Analyst Accepted Manuscript



This is an *Accepted Manuscript*, which has been through the Royal Society of Chemistry peer review process and has been accepted for publication.

Accepted Manuscripts are published online shortly after acceptance, before technical editing, formatting and proof reading. Using this free service, authors can make their results available to the community, in citable form, before we publish the edited article. We will replace this Accepted Manuscript with the edited and formatted Advance Article as soon as it is available.

You can find more information about *Accepted Manuscripts* in the **Information for Authors**.

Please note that technical editing may introduce minor changes to the text and/or graphics, which may alter content. The journal's standard <u>Terms & Conditions</u> and the <u>Ethical guidelines</u> still apply. In no event shall the Royal Society of Chemistry be held responsible for any errors or omissions in this *Accepted Manuscript* or any consequences arising from the use of any information it contains.



www.rsc.org/analyst

Analyst

MINIREVIEW

50

51

52

53

54

55

56

57

58

59 60

MALDI mass spectrometric imaging meets "omics": Recent advances in the fruitful marriage

A. C. Crecelius,^{ab *} U. S. Schubert^{ab} and F. von Eggeling^{bcde}

Analyst

Matrix-assisted laser desorption/ionization mass spectrometric imaging (MALDI MSI) is a method that allows the investigation of the molecular content of surfaces, in particular tissues, within its morphological context. The applications of MALDI MSI in the field of large-scale mass spectrometric studies, which are typically denoted by the suffix "omics", is steadily increasing. This is because, on one hand, technical advances regarding sample collection and preparation, matrix application, instrumentation, and data processing have enhanced molecular specificity and sensitivity of MALDI MSI; and, on the other hand, the focus of the "omics" community has moved from establishing an inventory of certain compound classes to exploring their spatial distribution to gain novel insights. Thus, the aim of this mini-review is twofold, to display the state-of-art in terms of technical aspects in MALDI MSI and to highlight selected applications within the last two years, which either have significantly advanced a certain "omics" field or have introduced a new one through pioneering efforts.

^aLaboratory of Organic and Macromolecular Chemistry (IOMC), Friedrich Schiller University Jena, Humboldtstraße 10, 07743 Jena, Germany.

^bJena Center for Soft Matter (JCSM), Friedrich Schiller University Jena, Philosophenweg 7, 07743 Jena, Germany, E-mail: anna.crecelius@unijena.de.

^cInstitute of Physical Chemistry, Friedrich Schiller University Jena, Helmholtzweg 4, 07743 Jena, Germany.

^dDepartment of Otorhinolaryngology, Jena University Hospital, Lessingstraße 2, 07743, Jena, Germany.

eLeibnitz Institute of Photonic Technology (IPHT), Albert-Einstein-Straße 9, 07745 Jena, Germany.



Anna C. Crecelius obtained her Ph.D. in 2002 under the supervision of Prof. Malcolm R. Clench at the Sheffield Hallam University (U.K.). She has conducted post-doctoral research stays at universities including Vanderbilt University (USA) and Ludwig Maximillians University Munich. Currently, she is a senior research scientist in the group of Prof. Ulrich S. Schubert at the Friedrich Schiller University Jena. Her main

research area is the development and application of mass spectrometric imaging techniques.

Ulrich S. Schubert studied chemistry in Frankfurt and Bayreuth and the Virginia Commonwealth University (USA). His Ph.D. studies were performed at the Universities of Bayreuth and Tampa (USA). After postdoctoral training with Jean-Marie Lehn at the University in Strasbourg (France), he moved to the TU



München and obtained his Habilitation in 1999. From 1999 to 2000 he was Professor at the Center for NanoScience, University of Munich, and from 2000 to 2007 Full-Professor at TU Eindhoven (The Netherlands). Currently he holds a chair at the Friedrich Schiller University Jena with research interest in nanoparticle systems as sensor and drug delivery devices,

supramolecular chemistry, inkjet printing of polymers, polymers for energy applications, and self-healing materials.



Ferdinand von Eggeling studied Biology and Chemistry in Erlangen and finished his Ph.D (1995) and his Habilitation (2003) at the Friedrich Schiller University Jena in Genetics. Since 2001 he was head of the Core Unit Chip Application (CUCA) at the Institute of Human Genetics. In 2009 he received the apl. Professor for Genetics at the Friedrich Schiller

University Jena. Currently he has an affiliation at the Institute of Physical Chemistry and the ENT-Department of the University Hospital in Jena. His main interest is in mass spectrometric imaging of different tumour entities and the biological characterisation of functional tissue components.

2

3

4

5

6

7

8

9

10

11

12

13

14

15

16

17

18

19

20

21

22

23

24

25

26

27

28

29

30

31

32

33

34

35

36

37

47

51

57

58

59 60

Introduction

One of the simplest instruments to generate images is a pinhole camera, which astronomers have been used in the 13th century to observe sunspots. In the 16th century the microscope was developed which allowed detecting small objects like mammalian eggs, sperms or bacteria. The next level of imaging was reached by the development of X-rays (1895) which enabled physicians to look into a body. Since 1973 magnetic resonance imaging is also used for the examination of organs or the whole body in 3D. Another medical imaging technique that produces also a three-dimensional image from functional processes in the body is positron emission tomography. With this imaging technique molecular processes could be made visible to a certain extent, however radioactive labels are required. An emerging label free technique is mass spectrometric imaging (MSI), which was developed at the end of the 20th century. Matrix-assisted laser desorption/ionization mass spectrometric imaging (MALDI MSI) was one of the first soft ionization techniques applied to it.^{1, 2} One key aspect of a successful MALDI MSI experiment is the procedure for the matrix application,³ and beforehand the right choice of matrix.⁴ Due to the increasing applications of ultra violet (UV) MALDI MSI in various "omics" field, the information, which matrix is suitable for which family of compound classes and mass range can be easily found in the literature. In particular in metabolomics, considerable efforts have been carried out in the last two years to discover new matrices, such as the versatile matrix 9-aminoacridine.⁵⁻⁷ Hence, Table 1 provides a snapshot of the current state-of-art of common and new UV MALDI MSI matrices, subdivided into the corresponding "omics" fields. We listed only one recent reference, published within the last two years, in Table 1 for each presented MALDI MSI matrix candidate based on the selected matrix application procedure. Additional information regarding suitable UV MALDI MSI matrices for animal tissue analysis can be found in the recent review by Thomas and Chaurand.⁸

38 In order to circumvent the disadvantages, such as lateral analyte 39 migration induced through matrix deposition,⁹ the possibility of 40 using heterocyclic based dyes,¹⁰ nanostructured indium tin oxide 41 coated glass slides,¹¹ or nanostructure-assisted laser 42 desorption/ionization¹² are promising alternatives, which can be 43 employed for the analysis of small molecules, e.g. in the fields 44 of peptidomics, metabolomics, glycomics, or plantomics. 45

Even though, UV MALDI MSI is more robust than infrared (IR) 46 MALDI MSI,¹³ its few applications should be presented in this mini-review. The advantage of IR MALDI MSI over UV 48 MALDI MSI is that no sample preparation is required, since the 49 physiological cell water of the biological tissue can be used as 50 matrix.¹⁴ During measurements, the evaporation of the physiological cell water can be prevented by employing an 52 atmospheric pressure (AP) ion source with a cooling stage.^{15, 16} 53 For improving the ionization yield, AP IR MALDI MSI can be 54 combined with an electrospray postionization step, such as 55 accomplished in matrix-assisted laser desorption electrospray 56 ionization (MALDESI).17-19

Despite the right choice of matrix, it should be kept in mind that the complete sample preparation protocol determines e.g. spectrum quality, spatial resolution, as well as reproducibility of the MALDI MSI experiments.^{8, 20, 21} Key aspects of sample handling and preparation include tissue processing (fresh frozen vs. embedded tissue),²² washing steps,^{23, 24} on-tissue chemistry (e.g. enzymatic digestion,^{25, 26} derivatization,²⁷ transfer to functionalized surfaces),²⁸ and instrumentation for the application of the matrix.^{3, 29-31} A variety of embedding media has been tested, ranking from gelatin,³² carboxymethylcellulose,³³ poly[*N*-(2-hydroxypropyl) methacryl amide],²² to eye yolk.³⁴ Hence, the optimization of all these parameters based on the type of sample, ranking from human, animal, plant, food tissue, cells, cosmetics, to polymeric materials, is essential for the outcome of the MALDI MSI experiment. No wonder that especially during the last year more and more efforts have been devoted to methodology optimization,^{3, 35-37} validation,^{27, 38} and standardization,³⁹ which is essential for translating e.g. biomedical applications of MALDI MSI into the clinics.40,41

One advancement in MALDI MSI has certainly contributed to the translation into the clinic research, the analysis of formalinfixed paraffin-embedded (FFPE) tissue.⁴² In comparison to fresh frozen tissue, for which MALDI MSI was originally developed in the field of proteomics,¹ FFPE tissue enables the storage at room temperature for a long period of time. However, several preparation steps additional sample (deparaffination, rehydration, antigen retrieval, and enzymatic digestion) are necessary in comparison to fresh frozen tissue.⁴³ Hence, a great number of publications were published recently to tackle this issue.¹⁴ For tissue preservation not only FFPE tissue is suitable, also heat treatment is efficient.44

Another feature, which is necessary for clinical applications, is the increased sample throughput.⁴⁵ One possibility is to use precoated slides, bypassing the matrix application after sectioning.⁴⁶ Finally, the correlation of the extracted ion images with the underlying histology represents an important aspect in the clinical setting towards personalized medicine.47 This can be achieved in different ways: (1) staining of the tissue before MALDI MSI analysis,⁴⁸ (2) removal of the matrix after MALDI MSI analysis and staining of the tissue⁴⁹ or (3) staining of a serial section.50 All three options have their advantages and disadvantage, e.g. option one is only applicable to certain stains, which are compatible with MALDI MSI, option two can lead to disrupter of the tissue integrity caused by the matrix removal, and option three can influence the co-registration step of ion and optical image. Hence, the right choice varies from case to case, e.g. head and neck tissue tears during matrix removal,⁵⁰ therefore option two is not applicable, and hematoxylin-eosin (H&E) staining is not compatible with MALDI MSI, therefore only option three is suitable.

Typically, the majority of studies belonging to one "omics" field are focusing on a single principal of mass analysis in order to fulfil the requirements for the specific compound class, as illustrated in Table 1. For example in proteomics, in which molecules of high molar mass are of interest, the time-of-flight Journal Name

nalyst Accepted Manuscri

(TOF) or TOF/TOF analyser, is generally employed due to the highest practical mass range.51 However, the TOF/TOF instruments have a limited precursor-ion selectivity for MS/MS experiments, which makes the on-tissue structural elucidation of the recorded ions in the performed MALDI MSI experiments challenging. For the analysis of small molecules, by means of metabolomics, plantomics, etc. an analyzer with high mass resolving power is so beneficial, that a loss in dynamic range is taken into account. Hence, Fourier-transform ion cyclotron resonance (FT-ICR) or Orbitrap analyzer are commonly used. However, the trend to achieve high, even towards cellular spatial resolution is creating, especially with these kind of instruments, new challenges. The question, which nowadays often arises is "how do I get fast meaningful results from these big datasets?", since the aim is to process and analyse these datasets in an efficient, fast and standardized manner. The MALDI MSI community is currently responding to this issue by suggesting various computational strategies.50, 52-58 Finally, in drug imaging,^{59, 60} besides ion traps (FT-ICR and Orbitrap), triple quadropole analyser is additionally in favour, due to its selected reaction monitoring capabilities.^{61, 62}

Since more and more research groups are employing MALDI MSI nowadays, new software has been developed to visualize (MIRION),⁶³ process (MSiReader,⁶⁴ OpenMSI⁶⁵), and to store⁶⁶ the generated datasets.

The mini-review will subsequently focus on selected applications of MALDI MSI. Publications within the last two years, starting from 2013 up to the first quarter of 2015 are considered, which either substituted a common "omics" field or introduced a new one owing to its potential.

Selected "omics" applications

Mass spectrometry has become an indispensable tool in the "omics" analysis due to its vast expansion. Often not only the identification and quantification of a certain compound class is of interest, but also its localization within the biological system, which cannot be determined by classical MS based approaches alone without any additional fractionation, extraction steps. As a consequence, MALDI MSI is gaining growing significance, in particularly in biological and clinical studies for improved diagnostic and therapeutic approaches.⁴⁵ Due to the rapidly growing number of publications in this field within the last two years, only significant applications of MALDI MSI in the different "omics" based areas will be discussed. For further biological applications of MALDI MSI, the review by Spengler is highly recommended, who covers the last three years.¹⁴

 Table 1. Overview of widely used and new MALDI MSI matrices, classified according to the "omics" field. (Time-of-flight, TOF; quadrupole time-of-flight, QTOF; fourier-transform ion cyclotron resonance, FT-ICR; ion mobility, IM)

"Omics" field	Compound class	Matrix	Matrix application procedure	Spatial resolution [µm]	Specimen	MS analyzer (ion mode)	Ref.
Proteomics	Proteins	Sinapinic acid	Automatic vibrational sprayer	80	Mouse brain	TOF/TOF (positive linear)	67
			Sublimation device followed by rehydration	50, 100	Human ulcers	TOF (positive linear)	68
			Pre-coated gold covered microscopic slides	10	Mouse brain and rat kidney	TOF (positive linear)	46
		2,5-Dihydroxyacetophenone	Sublimation device followed by recrystallization Automatic nozzle/air sprayer system	5	Mouse and rat brain	TOF and TOF/TOF (positive linear)	69
			Automatic nozzle sprayer	1	Mouse brain	TOF (transmission geometry)	70
	Peptides	α-Cyano-4-hydoxycinnamic acid	Automatic vibrational sprayer	150	Human knee synovial and cartilage tissue	IM (positive-V-mode)	71
				80	Rat muscles	TOF/TOF (positive reflector)	72
			Automatic pneumatic sprayer	100	Mouse brains	TOF/TOF (positive reflector)	73
Peptidomics	Peptides	2',4',6'-Trihydroxyacetophenone	Automatic vibrational sprayer	50-200	Rat intestine	TOF (positive linear)	74
	Neuropeptides	2,5-Dihydroxybenzoic acid	Airbrush	25	Stromatogastric nervous tissue of crabs	TOF/TOF (positive reflector) FT-ICR (positive)	75
				50	-	TOF/TOF (positive reflector)	76
		α-Cyano-4-hydoxycinnamic acid	Chemical Printer	50	Honeybees brains	TOF/TOF (positive reflector)	77
Metabolomics	Lipids	2,5-Dihydroxybenzoic acid	Sublimation device	10	Mammalian retina	TOF or TOF/TOF (positive reflector)	35
		Alkylated 2,5-dihydroxybenzoic acid	Capillary spraying device	50	Rat brain	TOF/TOF (positive, negative reflector)	78
		α-Cyano-4-hydoxycinnamic acid	Automatic vibrational sprayer	150	Mouse kidney (mouse model for fabry disease)	FT-ICR (positive)	79
			Automatic nozzle sprayer	70	Human colorectal cancer tissue	IM (positive-V-mode)	80
		Binary matrix of 2,5- dihydroxybenzoic acid and α- cyano-4-hydoxycinnamic acid	Automatic vibrational sprayer	150	Mouse liver (mouse model for HBV infection)	TOF (positive reflector)	81
		2,6-Dihydroxyacetophenone	Sublimation device	10	Mouse eyes (mouse model for stargardt disease)	FT-ICR (positive)	82

Analyst Accepted Manuscript

Analyst

		9-Aminoacridine	Automatic vibrational sprayer	50	Mouse kidney	TOF/TOF (pagative reflector)	5
		15.0		00 100 255		(liegative reflector)	92
		1,5-Diaminonapthalene	Sublimation device	80, 100, 255	Pig and mouse brain	FI-ICR	85
					homogenates	(positive)	
				10, 100	Mouse brain, xiphosphorus	TOF/TOF	84
					maculatus fish	(positive and	
						negative reflector)	
		1.8-Bis(dimethyl-	Sublimation device followed by	20, 1000	Human cancer tissue	FT-ICR	85
		amino)nanhthalana	recrystallization	20,1000	Trankin Gunder Hissue	(negative)	
		Owneitin	Automatic silentices lesson	200	Densine education de		86
		Quercitin	Automatic vibrational sprayer	200	Porcine adrenai giands	F1-ICK	80
						(positive, negative)	
		Curcumin	Airgun,	50, 100, 150	Human fingermarks,	Q-TOF	87
			Automatic pneumatic sprayer,		rat lung,	(positive)	
			Acoustic droplet ejection system		living skin equivalent	° тм ́	
			1		5 1	(positive)	
		Dithmonol	Ainhmach	10	Mouse hasia	(positive)	88
		Ditilianoi	Airbrush	10	wouse brain	11VI	00
						(negative)	
		Ag nanoparticles	Implanter	50	Rat heart	Orbitrap	89
			-			(positive, negative)	
		1.5-Napthalenediamine	Automatic vibrational spraver	50, 100, 200	Mouse and rat brains	TOF/TOF	90
		hydrochloride	l interesting the second spruyer	20, 100, 200	(MCAO rat model)	(negative reflector)	
			A	100	Det has in	TOF	01
		4-PhenyI-α-cyanocinnamic acid	Automatic pneumatic sprayer	100	Kat orain	I UF	91
		amide				(positive, negative	
						reflector)	
	Nucleotides	9-Aminoacridine	Automatic pneumatic spraver	50	Porcine eyes	FT-ICR	6
						(negative reflector)	
-	Nucleotideo	N (1 Nonhthul) athulanadiamina	a) Electrocomory demonition dervice	a) 10	Monos hasin Iridaan linan	TOE/TOE	92
	Inucleotides,	N-(1-Naphthyl) ethylenediannie	a) Electrospray deposition device	a) 10	Mouse brain, kidney, liver	IOF/IOF	1 12
	Lipids	dihydrochloride	b) Automatic vibrational sprayer	b) 25, 50, 100	(colorectal liver metastasis	(negative reflector)	
					model)		
	Fatty acids	Silver	Sputter coater	5, 50, 150	Mouse kidney, testis, liver,	TOF/TOF	93
					brain	(positive reflector)	
Glycomics	N-linked glycans	2.5-Dihydroxybenzoic acid	Automatic vibrational spraver	25	Mouse brain, human	FT-ICR	94
olycollics		_,=, =, =	· · · · · · · · · · · · · · · · · · ·		kidney	(positive)	
			Automotio nonale onnovien	100	Musing Iridness	TOE/TOE	05
			Automatic nozzie sprayer	100	Murine kidney	107/107	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
						(positive reflector)	
Plantomics	Metabolites	9-Aminoacridine	Sublimation device	50	Arabidopsis thaliana leaves	TOF	7
						(negative reflector)	
		1.8-Bis	Airbrush	50	Medicago truncatula roots	TOF/TOF	96
		(dimethyl-amino)naphthalene			and root nodules	(negative reflector)	
			Automotic vibuational annavan	50	Luning roots	(lieguirre reneetor)	07
		a-Cyano-4-nydoxycinnamic acid	Automatic vibrational sprayer	50	Lupine roots	Orbitrap	
						(positive)	
		2,5-Dihydroxybenzoic acid	Pneumatic sprayer	20	Grapes	Orbitrap	98
						(positive)	
		Binary matrix of 2.5-	Automatic vibrational spraver	35	Citrus sinensis grafted on	TOF/TOF	99
		dihydroxybenzoic acid and a-	1.5		citrus limonia petioles and	(positive reflector)	
		cvano-4-hydoxycinnamic acid			leaves	(r source remeetor)	
		1.5 Dismission and below	California dania	25	Combat	Orbiteren	32
		1,5-Diaminonapthalene	Sublimation device	25	Corn leafs	Orbitrap	32
						(negative)	
		Silica TLC powder	Dry coating technique	50	Eucalyptus stem	Orbitrap	100
						(negative)	
Foodomics	Fungal secondary	2.5-Dihydroxybenzoic acid	Pneumatic sprayer	15	Mushrooms	Orbitrap	33
roouonneo	metabolites	_,,				(positive)	
	nictabolites	TT 1	A	050		(positive)	101
	Proteins	α-Hydroxycinnamic acid	Automatic vibrational sprayer	250	Tomatoes	TOF/TOF	101
		and aniline				(positive linear)	
	Flavonoids	2',4',6'-Trihydroxyacetophenone	Automatic vibrational sprayer	70	Strawberries	TOF/TOF	102
						(negative reflector)	
Cosmetomics	Lipids	α-Cvano-4-hydoxycinnamic acid	Airbrush	100	Cosmetic products	Orbitrap	103
,					r	(positive negative)	
Matariamias	Linida	Dinory matrix of 2.5	Chamical printar	10 to 150	Ultra high molecular	TOE/TOE	104
wrater formes	Lipius	Dinary matrix Of 2,3-	Chemical primer	1010150	Unia-ingn Hiolecular		
		dinydroxybenzoic acid and α-			weight polyethylene joint	(positive reflector)	
		cyano-4-hydoxycinnamic acid			implants		
	Polymers	2,5-Dihydroxybenzoic acid	Pneumatic sprayer	20 to 100	Polymeric dialyzer	Orbitrap	105
					membranes	(positive)	

Proteomics

Even though, MALDI MSI has been extensively utilized in the field of proteomics since its discovery,^{1, 2} the analysis of large intact proteins (above 25 kDa) is still challenging.¹⁰⁶ Hence, more and more researchers are employing various on-tissue digestions techniques, developed for the specific tissue type they are working on^{25, 73, 107, 108} Additionally in 2013, a multi-center study has been set up to improve and validate the current protocols under the roof of the COST action BM1104. The idea to image tryptic peptides opened the door for analysing FFPE tissue samples, which are commonly archived in clinics with the corresponding meta-data (survival and treatment response). Therefore, it is obvious that the move of MALDI MSI towards clinical biomarker discovery is currently on its way,^{40, 42} substituted by robust methods,⁴³ and reference databases.¹⁰⁹ The clinical applications rank from various cancer types, such as

clear cell renal cell,¹¹⁰ heptatocellular,¹¹¹ thyroid,¹¹² prostate,¹¹³ pancreatic,¹¹⁴ salivary gland,¹¹⁵ breast and gastric carcinoma¹¹⁶ to other diseases, such as osteoarthritis,⁷¹ trauma,⁷² wounds,⁶⁸ cartilage,¹¹⁷ ectopic calcification,¹⁰⁷ in order to differentiate and classify pathological regions on the basis of known and unknown proteins. The findings are subsequently further validated by traditional histology.⁴⁷

MALDI MSI has been proven in the past as a useful tool in molecular neuroscience,^{118, 119} exploring the biomolecular mechanism of neurodegenerative disorders, such as amyotrophic lateral sclerosis,^{120, 121} parkinson's disease,¹²² and childhood absence epilepsy.¹²³

A recent example of MALDI MSI,¹⁰⁷ which helped in understanding the underlying biology of calcification is presented in Figure 1. The MALDI MSI data (Figure 1 B) were integrated with the histological observations (Figure 1 A) to

2

3

4

5

6

7

8

9

10

11

12

13

14

15

16

17

18

19

20

21

22

23

24

25

26

27

28

29 30

31 32 33

34

35

36

37

38

39

40

41

42

43

44

45

46

47

48

49

50

51

52

53

54

55

56

Journal Name

reveal molecular markers for morphological defined tissue areas, such as calgizzarin (m/z 11651) for epidermis, or thymosin beta-4 (TYB-4, m/z 4965) for papillary dermis or whole dermis in the case of diseased and healthy skin tissue, respectively. The subsequent assignment of the protein identities to the peaks was accomplished by bottom-up strategies using *in situ* digestion *via* hydrogel discs.¹²⁴



Fig. 1. MALDI MSI of a patient sample affected by pseudoxanthoma elasticum (PXE) in comparison to a control one. (A) Optical images of tissue sections after hematoxylin-eosin or alizarin red staining; (B) Seven extracted ion images of known and unknown proteins associated with ectopic calcification. Reprinted in a modified version with permission from ref.¹⁰⁷, D. Taverna, *et al.*, *Bone*, 2015, **74**, 83-94. Copyright 2015, Elsevier Inc.

The second approach commonly used in proteomics for protein identification, which is called top-down, has also been employed in MALDI MSI studies,⁶⁷ even the combination of both.¹²⁵ In top-down a mass spectrometer is used to fragment the proteins without any digestion step, e.g. in-source decay can be used, which is a metastable decay of molecules during the desorption/ionization process.⁶⁷ Although, all three approaches (bottom-up, top-down, combination of both) resulted in confident protein identifications, and consequently in the establishment of a public database,¹²⁶ it certainly remains an important issue to be solved in the future to push this technique towards a valuable tool for clinicians (grading, margins, prognosis, prediction of tumours) in the framework of personalized medicine.

Peptidomics

Analyst

The MS-based "omics" discipline that focuses on the comprehensive analysis of peptides involved in cell-to-cell communications is often referred to as peptidomics. There are not many MALDI MSI studies in this field presumably due to the low abundance of peptides, and especially neuropeptides, which are hampering the analysis. However, MALDI MSI with its high specificity is certainly a powerful method for localizing neuropeptides to identify neuronal signalling pathways^{118, 127} or exploring neurodegenerative diseases, such as parkinson's,¹²⁸⁻¹³⁰ alzheimer's,^{131, 132} and huntington disease.¹³³ The resulting molecular knowledge is important to understand for example how the human nervous system enables us to interact with our environment. A common used model system in this respect is the stromatogastric nervous system of the Johns crab cancer borealis, which consists of a set of distinct but interacting motor circuits. A recent MALDI MSI study⁷⁶ identified 57 neuropeptides originating from eleven different neuropeptide families in stomatogastric ganglion tissue. The spatial localization of e.g. NFDEIDRSGFGFA from the orcokinin neuropeptide family (m/z 1474.6), and HIGSLYRa from the YRamide neuropeptide family (m/z 844.5) were determined as predominantly localized in the central region of the ganglion, where the neutrophil is formed, as shown in Figure 2 B and C, respectively.



Fig. 2. MALDI MSI analysis of neuropeptides in stomatogastric ganglion tissue, extracted from a John crab *cancer borealis*. (A) Optical image prior matrix coating; (B) and (C) two selected ion images: NFDEIDRSGFGFA from the orcokinin neuropeptide family (*m*/z 1474.6), and HIGSLYRa from the YRamide neuropeptide family (*m*/z 844.5), respectively. Reprinted in a modified version with permission from ref.⁷⁶, R. Chen *et al., Rapid Commun. Mass Spectrom.*, 2014, **28**, 2437-2444. Copyright 2014, John Wiley & Sons, Ltd.

Current limitations associated with identification of MALDI MSI measured peaks might be tackled by using the approach presented by Minerva *et al.*¹³⁴ in an obese mouse model. The strategy was based on high-resolution MALDI MSI, MS/MS and LC-MS, facilitating the identification of 46 peptides out of 136 detected signals by MALDI MSI.

Furthermore, to address the drawbacks originating from the sample preparation, as discussed in the introduction section, prespotted targets can be used, as shown by the group of Salzet.¹³⁵ They successfully analysed endogenous peptides on targets prespotted with ionic matrices. Another possibility is to use nanostructure-initiator chips, although, a recent study has proven that MALDI MSI is superior for analyzing neuropeptides leading to twelve identified neuropeptide distributions compared to none in using nanostructure-initiator chips.¹³⁶

2

3

4

5

6

7

8

9

10

11

12

13

14

15

16

17

Metabolomics

Metabolomics is considered as one of the later "omics" technologies that provides additional functional information for understanding biological systems. The metabolome consists of small molecular building blocks (e.g., amino acids, nucleotides), metabolic intermediates (e.g., fatty acids), and structural and signalling elements (e.g., lipids). Since these small molecules are easily detectable via MALDI MSI, the last two years were characterized by a strong interest in this "omics" field, 137-139 with special emphasis in the tumour-specific metabolism.¹⁴⁰ Since lipids, which are classified as a subset of metabolomics, are playing many important roles in cancer progressing,¹⁴¹ their spatial localization has been investigated in colorectal,⁸⁰ clear cell renal cell,¹¹⁰, thyroid, gastric, lung, esophageal, breast,⁸⁵ head and neck cancer,50, 142 as well as xenografts.143, 144 Compared to the list of proteomic MALDI MSI studies in cancer research, as presented two sections above, this list is nearly as long. Moreover, the subsequent combination of both "omics" fields has already been started, e.g. by exploring protein and lipid markers, which differentiate tumour from non-tumour regions within one MALDI MSI study.¹¹⁰ In particular, in cancer research, the correlation of the lipidomic organization revealed by MALDI MSI with the underlying histology is very important to gain further information of histological structures to improve personalized medicine. In the case of head and neck cancer, the spatial molecular characterization is important, since half of the patients develop a locoregional recurrence although radical therapy was prescribed. Figure 3 shows exemplary a correlation of molecular and histological information.⁵⁰



Fig. 3. MALDI FT-ICR MSI analysis of a human head and neck tumour tissue. Comparison of (A) metabolic segmentation map generated by the MSI data, and (B) histopathology (hematoxylin-eosin stain). Reprinted in a modified version with permission from ref.⁵⁰, L. Krasny *et al., J. Am. Soc. Mass Spectrom.*, 2015, **26**, 36-43. Copyright 2015, Springer.

With the help of computational algorithms, the head and neck tissue sample was subdivided into six clusters based on the spectral similarities (Figure 3 A). The thereby detected heterogeneity of the functional lipidome was reflected in the morphology, as observed in the H&E stain (Figure 3 B). To enable such a comparison of spatially defined molecular and histological signatures a registration step of the MALDI MSI dataset to the histological stain is essential, which was performed in this case manually on three defined landmarks. Alternatively, an automated registration procedure can be performed, ¹⁴⁵ which ultimately facilitates the correlation to anatomical atlases. ¹⁴⁶ And

Page 6 of 12

beyond this, the image fusion of extracted ion images with H&E stains generated by MALDI MSI and microscopy, respectively, can assist in predicting ion distributions in tissue areas that were not analyzed by MALDI MSI.¹⁴⁷

Besides, cancer applications, various other diseases, such as infections of hepatitis B virus,⁸¹ atherosclerosis,¹⁴⁸ fabry,⁷⁹ peridontal,¹⁴⁹ alzheimer's,¹⁵⁰⁻¹⁵² epilepsia,¹⁵³ stroke,¹⁵⁴ schizophrenia,¹⁵⁵ and stargardt disease⁸² have been investigated to shade light into the underlying disease mechanism. Within the spatial mapping of lipids, certain classes, such as phospholipids,¹⁵⁶ which can degrade in time,³⁶ sphingolipids,¹⁵⁷ and ceramides^{158, 159} have been extensively investigated. Even the possibility to introduce a wavelength-tuneable postionization laser to increase the ion yields of lipids.¹⁶⁰

As discussed for the two earlier "omics" fields, in metabolomics is the identification of the detected species directly on the analysed tissue as well crucial. Generally, two approaches are possible: 1) MS identification based on the high mass accuracy obtained from an orbitrap or an FT-ICR MS instrument,¹⁶¹ and 2) MS/MS fragmentation patterns enabling the differentiation between isobaric species.¹⁶²

Nowadays, ion mobility (IM) instruments are often used in MALDI MSI,¹⁶³ owing to several advantages, such as an improved signal-to-noise ratio caused by the physical separation of the noise, a larger peak capacity, and the possibility to separate isomers on the basis of shape differences. The latter feature beyond doubt can facilitate the identification procedure.

Besides the identification, the number of detected metabolites is important, which can be increased by carrying out the MALDI MSI analysis in both, positive and negative ionisation mode, using certain matrices (1,5-diaminonaphthalene,⁸⁴ quercetin,⁸⁶ dithranol,⁸⁸ silver nanoparticles¹⁶⁴ or the combination of two (α cyano-4-hydoxycinnamic acid and 9-aminoacrdine).¹⁶⁵

To go beyond the *in situ* visualization of metabolic changes, the utilization of additional chemical imaging technique,¹⁶⁶ has been shown as a promising tool, e.g. for analysing bacterial biofilms,¹⁶⁷ three-dimensional cell cultures,¹⁶⁸ mouse brain,¹⁶⁹ or rat spinal cord sections.¹⁷⁰ Novel designs of mass spectrometers even allow the acquisition of two imaging modi in one instrument,^{170, 171} promoting the idea of multimodal imaging to understand complex biological systems.

Within the reported lipidomic MALDI MSI studies, insects are the smallest animal bodies investigated, ranking from complete insect bodies, such as *drosophila melanogaster* flies to *paderus riparius* beetles.¹⁷²⁻¹⁷⁴ The gained knowledge can possibly help in understanding mechanistic and physiological principals, explaining the recent interest in this class of invertebrates.

At the end of this section, the developments towards quantitative MALDI MSI should be addressed. Certainly, there is still space for improvements; however, useful strategies in metabolomics as well as pharmacogenomics have already established and the reader is revered to the references listed.^{5, 83, 175, 176} Among these methods, one strategy is to use a calibration curve generated from the deuterated analogue to quantify the absolute concentration of a target compound. In the case of acetylcholine (ACh), a neurotransmitter, which can be used to identify cholinergic

Journal Name

Analyst

neurons in the central nervous system, MALDI MSI was performed in parallel on a sagittal mouse brain section of a control and a treated animal (10 mg/kg of the cholinesterase inhibitor tarcine), as shown in Figure 4.¹⁷⁷ The relative concentration of ACh is visualized in the extracted ion images, (Figure 4 A), and the absolute concentrations in the different brain areas is calculated using the deuterated standard spotted on control sections (Figure 4 B). From this, it could be demonstrated that the administration of tracine caused overall a seven-times increase of ACh in the mouse brain. Typically, the concentration of ACh is determined by quimioluminiscent, electro-chemical, fluorescent, and high-performance liquid chromatography coupled to electrospray mass spectrometry.¹⁷⁸ However, none of these techniques enabled the spatial quantification of ACh in such a way, as possible by MALDI MSI.



Fig. 4. MALDI MSI analysis of a sagittal mouse brain section to quantify (A) the relative and (B) the absolute concentration change of the neurotransmitter ACh in different brain areas (hippocampus, HIPP; caudate putamen, CP; cerebral cortex, CTX; thalamus, TH) induced through the administration of 10 mg/kg tracine. Reprinted in a modified version with permission from ref.¹⁷⁷, M. Shariatgorji *et al.*, *Neuron*, 2014, **84**, 697-707. Copyright 2014, Elsevier Inc.

The considered study¹⁷⁷ is two-fold remarkable, firstly due to the link of the two "omics" fields metabolomics and pharmacogenomics, and secondly due to the aspect of absolute quantification.

Other neurotransmitter, besides ACh, such as e.g. γ -amino butyric acid are only detectable through a derivatization step,¹⁷⁷ which is nowadays often applied in MALDI MSI studies to allow the successful analysis of e.g. amino acids,^{27, 179} or

pharmaceuticals.¹⁸⁰ MALDI MSI has already been employed as a tool to close the gap between metabolome changes in response to drug administration and certainly will be continued in the future in clinical settings.⁶²

Besides the impressive applications of MALDI MSI in medicine, its potential in forensic science has already been proven, e.g. to gain chemical information on latent fingermarks to help in convicting suspects, when the typical matching of the patterns fails.¹⁸¹ Further developments in this domain are focused on replacing the use of organic matrices to overcome disadvantages, which are linked with its use, such as the difficulties to get reproducible signal intensities, or the circumstance of masking analyte signals.¹⁸², ¹⁸³

Glycomics

Glycomics is focusing on the isolation and characterization of glycans, which nowadays are routinely analysed by MS based methods, providing both, qualitative and quantitative information employing top-down techniques.¹⁸⁴ In order to understand the roles of N-glycans in the physiology and molecular pathology of diseases, MALDI MSI of N-linked glycans was developed within the last two years, emerging from profiling⁹⁴ to MALDI MSI of FFPE tissues.^{95, 185, 186}

Plantomics

Plantomics describes the application of "omics" technologies in plant science to which the analysis of plant metabolites by MALDI MSI certainly counts. Often there exists an overlap with foodomics, as e.g. recognizable in the next section in this minireview.

The crucial step in plantomics is certainly the sample preparation. Two simple questions are arising in this contest: "how do I get intact sections from my sample, and which matrix can I use?" Commonly, animal and human tissue is cut in a cryomicrotome at 10 to 20 µm tissue thickness, however plant tissue is more demanding, especially if fragile leaves or petals are cut. Hence, a typical thickness can vary from 20 up to 100 µm. In the case of even uneven leaves, the imprinting onto porous PTFE prior matrix application is recommended to circumvent a broadening of the peak shape due to variations of the recorded time-of-flight of the ions when originating from different tissue heights.¹⁸⁷ Plant tissue compared to animal and human tissue is special, since it consists of many different cell types; therefore, the right choice of matrix is crucial. As presented in Table 1, a variety of matrices have already been investigated in plantomics, ranking from 9-aminoacridine⁷ and diaminonapthalene³² for the negative ion mode to common MALDI MSI matrices for the positive ion mode, such as α cyano-4-hydroxycinnamic acid,⁹⁷ 2,5-dihydroxybenzoic acid,⁹⁸ or the combination of both.99 Even the use of silica TLC powder¹⁰⁰ according to the protocol described by Puolitaival et al.¹⁸⁸ was successfully employed. Another possibility is to use no matrix, however only applicable if the plant metabolites have chromophores, which absorb the incident laser light.¹⁸⁹ Since only recent studies have been discussed here, the review by

Bjarnholt *et al.*¹⁹⁰ is recommended for further reading, who covers publications up to the end of 2013.

Foodomics

1

2

3

4

5

6

7

8

Foodomics is the comprehensive, high-throughput approach for the exploitation of food science in the light of an improvement of human nutrients.¹⁹¹ The main objective of this new approach is to improve human health and well-being. A variety of tissue types have been investigated by MALDI MSI ranking from barley,¹⁹² blueberry,¹⁹³ apple,¹⁹⁴ tomatoes,¹⁰¹ to mushrooms³³ explore the spatial distribution of mainly small organic molecules, such as lipids, flavonoids, fungal secondary metabolites, or amino acids.¹⁹⁵ An example of the MALDI surface analysis of fruits is presented in Figure 5.



Fig. 5. Localization of citric acid C₆H₇O₇ ([M-H]⁻ m/z 191) in strawberries (*Fragaria* × ananassa) of two development stages (G2: green fruit; R: full-ripe red fruit).¹⁰²

Strawberries are fruits, which are widely appreciated for their aroma, red color, juicy texture and sweetness. The acidity comes mainly from citric acid which comprises about 88 % of the acid content, along with malic acid and ellagic acid. When strawberries ripen, the acidity decreases. To visualize this change in concentration and to figure out its localization we performed MALDI MSI on garden strawberries (Fragaria × ananassa) and could show that citric acid is homogenously distributed in green fruits (Fig. 5 G2), and only at the skin in the full-ripe red fruit (Fig. 5 R).¹⁰² This example shows very nicely the potential of food imaging, and since the current spatial resolution of MALDI MSI is sufficient for analysing food, it can be expected that this technique will find its way as an analytical tool for the quality control of food products, besides novel ambient ionization techniques, which do not require any sample preparation.

Cosmetomics

Cosmetic products are gaining more and more importance in our daily life to improve e.g. the skin care, or odor of our body due to the rapid increase of our population. Hence, analytical methods are required to control their quality. Due to the complexity of cosmetics advanced characterization techniques, such as high-performance liquid chromatography coupled to mass spectrometry, gas chromatography mass spectrometry, and inductively coupled plasma mass spectrometry are routinely employed.¹⁹⁶ The application of MALDI MSI as a quality control tool of cosmetic products was presented by de Oliveira *et al.*¹⁰³ Upon the lipid profiles it was possible to test if a lipstick or eyeliner was expired or not. The imaging capabilities of MALDI MSI in the area of cosmetomics have certainly to be investigated

further to fulfil the requirements as a robust quality control technique in the cosmetic industry. However, in cosmetomics not only the quality of the cosmetic products is of interest, but also e.g. the penetration rate of cosmetics into the skin. The potential of MALDI MSI in the spatial analysis of skin has already been demonstrated,¹⁹⁷⁻¹⁹⁹ and hence now it is the right time to determine e.g. the penetration depth of certain sun-cream ingredients into the skin.

Materiomics

Materiomics is defined as the comprehensive study of material systems, including polymer systems, also known as polymeromics,²⁰⁰ connecting physiochemical material properties with material characteristics and functions. Besides, polymeric surfaces, materials, such as ceramic or metal are investigated in this "omics" discipline for their later application, which often comprises of biological environments. The characterization of polymer surfaces by MALDI MSI is certainly possible, when the right sample preparation technique is figured out.²⁰¹ For example, in the case of a negative photoresist layer,²⁰² which is generally used to manufacture printed circuit boards, the main component novolac, the active component benzophenone, and the solvent tetrahydrofuran were mixed with the matrix dithranol and the salt additive LiTFA, and spin-coated onto an ITOconductive glass slide. In another application the best way to analyse ultra-high molecular weight poly(ethylene) (UHMW-PE) joint implants was to slice them at 14 to 16 µm in a cryomicrotome and to apply a binary matrix consisting of 2,5dihydroxybenzoic acid and α -cyano-4-hydoxycinnamic acid in e.g. potassium chloride saturated methanol using a chemical printer.¹⁰⁴ The interesting point in this study was to visualize the material failure and to connect it to the biological implication.



Fig. 6. MALDI MSI analysis of a ultra-high molecular weight poly(ethylene) (UHMW-PE) hip joint explant. Reprinted in a modified version with permission from ref.¹⁰⁴, S. M. Froehlich *et al.*, *Anal. Chem.*, 2014, **86**, 9723-9732. Copyright 2014, American Chemical Society.

For this, a piece of a hip joint explant was sliced and serial sections were analysed by MALDI-MSI for the spatial lipid distributions inside the material. Figure 6 shows the 3D reconstruction of cholesterol $[M-H_2O+H]^+$ at m/z 369 on four

2

3

4

5

6

7

8

9

10

11

12

13

14

15

16

17

18

19

20

21

22

23

24

25

26

27

28

29

30

31

32

33

34

35

36

37

38

39

40

41

42

43

44

45

46

47

48

49

50

51

52

53

54

55

56

57

58 59 60 2.

3.

4

5.

6.

7.

8.

9.

10.

32.

consecutive UHMW-PE slices. It is clearly visible that cholesterol diffuses into the material possibly caused by mechanical stress during implantation in the patient. Subsequent follow up studies by e.g. nanoindentation or fourier-transform infrared spectroscopy (FT-IR) can might reveal further insides in this material wearout.

The "omics" field materiomics is still in it's infancy, however the possibility to gain spatial molecular information on materials by MALDI MSI and to correlate these findings with common used techniques in material science, such as e.g. indentation or FT-IR seems to be a promising way to proceed.

Conclusions

In total, over 150 publications have been covered in this minireview, published between 2013 and 2015. Figure 7 summarizes the cited publications according to the different "omics" fields per year. From this it can be clearly seen that within the last two years most efforts were undertaken in the field of metabolomics with strong emphasis on methodology improvements.



In the end the present mini-review represents an attempt to provide a flavor of possible future directions of MALDI MSI in a variety of different "omics" fields to enable the readership to place this emerging technique into perspectives. Since steadily new "omics" areas are emerging, the type of samples as well as compound classes analysed by MALDI MSI will increase. This will consequently lead to the development of new sample preparation techniques, processing steps, as well as new mass spectrometers for MALDI MSI to fulfil the future needs to move this technique from the academic side to industry, e.g. as a potential quality control tool by employing standardized protocols.³⁹ The recent possibility of sharing, exchanging MALDI MSI datasets on a public repository is certainly one-step towards this direction leading to multicentre studies.^{66, 203}

Acknowledgements

The authors regret that space constrains prevented to cite all recent publications related to MALDI MSI. Financial support of the DFG (grand no. EG 102/4-1, EG 102/5-1, and SCHU

1229/15-1), the Thüringer Kultusministerium (grand no. B515-07008), as well as the Ernst-Abbe foundation are acknowledged.

References

- R. M. Caprioli, T. B. Farmer and J. Gile, *Anal. Chem.*, 1997, 69, 4751-4760.
 - B. Spengler, M. Hubert and R. Kaufmann, Proceedings of the 42nd Annual Conference on Mass Spectrometry and Allied Topics, Chicago, IL, 1994.
 - E. Gemperline, S. Rawson and L. Li, *Anal. Chem.*, 2014, 86, 10030-10035.
 - R. J. Goodwin, J Proteomics, 2012, 75, 4893-4911.
 - C. Marsching, R. Jennemann, R. Heilig, H. J. Grone, C. Hopf and R. Sandhoff, *J. Lipid Res.*, 2014, 55, 2343-2353.
 - N. Sun, A. Ly, S. Meding, M. Witting, S. M. Hauck, M. Ueffing, P. Schmitt-Kopplin, M. Aichler and A. Walch, *Proteomics*, 2014, 14, 913-923.
 - R. Shroff, K. Schramm, V. Jeschke, P. Nemes, A. Vertes, J. Gershenzon and A. Svatos, *Plant J*, 2015, 81, 961-972.
 - A. Thomas and P. Chaurand, Bioanalysis, 2014, 6, 967-982.
 - D. M. Anderson, K. A. Floyd, S. Barnes, J. M. Clark, J. I. Clark, H. McHaourab and K. L. Schey, *Anal. Bioanal. Chem.*, 2015, 407, 2311-2320.
 - K. Arafah, R. Longuespee, A. Desmons, O. Kerdraon, I. Fournier and M. Salzet, *Omics*, 2014, 18, 487-498.
- C. Lopez de Laorden, A. Beloqui, L. Yate, J. Calvo, M. Puigivila, J. Llop and N. C. Reichardt, *Anal. Chem.*, 2015, 87, 431-440.
- L. Krasny, O. Benada, M. Strnadova, K. Lemr and V. Havlicek, Anal. Bioanal. Chem., 2015, 407, 2141-2147.
- Y. Li, B. Shrestha and A. Vertes, *Anal. Chem.*, 2008, 80, 407-420.
- 14. B. Spengler, Anal. Chem., 2015, 87, 64-82.
- A. Pirkl, J. Soltwisch, F. Draude and K. Dreisewerd, *Anal. Chem.*, 2012, 84, 5669-5676.
- A. Rompp, K. C. Schafer, S. Guenther, Z. Wang, M. Kostler, A. Leisner, C. Paschke, T. Schramm and B. Spengler, *Anal Bioanal. Chem.*, 2013, 405, 6959-6968.
- 17. M. Nazari and D. C. Muddiman, Anal. Bioanal. Chem., 2015, 407, 2265-2271.
- M. T. Bokhart, E. Rosen, C. Thompson, C. Sykes, A. D. Kashuba and D. C. Muddiman, *Anal. Bioanal. Chem.*, 2015, 407, 2073-2084.
- F. Meier, K. P. Garrard and D. C. Muddiman, *Rapid. Commun.* Mass Spectrom., 2014, 28, 2461-2470.
- C. Eriksson, N. Masaki, I. Yao, T. Hayasaka and M. Setou, *Mass Spectrom. (Tokyo)*, 2013, 2, S0022.
- M. Martin-Lorenzo, B. Balluff, A. Sanz-Maroto, R. J. van Zeijl, F. Vivanco, G. Alvarez-Llamas and L. A. McDonnell, *J Proteomics*, 2014, 108, 465-468.
- M. Strohalm, J. Strohalm, F. Kaftan, L. Krasny, M. Volny, P. Novak, K. Ulbrich and V. Havlicek, *Anal. Chem.*, 2011, 83, 5458-5462.
- A. Thomas, N. H. Patterson, J. Laveaux Charbonneau and P. Chaurand, J. Mass Spectrom., 2013, 48, 42-48.
- B. Enthaler, T. Bussmann, J. K. Pruns, C. Rapp, M. Fischer and J. P. Vietzke, *Rapid Commun. Mass Spectrom.*, 2013, 27, 878-884.
- O. J. Gustafsson, J. S. Eddes, S. Meding, S. R. McColl, M. K. Oehler and P. Hoffmann, *Rapid Commun. Mass Spectrom.*, 2013, 27, 655-670.
- H. C. Diehl, B. Beine, J. Elm, D. Trede, M. Ahrens, M. Eisenacher, K. Marcus, H. E. Meyer and C. Henkel, *Anal. Bioanal. Chem.*, 2015, 407, 2223-2243.
- M. L. Manier, J. M. Spraggins, M. L. Reyzer, J. L. Norris and R. M. Caprioli, *J. Mass Spectrom.*, 2014, 49, 665-673.
- E. Fournaise and P. Chaurand, Anal. Bioanal. Chem., 2015, 407, 2159-2166.
- X. D. Wang, J. Han, J. C. Yang, J. X. Pan and C. H. Borchers, *Chem Sci*, 2015, 6, 729-738.
- 30. R. M. A. Heeren, Int. J. Mass Spectrom., 2015, 377, 672-680.
- M. Stoeckli and D. Staab, J. Am. Soc. Mass Spectrom., 2015, 26, 911-914.
 - A. R. Korte and Y. J. Lee, J. Mass Spectrom., 2014, 49, 737-741.

66.

67.

68.

69.

70.

73.

74.

75.

76.

77.

78.

79

80.

81.

84.

85.

86.

87.

88.

89.

90.

91.

92.

93.

94.

- 1 33. D. R. Bhandari, T. Shen, A. Rompp, H. Zorn and B. Spengler, Anal. 2 Bioanal. Chem., 2014, 406, 695-704. P. Sosnowski, OurCon II 2014 Imaging Mass Spectrometry 3 34. Conference, Antalya, Turkey, 2014. 4 35. A. Ly, C. Schone, M. Becker, J. Rattke, S. Meding, M. Aichler, D. 5 Suckau, A. Walch, S. M. Hauck and M. Ueffing, Histochem. Cell 6 Biol., 2015, 143, 453-462. 7 36. N. H. Patterson, A. Thomas and P. Chaurand, J. Mass Spectrom., 2014, 49, 622-627. 8 37. D. R. Ahlf Wheatcraft, X. Liu and A. B. Hummon, J. Vis. Exp., 9 2014, DOI: 10.3791/52313. 10 38. M. K. Passarelli, J. Wang, A. S. Mohammadi, R. Trouillon, I. Gilmore and A. G. Ewing, Anal. Chem., 2014, 86, 9473-9480. 11 L. A. McDonnell, A. Rompp, B. Balluff, R. M. Heeren, J. P. Albar, 39. 12 P. E. Andren, G. L. Corthals, A. Walch and M. Stoeckli, Anal. 13 Bioanal. Chem., 2015, 407, 2035-2045. 14 J. Kriegsmann, M. Kriegsmann and R. Casadonte, Int. J. Oncol., 40. 2015, 46, 893-906. 15 V. Mainini, M. Lalowski, A. Gotsopoulos, V. Bitsika, M. Baumann 41. 16 and F. Magni, Methods Mol. Biol., 2015, 1243, 139-164. 17 42. K. Gorzolka and A. Walch, Histol. Histopathol., 2014, 29, 1365-18 1376. 43. G. De Sio, A. J. Smith, M. Galli, M. Garancini, C. Chinello, F. 19 Bono, F. Pagni and F. Magni, Mol. Biosyst., 2015, 11, 1507-1514. 20 44. R. J. Goodwin, A. M. Lang, H. Allingham, M. Boren and A. R. Pitt, 21 Proteomics, 2010, 10, 1751-1761. M. M. Gessel, J. L. Norris and R. M. Caprioli, J Proteomics, 2014, 22 45. 107, 71-82. 23 46. J. H. Yang and R. M. Caprioli, J. Mass Spectrom., 2014, 49, 417-24 422. 25 47 M. Aichler and A. Walch, Lab. Invest., 2015, 95, 422-431. 48. P. Chaurand, S. A. Schwartz, D. Billheimer, B. J. Xu, A. Crecelius 26 and R. M. Caprioli, Anal. Chem., 2004, 76, 1145-1155. 27 49 A. C. Crecelius, D. S. Cornett, R. M. Caprioli, B. Williams, B. M. 28 Dawant and B. Bodenheimer, J. Am. Soc. Mass Spectrom., 2005, 29 16, 1093-1099. 50. L. Krasny, F. Hoffmann, G. Ernst, D. Trede, T. Alexandrov, V. 30 Havlicek, O. Guntinas-Lichius, F. von Eggeling and A. C. 31 Crecelius, J. Am. Soc. Mass Spectrom., 2015, 26, 36-43. 32 J. Pol, M. Strohalm, V. Havlicek and M. Volny, Histochem. Cell 51. Biol., 2010, 134, 423-443. 33 52. D. F. Smith, C. Schulz, M. Konijnenburg, M. Kilic and R. M. 34 Heeren, Anal. Bioanal. Chem., 2015, 407, 2321-2327. 35 53. M. Schwartz, B. Meyer, B. Wirnitzer and C. Hopf, Anal. Bioanal. 36 Chem., 2015, 407, 2255-2564. A. D. Palmer, J. Bunch and I. B. Styles, J. Am. Soc. Mass 54. 37 Spectrom., 2015, 26, 315-322. 38 55. F. Tang, Y. Chen, T. G. Li, J. M. He, Z. Abliz, G. Huang and X. H. 39 Wang, Chinese Chem. Lett., 2014, 25, 1331-1335. 40 56. I. Klinkert, K. Chughtai, S. R. Ellis and R. M. A. Heeren, Int. J. Mass Spectrom., 2014, 362, 40-47. 41 57. M. F. Robbe, J. P. Both, B. Prideaux, I. Klinkert, V. Picaud, T. 42 Schramm, A. Hester, V. Guevara, M. Stoeckli, A. Roempp, R. M. 43 A. Heeren, B. Spengler, O. Gal and S. Haan, Eur J Mass Spectrom, 44 2014, 20, 351-360. 58. T. E. Fehniger, F. Suits, A. Vegvari, P. Horvatovich, M. Foster and 45 G. Marko-Varga, Proteomics, 2014, 14, 862-871. 46 E. Patel, L. M. Cole, R. Bradshaw, A. Batubara, C. A. Mitchell, S. 59. 47 Francese and M. R. Clench, Bioanalysis, 2015, 7, 91-101. 48 60. A. Nilsson, R. J. Goodwin, M. Shariatgorji, T. Vallianatou, P. J. Webborn and P. E. Andren, Anal. Chem., 2015, 87, 1437-1455. 49 61. M. Poetzsch, A. E. Steuer, A. T. Roemmelt, M. R. Baumgartner 50 and T. Kraemer, Anal. Chem., 2014, 86, 11758-11765. 51 A. Buck and A. Walch, Bioanalysis, 2014, 6, 1241-1253. 62. C. Paschke, A. Leisner, A. Hester, K. Maass, S. Guenther, W. 63. 52 Bouschen and B. Spengler, J. Am. Soc. Mass Spectrom., 2013, 24, 53 1296-1306. 54 64. G. Robichaud, K. P. Garrard, J. A. Barry and D. C. Muddiman, J. 55 Am. Soc. Mass Spectrom., 2013, 24, 718-721. O. Rubel, A. Greiner, S. Cholia, K. Louie, E. W. Bethel, T. R. 65. 56 Northen and B. P. Bowen, Anal. Chem., 2013, 85, 10354-10361. 57 58
- A. Rompp, R. Wang, J. P. Albar, A. Urbani, H. Hermjakob, B. Spengler and J. A. Vizcaino, *Anal. Bioanal. Chem.*, 2015, 407, 2027-2033.
- R. Ait-Belkacem, C. Berenguer, C. Villard, L. Ouafik, D. Figarella-Branger, O. Chinot and D. Lafitte, *Proteomics*, 2014, 14, 1290-1301.
- D. Taverna, A. C. Pollins, G. Sindona, R. M. Caprioli and L. B. Nanney, *J. Proteome Res.*, 2015, 14, 986-996.
- J. Yang, A. Zavalin and R. M. Caprioli, 62th ASMS Conference on Mass Spectrometry and Allied Topics, Baltimore, U.S.A., 2014.
- A. Zavalin, J. Yang, K. Hayden, M. Vestal and R. M. Caprioli, Anal. Bioanal. Chem., 2015, 407, 2337-2342.
- B. Cillero-Pastor, G. B. Eijkel, F. J. Blanco and R. M. Heeren, *Anal. Bioanal. Chem.*, 2014, 407, 2213-2222.
- O. Klein, K. Strohschein, G. Nebrich, J. Oetjen, D. Trede, H. Thiele, T. Alexandrov, P. Giavalisco, G. N. Duda, P. von Roth, S. Geissler, J. Klose and T. Winkler, *Proteomics*, 2014, 14, 2249-2260.
 - B. Heijs, R. J. Carreira, E. A. Tolner, A. H. de Ru, A. M. van den Maagdenberg, P. A. van Veelen and L. A. McDonnell, *Anal. Chem.*, 2015, 87, 1867-1875.
 - S. M. Hong, M. Tanaka, S. Yoshii, Y. Mine and T. Matsui, *Anal. Chem.*, 2013, 85, 10033-10039.
 - H. Ye, L. Hui, K. Kellersberger and L. Li, J. Am. Soc. Mass Spectrom., 2013, 24, 134-147.
 - R. Chen, C. Ouyang, M. Xiao and L. Li, *Rapid Commun. Mass Spectrom.*, 2014, 28, 2437-2444.
 - M. Pratavieira, A. R. da Silva Menegasso, A. M. Garcia, D. S. Dos Santos, P. C. Gomes, O. Malaspina and M. S. Palma, *J. Proteome Res.*, 2014, 13, 3054-3064.
 - D. A. Stoyanovsky, L. J. Sparvero, A. A. Amoscato, R. R. He, S. Watkins, B. R. Pitt, H. Bayir and V. E. Kagan, *Rapid Commun. Mass Spectrom.*, 2014, 28, 403-412.
 - L. Kuchar, H. Faltyskova, L. Krasny, R. Dobrovolny, H. Hulkova, J. Ledvinova, M. Volny, M. Strohalm, K. Lemr, L. Kryspinova, B. Asfaw, J. Rybova, R. J. Desnick and V. Havlicek, *Anal. Bioanal. Chem.*, 2015, 407, 2283-2291.
 - R. Mirnezami, K. Spagou, P. A. Vorkas, M. R. Lewis, J. Kinross,
 E. Want, H. Shion, R. D. Goldin, A. Darzi, Z. Takats, E. Holmes,
 O. Cloarec and J. K. Nicholson, *Mol. Oncol.*, 2014, 8, 39-49.
 - E. S. Park, J. H. Lee, J. H. Hong, Y. K. Park, J. W. Lee, W. J. Lee, J. W. Lee, K. P. Kim and K. H. Kim, *PLoS One*, 2014, 9, e103955.
- D. M. Anderson, Z. Ablonczy, Y. Koutalos, J. Spraggins, R. K. Crouch, R. M. Caprioli and K. L. Schey, J. Am. Soc. Mass Spectrom., 2014, 25, 1394-1403.
 L. Jadoul, R. Longuespee, A. Noel and E. De Pauw, Anal. Bioanal.
 - L. Jadoul, R. Longuespee, A. Noel and E. De Pauw, *Anal. Bioanal. Chem.*, 2015, 407, 2095-2106.
 - A. Thomas, J. L. Charbonneau, E. Fournaise and P. Chaurand, Anal. Chem., 2012, 84, 2048-2054.
 - S. Guo, Y. M. Wang, D. Zhou and Z. L. Li, *Sci. Rep.*, 2014, 4, 5959.
 X. Wang, J. Han, J. Pan and C. H. Borchers, *Anal. Chem.*, 2014, 86, 638-646.
 - S. Francese, R. Bradshaw, B. Flinders, C. Mitchell, S. Bleay, L. Cicero and M. R. Clench, *Anal. Chem.*, 2013, 85, 5240-5248.
 - H. Kettling, S. Vens-Cappell, J. Soltwisch, A. Pirkl, J. Haier, J. Muthing and K. Dreisewerd, *Anal. Chem.*, 2014, 86, 7798-7805.
 - S. N. Jackson, K. Baldwin, L. Muller, V. M. Womack, J. A. Schultz, C. Balaban and A. S. Woods, *Anal. Bioanal. Chem.*, 2014, 406, 1377-1386.
 - H. H. Liu, R. Chen, J. Y. Wang, S. M. Chen, C. Q. Xiong, J. N. Wang, J. Hou, Q. He, N. Zhang, Z. X. Nie and L. Q. Mao, *Anal. Chem.*, 2014, 86, 10114-10121.
 - A. Fulop, M. B. Porada, C. Marsching, H. Blott, B. Meyer, S. Tambe, R. Sandhoff, H. D. Junker and C. Hopf, *Anal. Chem.*, 2013, 85, 9156-9163.
 - J. Wang, S. Qiu, S. Chen, C. Xiong, H. Liu, J. Wang, N. Zhang, J. Hou, Q. He and Z. Nie, *Anal. Chem.*, 2015, 87, 422-430.
 - M. Dufresne, A. Thomas, J. Breault-Turcot, J. F. Masson and P. Chaurand, *Anal. Chem.*, 2013, 85, 3318-3324.
 - T. W. Powers, E. E. Jones, L. R. Betesh, P. R. Romano, P. Gao, J.
 A. Copland, A. S. Mehta and R. R. Drake, *Anal. Chem.*, 2013, 85, 9799-9806.

59 60

2

3

4

5

6

7

8

9

28

29

59 60

- H. Ye, E. Gemperline, M. Venkateshwaran, R. B. Chen, P. M. Delaux, M. Howes-Podoll, J. M. Ane and L. J. Li, *Plant J*, 2013, 75, 130-145.
- 97. N. Rudolph-Mohr, S. Gottfried, M. Lamshöft, S. Zühlke, S. E. Oswald and M. Spiteller, *Geoderma*, 2015, 239–240, 257-264.
- 98. A. Berisha, S. Dold, S. Guenther, N. Desbenoit, Z. Takats, B. Spengler and A. Rompp, *Rapid Commun. Mass Spectrom.*, 2014, 28, 1779-1791.
- 99. M. S. Soares, D. F. da Silva, M. R. Forim, M. F. da Silva, J. B.
 Fernandes, P. C. Vieira, D. B. Silva, N. P. Lopes, S. A. de Carvalho,
 A. A. de Souza and M. A. Machado, *Phytochemistry*, 2015, 115, 161-170.
 100 P. Araujo, M. S. Ferreira, D. N. de Oliveira, L. Pereira, A. C.
- 13 100. P. Araujo, M. S. Ferreira, D. N. de Oliveira, L. Pereira, A. C.
 14 Sawaya, R. R. Catharino and P. Mazzafera, *Anal. Chem.*, 2014, 86, 3415-3419.
- 101. M. Bencivenni, A. Faccini, R. Zecchi, F. Boscaro, G. Moneti, A. Dossena and S. Sforza, *J. Mass Spectrom.*, 2014, 49, 1264-1271.
- 17 102. D. Hölscher, T. Hoffmann, B. Schneider, T. C. Fischer, H. Flachowsky, W. Schwab, U. S. Schubert and A. C. Crecelius, unpublished work.
- 103. D. N. de Oliveira, S. de Bona Sartor, M. S. Ferreira and R. R. Catharino, *Materials*, 2013, 6, 1000-1010.
 21 104. S. M. Frohlich, V. M. Archodoulaki, G. Allmaier and M. Marchetti-
- 21104.S. M. Frohlich, V. M. Archodoulaki, G. Allmaier and M. Marchetti-22Deschmann, Anal. Chem., 2014, 86, 9723-9732.
- 105. K. Krueger, C. Terne, C. Werner, U. Freudenberg, V. Jankowski, W. Zidek and J. Jankowski, *Anal. Chem.*, 2013, 85, 4998-5004.
- 24 106. J. J. Nicklay, G. A. Harris, K. L. Schey and R. M. Caprioli, *Anal. Chem.*, 2013, 85, 7191-7196.
- 26 107. D. Taverna, F. Boraldi, G. De Santis, R. M. Caprioli and D. Quaglino, *Bone*, 2015, 74C, 83-94.
 27 108 R. Gillera Basta and P. M. Harran, J. Partagua, Pag. 2014, 13.
 - 108. B. Cillero-Pastor and R. M. Heeren, *J. Proteome Res.*, 2014, 13, 325-335.
 - 109. S. Meding, K. Martin, O. J. Gustafsson, J. S. Eddes, S. Hack, M. K. Oehler and P. Hoffmann, *J. Proteome Res.*, 2013, 12, 308-315.
- 30
 Oehler and P. Hoffmann, J. Proteome Res., 2013, 12, 308-315.

 31
 110.
 E. E. Jones, T. W. Powers, B. A. Neely, L. H. Cazares, D. A. Troyer, A. S. Parker and R. R. Drake, Proteomics, 2014, 14, 924-935.

 33
 111.
 C. Marquardt, T. Tolstik, C. Bielecki, R. Kaufmann, A. C.
- 111. C. Marquardt, T. Tolstik, C. Bielecki, R. Kaufmann, A. C. Crecelius, U. S. Schubert, U. Settmacher, A. Stallmach and O. Dirsch, Z. Gastroenterol., 2015, 53, 33-39.
- 35 112.
 36 37 J12.
 37 J12.
 36 J13.
 37 J12.
 36 J13.
 37 J12.
 37 J12.
 37 J12.
 38 J12.
 38 J12.
 39 J12.
 30 J12.
 31 J12.
 32 J12.
 33 J12.
 34 J2.
 35 J12.
 35 J13.
 36 J12.
 37 J12.
- 113.
 B. Flatley, P. Malone and R. Cramer, *Biochim. Biophys. Acta*, 2014, 1844, 940-949.
- 114. V. Rebours, J. Le Faouder, S. Laouirem, M. Mebarki, M. Albuquerque, J. M. Camadro, T. Leger, P. Ruszniewski, P. Levy, V. Paradis, P. Bedossa and A. Couvelard, *Pancreatology*, 2014, 14, 117-124.
 115. C. Erret, O. Cuptings Lighting L. Hauberg Lette, D. Trede, M.
- 42115.G. Ernst, O. Guntinas-Lichius, L. Hauberg-Lotte, D. Trede, M.43Becker, T. Alexandrov and F. von Eggeling, *Head & Neck*, 2014,44DOI: 10.1002/hed.23713.
- 45 116. B. Balluff, C. K. Frese, S. K. Maier, C. Schone, B. Kuster, M. Schmitt, M. Aubele, H. Hofler, A. M. Deelder, A. J. Heck, P. C. Hogendoorn, J. Morreau, A. Maarten Altelaar, A. Walch and L. A. McDonnell, *J. Pathol.*, 2015, 235, 3-13.
- 48 117. M. J. Peffers, B. Cillero-Pastor, G. B. Eijkel, P. D. Clegg and R. M. Heeren, *Arthritis Res. Ther.*, 2014, 16, R110.
- 118.
 J. Hanrieder, N. T. Phan, M. E. Kurczy and A. G. Ewing, ACS

 50
 Chem. Neurosci., 2013, 4, 666-679.
- 51
 119.
 J. Hanrieder, P. Malmberg and A. G. Ewing, *Biochim Biophys.*

 52
 Acta, 2015, 1854, 718-731.

 120
 Interface
 Interface
- 120. J. Hanrieder, T. Ekegren, M. Andersson and J. Bergquist, J. Neurochem., 2013, 124, 695-707.
 54 121 F. Acquadro I. Caron M. Tortarolo F. M. Bucci, C. Bendotti and C. Be
- 54121.E. Acquadro, I. Caron, M. Tortarolo, E. M. Bucci, C. Bendotti and55D. Corpillo, J. Proteome Res., 2014, 13, 1800-1809.56122K. Skold, M. Svensson, A. Nilsson, X. Zhang, K. Nydahl, R. M.
- 56 122. K. Skold, M. Svensson, A. Nilsson, X. Zhang, K. Nydahl, R. M. Caprioli, P. Svenningsson and P. E. Andren, J. Proteome Res., 2006, 5, 262-269.

- M. Lagarrigue, T. Alexandrov, G. Dieuset, A. Perrin, R. Lavigne, S. Baulac, H. Thiele, B. Martin and C. Pineau, *J. Proteome Res.*, 2012, 11, 5453-5463.
- 124. G. A. Harris, J. J. Nicklay and R. M. Caprioli, *Anal. Chem.*, 2013, 85, 2717-2723.
- S. K. Maier, H. Hahne, A. M. Gholami, B. Balluff, S. Meding, C. Schoene, A. K. Walch and B. Kuster, *Mol. Cell. Proteomics*, 2013, 12, 2901-2910.
- L. A. McDonnell, A. Walch, M. Stoeckli and G. L. Corthals, J. Proteome Res., 2014, 13, 1138-1142.
- 127. J. Hanrieder, P. Malmberg and A. G. Ewing, *Biochim. Biophys. Acta*, 2015, 1854, 718-731.
- 128. J. Hanrieder, A. Ljungdahl, M. Falth, S. E. Mammo, J. Bergquist and M. Andersson, *Mol. Cell. Proteomics*, 2011, 10, M111.009308.
- 129. A. Ljungdahl, J. Hanrieder, M. Falth, J. Bergquist and M. Andersson, *PLoS One*, 2011, 6, e25653.
- M. Stoeckli, D. Staab, M. Staufenbiel, K. H. Wiederhold and L. Signor, *Anal. Biochem.*, 2002, 311, 33-39.
- M. Stoeckli, R. Knochenmuss, G. McCombie, D. Mueller, T. Rohner, D. Staab and K. H. Wiederhold, *Methods Enzymol.*, 2006, 412, 94-106.
- Y. Arribat, Y. Talmat-Amar, A. Paucard, P. Lesport, N. Bonneaud, C. Bauer, N. Bec, M. L. Parmentier, L. Benigno, C. Larroque, P. Maurel and F. Maschat, *Acta Neuropathol. Commun.*, 2014, 2, 86.
- 134. L. Minerva, K. Boonen, G. Menschaert, B. Landuyt, G. Baggerman and L. Arckens, *Anal. Chem.*, 2011, 83, 7682-7691.
- 135. D. Bonnel, J. Franck, C. Meriaux, M. Salzet and I. Fournier, *Anal. Biochem.*, 2013, 434, 187-198.
- R. M. Sturm, T. Greer, R. Chen, B. Hensen and L. Li, *Anal. Methods*, 2013, 5, 1623-1628.
- 137. D. Gode and D. A. Volmer, *Analyst*, 2013, 138, 1289-1315.
- 138. S. R. Ellis, S. H. Brown, M. In Het Panhuis, S. J. Blanksby and T. W. Mitchell, *Prog. Lipid Res.*, 2013, 52, 329-353.
- 139. Y. Fujimura and D. Miura, *Metabolites*, 2014, 4, 319-346.
- T. J. Dekker, E. A. Jones, W. E. Corver, R. J. van Zeijl, A. M. Deelder, R. A. Tollenaar, W. E. Mesker, H. Morreau and L. A. McDonnell, *Anal. Bioanal. Chem.*, 2015, 407, 2167-2176.
- 141. A. Z. Fernandis and M. R. Wenk, *J. Chromatogr. B*, 2009, 877, 2830-2835.
- 142. Y. Uchiyama, T. Hayasaka, N. Masaki, Y. Watanabe, K. Masumoto, T. Nagata, F. Katou and M. Setou, *Anal. Bioanal. Chem.*, 2014, 406, 1307-1316.
- J. Cimino, D. Calligaris, J. Far, D. Debois, S. Blacher, N. E. Sounni,
 A. Noel and E. De Pauw, *Int. J. Mol. Sci.*, 2013, 14, 24560-24580.
- R. Fernandez, S. Lage, B. Abad-Garcia, G. Barcelo-Coblijn, S. Teres, D. H. Lopez, F. Guardiola-Serrano, M. L. Martin, P. V. Escriba and J. A. Fernandez, *J. Am. Soc. Mass Spectrom.*, 2014, 25, 1237-1246.
- 145. W. M. Abdelmoula, K. Skraskova, B. Balluff, R. J. Carreira, E. A. Tolner, B. P. Lelieveldt, L. van der Maaten, H. Morreau, A. M. van den Maagdenberg, R. M. Heeren, L. A. McDonnell and J. Dijkstra, *Anal. Chem.*, 2014, 86, 9204-9211.
- 146. N. Verbeeck, J. Yang, B. De Moor, R. M. Caprioli, E. Waelkens and R. Van de Plas, *Anal. Chem.*, 2014, 86, 8974-8982.
- 147. R. Van de Plas, J. Yang, J. Spraggins and R. M. Caprioli, *Nat. Methods*, 2015, 12, 366-372.
- 148. J. Castro-Perez, N. Hatcher, N. Kofi Karikari, S. P. Wang, V. Mendoza, H. Shion, A. Millar, J. Shockcor, M. Towers, D. McLaren, V. Shah, S. Previs, K. Akinsanya, M. Cleary, T. P. Roddy and D. G. Johns, *Rapid Commun. Mass Spectrom.*, 2014, 28, 2471-2479.
- H. Hirano, N. Masaki, T. Hayasaka, Y. Watanabe, K. Masumoto, T. Nagata, F. Katou and M. Setou, *Anal. Bioanal. Chem.*, 2014, 406, 1355-1363.
- D. Yuki, Y. Sugiura, N. Zaima, H. Akatsu, S. Takei, I. Yao, M. Maesako, A. Kinoshita, T. Yamamoto, R. Kon, K. Sugiyama and M. Setou, *Sci. Rep.*, 2014, 4, 7130.
- D. Yuki, Y. Sugiura, N. Zaima, H. Akatsu, Y. Hashizume, T. Yamamoto, M. Fujiwara, K. Sugiyama and M. Setou, *Neuroscience*, 2011, 193, 44-53.

2

3

4

5

6

7

8

9

10

11

12

13

14

15

16

17

18

19

20

21

22

23

24

25

26

27

28

29

30

37

58

59 60 Analyst

- M. Shariatgorji, P. Svenningsson and P. E. Andren, *Neuropsychopharmacology.*, 2014, 39, 34-49.
 Y. Sugiura, R. Taguchi and M. Setou, *PLoS One*, 2011, 6, e17952.
 J. A. Hankin, S. E. Farias, R. M. Barkley, K. Heidenreich, L. C. Frey, K. Hamazaki, H. Y. Kim and R. C. Murphy, *J. Am. Soc. Mass*
- Spectrom., 2011, 22, 1014-1021.
 J. Matsumoto, Y. Sugiura, D. Yuki, T. Hayasaka, N. Goto-Inoue, N. Zaima, Y. Kunii, A. Wada, Q. Yang, K. Nishiura, H. Akatsu, A. Hori, Y. Hashizume, T. Yamamoto, K. Ikemoto, M. Setou and S. Niwa, Anal. Bioanal. Chem., 2011, 400, 1933-1943.
- 156. L. J. Sparvero, A. A. Amoscato, C. E. Dixon, J. B. Long, P. M. Kochanek, B. R. Pitt, H. Bayir and V. E. Kagan, *Chem. Phys. Lipids*, 2012, 165, 545-562.
- 157. E. E. Jones, S. Dworski, D. Canals, J. Casas, G. Fabrias, D. Schoenling, T. Levade, C. Denlinger, Y. A. Hannun, J. A. Medin and R. R. Drake, *Anal. Chem.*, 2014, 86, 8303-8311.
- A. Roux, L. Muller, S. N. Jackson, K. Baldwin, V. Womack, J. G. Pagiazitis, J. R. O'Rourke, P. K. Thanos, C. Balaban, J. A. Schultz, N. D. Volkow and A. S. Woods, ACS Chem. Neurosci., 2015, 6, 247-259.
- A. S. Woods, B. Colsch, S. N. Jackson, J. Post, K. Baldwin, A. Roux, B. Hoffer, B. M. Cox, M. Hoffer, V. Rubovitch, C. G. Pick, J. A. Schultz and C. Balaban, ACS Chem. Neurosci., 2013, 4, 594-600.
- 160. J. Soltwisch, H. Kettling, S. Vens-Cappell, M. Wiegelmann, J. Muthing and K. Dreisewerd, *Science*, 2015, 348, 211-215.
- 161. D. M. Anderson, D. Mills, J. Spraggins, W. S. Lambert, D. J. Calkins and K. L. Schey, *Mol. Vis.*, 2013, 19, 581-592.
- A. Thomas, N. H. Patterson, M. M. Marcinkiewicz, A. Lazaris, P. Metrakos and P. Chaurand, *Anal. Chem.*, 2013, 85, 2860-2866.
- S. N. Jackson, D. Barbacci, T. Egan, E. K. Lewis, J. A. Schultz and A. S. Woods, *Anal. Methods*, 2014, 6, 5001-5007.
- L. Muller, A. Kailas, S. N. Jackson, A. Roux, D. C. Barbacci, J. A. Schultz, C. D. Balaban and A. S. Woods, *Kidney Int.*, 2015, DOI: 10.1038/ki.2015.3.
- B. Rocha, B. Cillero-Pastor, G. Eijkel, A. L. Bruinen, C. Ruiz-Romero, R. M. Heeren and F. J. Blanco, *Proteomics*, 2015, 15, 702-713.
- 31
 166.
 R. Masyuko, E. J. Lanni, J. V. Sweedler and P. W. Bohn, Analyst, 2013, 138, 1924-1939.
- 33
 167.
 R. N. Masyuko, E. J. Lanni, C. M. Driscoll, J. D. Shrout, J. V.

 34
 Sweedler and P. W. Bohn, *Analyst*, 2014, 139, 5700-5708.
- 34
 168.
 D. R. Ahlf, R. N. Masyuko, A. B. Hummon and P. W. Bohn, Analyst, 2014, 139, 4578-4585.

 36
 169.
 T. W. Bocklitz, A. C. Crecelius, C. Matthaus, N. Tarcea, F. von
 - T. W. Bocklitz, A. C. Crecelius, C. Matthaus, N. Tarcea, F. von Eggeling, M. Schmitt, U. S. Schubert and J. Popp, *Anal. Chem.*, 2013, 85, 10829-10834.
- 38
 2013, 83, 1029-10834.

 39
 170.
 E. J. Lanni, S. J. Dunham, P. Nemes, S. S. Rubakhin and J. V. Sweedler, J. Am. Soc. Mass Spectrom., 2014, 25, 1897-1907.
- 40171.M. Lorenz, O. S. Ovchinnikova, V. Kertesz and G. J. Van Berkel,41Rapid Commun. Mass Spectrom., 2013, 27, 1429-1436.
- 172.F. Kaftan, V. Vrkoslav, P. Kynast, P. Kulkarni, S. Bocker, J.
Cvacka, M. Knaden and A. Svatos, J. Mass Spectrom., 2014, 49,
223-232.
- 44
 173.
 A. C. Niehoff, H. Kettling, A. Pirkl, Y. N. Chiang, K. Dreisewerd

 45
 and J. Y. Yew, *Anal. Chem.*, 2014, 86, 11086-11092.
- 46174.D. R. Bhandari, M. Schott, A. Rompp, A. Vilcinskas and B.
Spengler, Anal. Bioanal. Chem., 2015, 407, 2189-2201.
- 47
 175.
 S. R. Ellis, A. L. Bruinen and R. M. A. Heeren, Anal. Bioanal. Chem., 2014, 406, 1275-1289.
- 49
 176.
 T. Porta, A. Lesur, E. Varesio and G. Hopfgartner, Anal. Bioanal. Chem., 2015, 407, 2177-2187.

 50
 177
 177
- 178.
 178.
 178.
 178.
 178.
 178.
 178.
 179.
 179.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.
 170.</l
- 55 179. S. Toue, Y. Sugiura, A. Kubo, M. Ohmura, S. Karakawa, T. Mizukoshi, J. Yoneda, H. Miyano, Y. Noguchi, T. Kobayashi, Y. Kabe and M. Suematsu, *Proteomics*, 2014, 14, 810-819.
 57 180. B. Elinders, L. Morrall, P. S. Marshell, L. E. Banchew, and M. P.
 - 180. B. Flinders, J. Morrell, P. S. Marshall, L. E. Ranshaw and M. R. Clench, *Anal. Bioanal. Chem.*, 2015, 407, 2085-2094.

- S. Francese, R. Bradshaw, L. S. Ferguson, R. Wolstenholme, M. R. Clench and S. Bleay, *Analyst*, 2013, 138, 4215-4228.
- B. L. Walton and G. F. Verbeck, Anal. Chem., 2014, 86, 8114-8120.
 X. Tang, L. Huerg, W. Zing, and Y. Tang, J. Huerg, W. Zing, and Y. Tang, J. Huerg, W. Zing, and Y. Tang, an
- 184. D. Kolarich, B. Lepenies and P. H. Seeberger, *Curr Opin Chem Biol*, 2012, 16, 214-220.
 185. T. W. D. L. S. M. C. M. S. M.
- 186. S. Toghi Eshghi, S. Yang, X. Wang, P. Shah, X. Li and H. Zhang, ACS Chem Biol, 2014, 9, 2149-2156.
 187. D. L. Harris, C. N. Yang, C. Yu, and T. J. Shah, X. Li and H. Zhang, ACS Chem Biol, 2014, 9, 2149-2156.
- P. J. Horn, C. N. James, S. K. Gidda, A. Kilaru, J. M. Dyer, R. T. Mullen, J. B. Ohlrogge and K. D. Chapman, *Plant Physiol.*, 2013, 162, 1926-1936.
- S. M. Puolitaival, K. E. Burnum, D. S. Cornett and R. M. Caprioli, J. Am. Soc. Mass Spectrom., 2008, 19, 882-886.
- 189. D. Holscher, S. Dhakshinamoorthy, T. Alexandrov, M. Becker, T. Bretschneider, A. Buerkert, A. C. Crecelius, D. De Waele, A. Elsen, D. G. Heckel, H. Heklau, C. Hertweck, M. Kai, K. Knop, C. Krafft, R. K. Maddula, C. Matthaus, J. Popp, B. Schneider, U. S. Schubert, R. A. Sikora, A. Svatos and R. L. Swennen, *Proc. Natl. Acad. Sci. USA*, 2014, 111, 105-110.
- N. Bjarnholt, B. Li, J. D'Alvise and C. Janfelt, *Nat. Prod. Rep.*, 2014, 31, 818-837.
- 191. F. Capozzi and A. Bordoni, *Genes Nutr.*, 2013, 8, 1-4.
- M. Peukert, A. Matros, G. Lattanzio, S. Kaspar, J. Abadia and H. P. Mock, *New Phytol.*, 2012, 193, 806-815.
- 193. Y. Yoshimura, H. Enomoto, T. Moriyama, Y. Kawamura, M. Setou and N. Zaima, *Anal. Bioanal. Chem.*, 2012, 403, 1885-1895.
- P. Franceschi, Y. Dong, K. Strupat, U. Vrhovsek and F. Mattivi, J. *Exp. Bot.*, 2012, 63, 1123-1133.
- 195. E. Handberg, K. Chingin, N. Wang, X. Dai and H. Chen, *Mass Spectrom. Rev.*, 2014, DOI: 10.1002/mas.21424.
- 196. X. L. Zhang, N. N. Wang, Y. F. Zhou, Y. Liu, J. H. Zhang and H. W. Chen, *Anal. Methods*, 2013, 5, 311-315.
- 197. B. Enthaler, M. Trusch, M. Fischer, C. Rapp, J. K. Pruns and J. P. Vietzke, *Anal. Bioanal. Chem.*, 2013, 405, 1159-1170.
- A. Mess, B. Enthaler, M. Fischer, C. Rapp, J. K. Pruns and J. P. Vietzke, *Talanta*, 2013, 103, 398-402.
- B. Enthaler, J. K. Pruns, S. Wessel, C. Rapp, M. Fischer and K. P. Wittern, *Anal. Bioanal. Chem.*, 2012, 402, 1159-1167.
- 200. E. Altuntas and U. S. Schubert, *Anal. Chim. Acta*, 2014, 808, 56-69.
- 201. A. C. Crecelius, J. Vitz and U. S. Schubert, *Anal. Chim. Acta*, 2014, 808, 10-17.
- A. C. Crecelius, R. Steinacker, A. Meier, T. Alexandrov, J. Vitz and U. S. Schubert, *Anal. Chem.*, 2012, 84, 6921-6925.
- 203. A. Rompp, J. P. Both, A. Brunelle, R. M. Heeren, O. Laprevote, B. Prideaux, A. Seyer, B. Spengler, M. Stoeckli and D. F. Smith, *Anal. Bioanal. Chem.*, 2015, 407, 2329-2335.