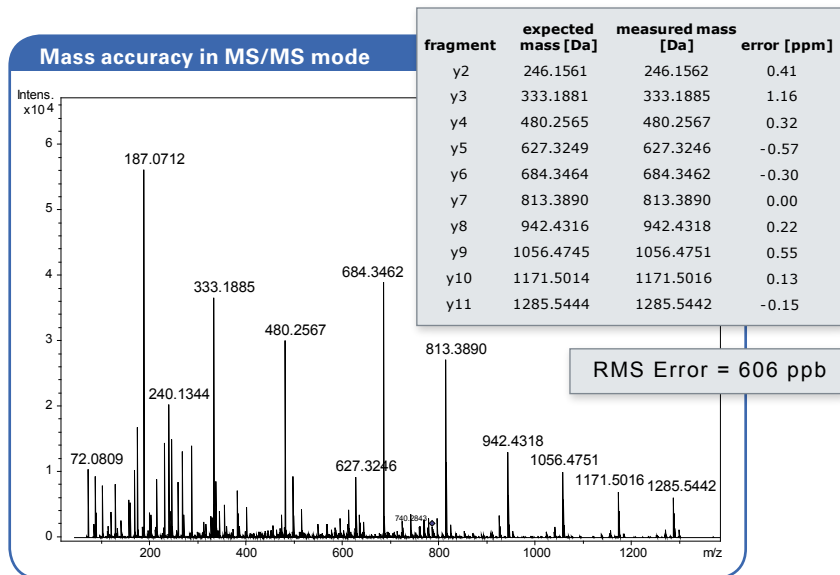
The same extreme high mass accuracy is available in MS/MS mode providing high confidence in de novo sequencing.

Intact protein analysis

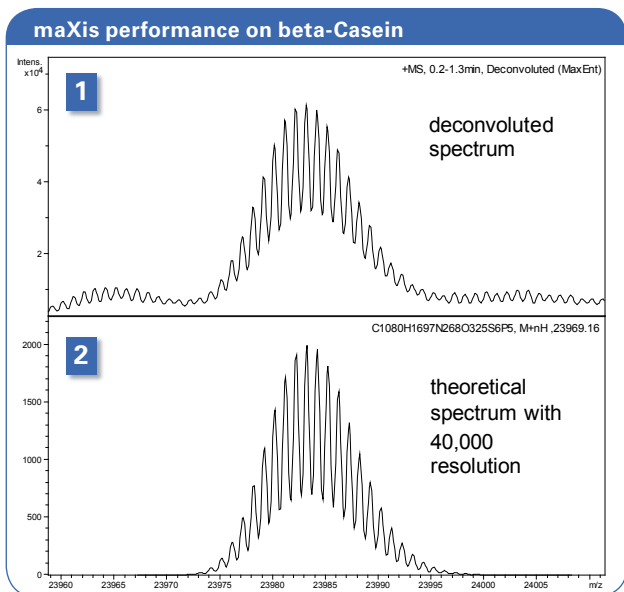
Analysis of intact proteins requires outstanding resolution capabilities at high mass ranges. maXis high resolution power accompanied by extended mass range and high mass accuracy allows for precise protein analysis.



Resolve isobaric peaks. Mass resolution achieved 50,000 FWHM. Isobaric peptide peaks with a very small mass difference of 51 mDa are clearly resolved.



MS/MS spectrum of peptide GluFib (2 pmol/μl).



Analysis of β-Casein with a molecular weight of 24 kDa is performed with a mass accuracy of $\Delta m_w = 1.5$ ppm. The deconvoluted spectrum (1) shows close similarity to the theoretical isotopic pattern (2).

Mass accuracy in a proteomics study

OK	Accession	Protein	MW [kDa]	Scores	Peptides	SC	RM
✓	gi 6730181	Chain A, Crystal Structure of C418a,C419a Mutant...	85.1	1816.9 (M:1816.9)	28	47.2	
✓	gi 15834378	chaperonin GroEL [Escherichia coli O157:H7 str. S...	57.3	1725.5 (M:1725.5)	23	62.0	
✓	gi 49258331	Chain A, E. Coli Elongation Factor EF-Tu Complex...	43.1	1528.5 (M:1528.5)	19	64.4	
✓	gi 83586981	COG4771: Outer membrane receptor for ferriente...	82.1	1476.5 (M:1476.5)	20	42.5	
✓	gi 15799694	molecular chaperone DnaK [Escherichia coli O157:...	69.1	1411.4 (M:1411.4)	22	48.4	
✓	gi 15799798	pyruvate dehydrogenase subunit E1 [Escherichia c...	99.6	1257.0 (M:1257.0)	25	33.9	
✓	gi 75237909	COG0039: Malate/lactate dehydrogenases [Escher...	32.3	1117.0 (M:1117.0)	13	74.7	
✓	gi 75230020	COG0148: Enolase [Escherichia coli O157:H7]	39.1	1044.4 (M:1044.4)	12	49.7	
✓	gi 15800816	outer membrane protein A [Escherichia coli O157:...	37.2	980.8 (M:980.8)	14	53.2	
✓	gi 15804222	α-mannosidase 4 [Escherichia coli O157:H7]	41.4	920.8 (M:920.8)	17	51.8	

Peptide OK	Cmpd.	m/z meas.	Mr calc.	z	Δ m/z [ppm]	Rt [min]	Scores	Sequence
✓	2331	903.1172	2706.3269	3	0.30	69.91	138.0 (M:138.0)	K.IEAGYVAVGQNAVGTDLVQWDI
✓	2458	771.3810	3081.4944	4	0.14	72.36	114.5 (M:114.5)	R.FDHSIVGNWSPALNISQGLC
✓	2756	983.5106	1965.0095	2	-1.45	78.10	97.8 (M:97.8)	K.EISPSYIVGLSATVDVTK.N
✓	1678	662.0219	1983.0459	3	-1.03	57.47	93.0 (M:93.0)	R.GMGPENTLILIDKPVSSR.N
✓	1773	545.6220	1633.8424	3	1.09	59.29	91.0 (M:91.0)	K.NVSLTGGVDNLFDKR.L
✓	1317	937.7875	2810.3352	3	1.93	50.54	86.7 (M:86.7)	R.MKDLSSNTQALGTGNTGGADI
✓	2944	661.3279	1980.9581	3	1.88	81.83	84.9 (M:84.9)	R.WDFAPLQGLEAGYSR.Q
✓	1486	717.3905	1432.7674	2	-0.68	53.78	78.9 (M:78.9)	R.YNGAAGGVNITTK.K
✓	3383	1065.5412	3193.6039	3	-0.67	91.98	77.8 (M:77.8)	K.AVVEGLEGLNVPVSEVMVMT
✓	782	599.9475	1796.8190	3	0.92	40.29	77.5 (M:77.5)	K.TQADAVDINGSHQ2SAR.L
✓	2995	994.4329	1786.8526	2	-0.76	74.97	72.6 (M:72.6)	R.NFSLTQGLGEFSPR.L
✓	2883	654.3306	1306.6459	2	0.60	83.64	66.9 (M:66.9)	R.DGMILAGVTWFR.N
✓	1998	643.2864	1284.5597	2	-1.16	63.58	63.5 (M:63.5)	R.TWVMSVNIHF.E
✓	780	589.8122	1177.6091	2	0.60	40.28	62.5 (M:62.5)	R.AGTAYTLPAQR.E
✓	235	492.2617	982.5084	2	0.50	29.39	52.3 (M:52.3)	K.GQPVAQPTK.E
✓	2002	739.8776	1477.7413	2	-0.42	63.62	43.1 (M:43.1)	K.NVSLTGGVDNLFDKR.R
✓	569	411.7221	821.4283	2	1.61	36.20	40.5 (M:40.5)	R.LVGNLDK.T
✓	1782	624.6563	1870.9465	3	0.30	59.42	24.5 (M:24.5)	K.APSLVQTNPNVLYSK.G
✓	1044	416.2317	830.4498	2	-1.12	45.36	21.9 (M:21.9)	R.DVSEIR.T

Screening of an *E. coli* lysate with a mass accuracy typically below 1 ppm – obvious advantages for confidence in protein ID and quantitation.

Technical Specifications

Cutting-edge performance

- First ever ultra-high resolution time-of-flight technology; UHR-TOF
- Outstanding combination of mass accuracy, resolution and speed without compromise
- Dual ion funnel Q-q front end
- SmartFormula 3D, the novel combination of accurate mass of parent and fragment ions with True Isotopic Pattern (TIP™)
- Wide dynamic range for ultra-stable accurate mass
- IonCooler™ technology for full MS/MS bandwidth
- Dimensions 800 x 1320 x 2850 mm, weight 500 kg

Source options

- APCI atmospheric pressure chemical ionization source
- ESI/APCI multimode source
- APPI atmospheric pressure photo ionization source
- Online / offline NanoElectrospray sources
- CE/MS coupling with grounded ESI needle
- Direct GC coupling

Analytical performance

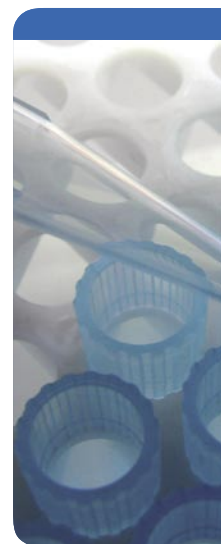
- Mass accuracy < 1 ppm (typically 600 - 800 ppb) RMS Error
- High resolution EIC with typically 1.5 mDa window
- Mass resolution 40,000 (FWHM), typically 50,000 FWHM at ultra performance LC speed
- Mass range 50 – 20,000 m/z
- Advanced temperature compensation
- Acquisition rate up to 20 Hz (profile and peak detected spectra to disk)

Compass & application software suites

- Integrated LC-MS/MS control and data processing incl. SmartFormula 3D
- MetaboliteTools™ for metabolite identification
- TargetAnalysis™ – for multi-target compound screening
- BioTools™ / RapiDeNovo™ software for protein data interpretation
- ProteinScape™ database system for proteome project management
- Compass OpenAccess™: Walk-up LC/MS chemical formula generation

Support of HPLC and sample inlet systems from the following vendors:
Bruker EASY-nLC, Advion TriVersa NanoMate, Agilent, Dionex, VWR/Hitachi, Waters (incl. UPLC), Autosamplers from CTC

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