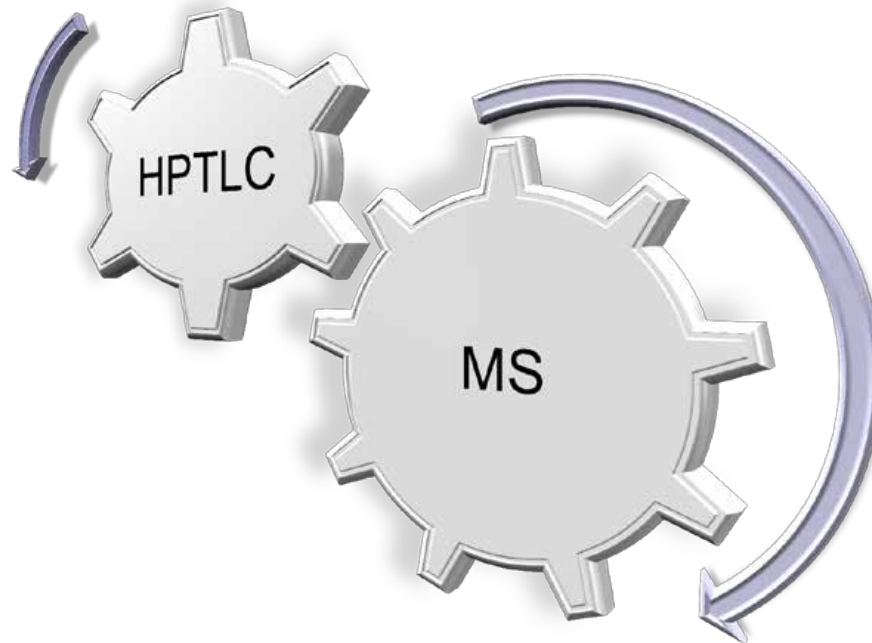


HPTLC-MS

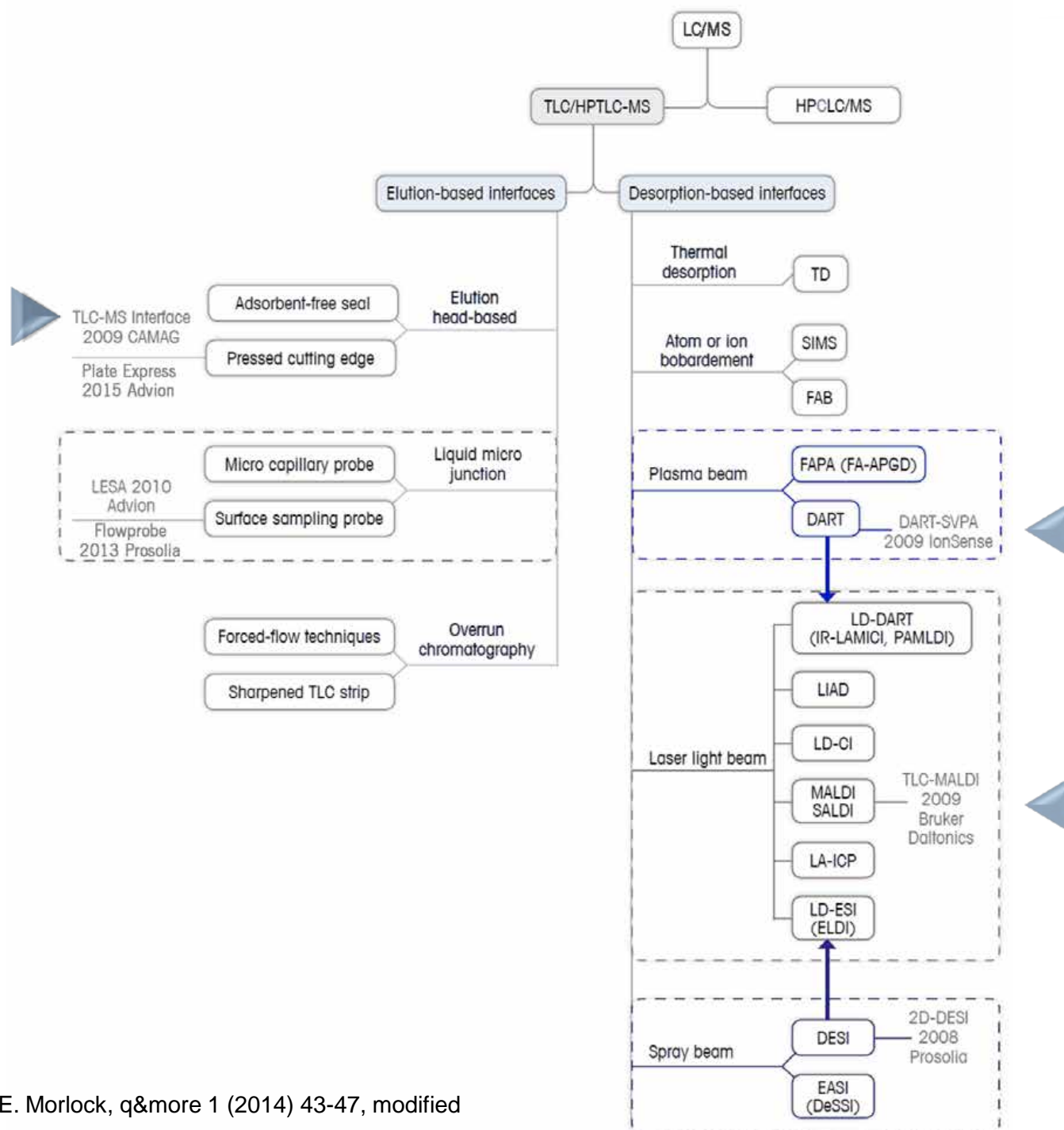
Overview, quantitation and comparison



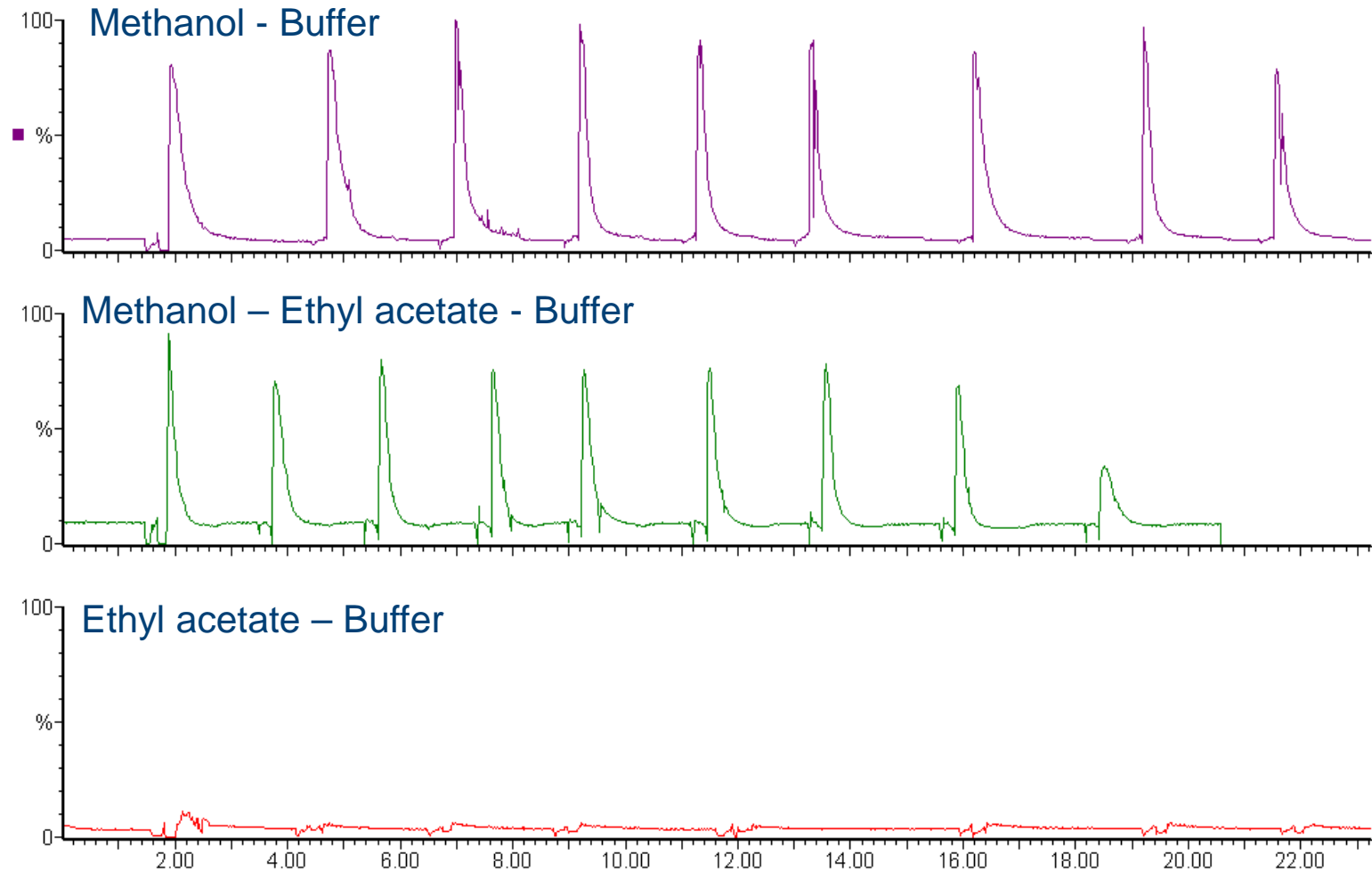
Gertrud Morlock, Chair of Food Science



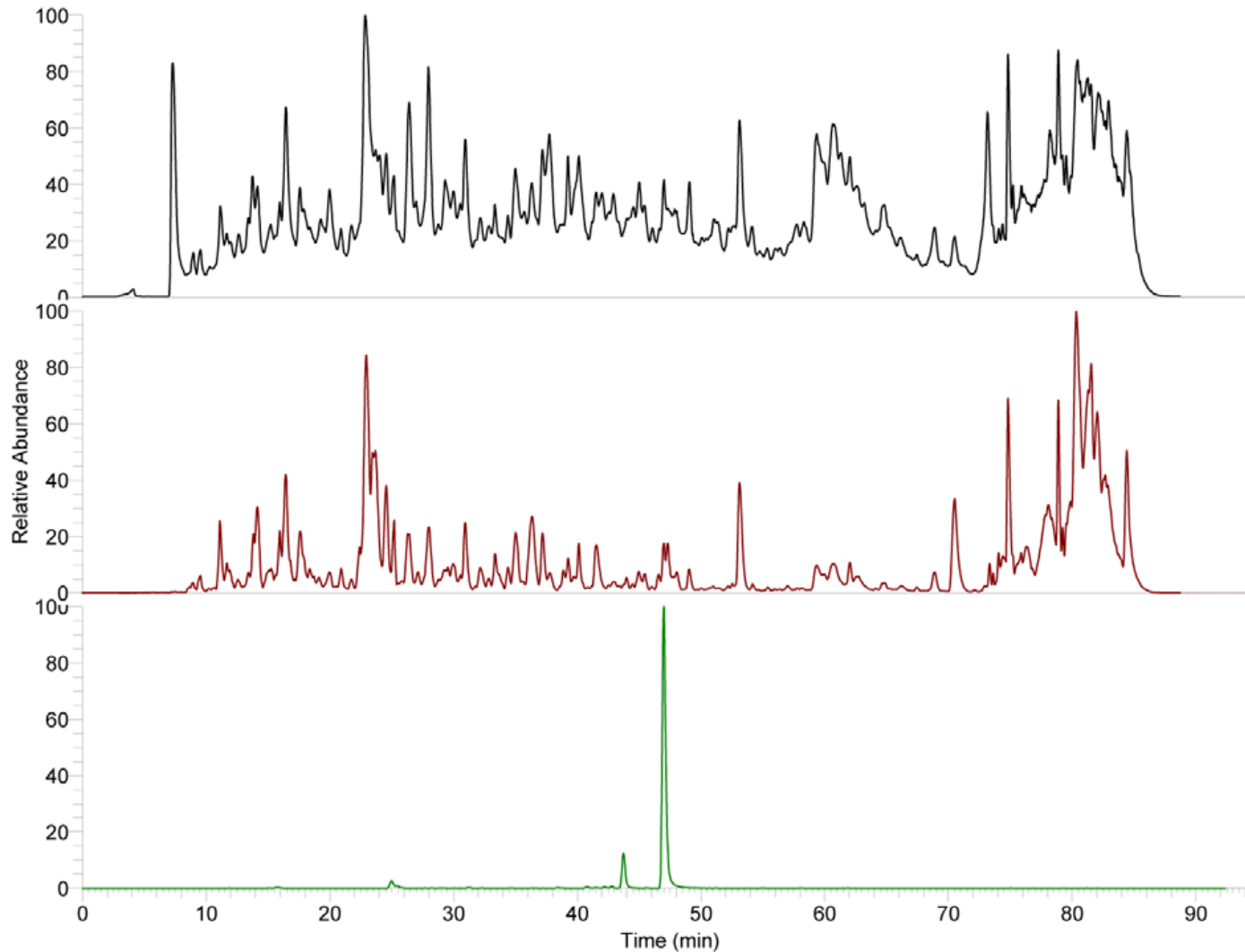
Justus Liebig University Giessen



Solubility *versus* elution power



MS chromatograms → chronograms



Total Ion
Chromatogram
(TIC)

Generated by
summing the intensity of
all peaks in each mass
spectrum and graphing
this sum over time

Base Peak
Chromatogram

Generated by
graphing the intensity
of the base peak in each
spectrum over time

Less noise
More contrast

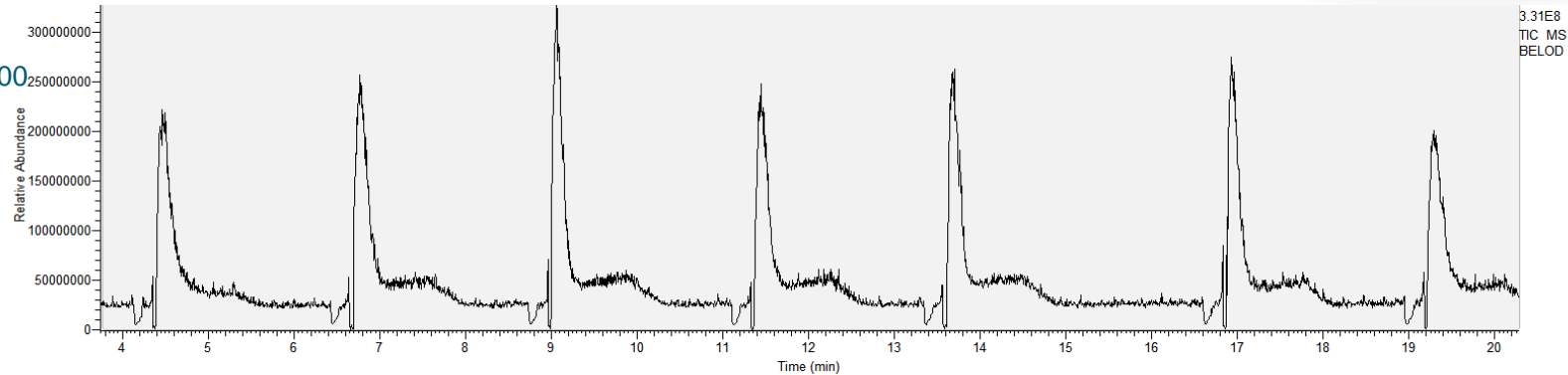
Extracted Ion
Chromatogram
 $m/z = 704.36$
 ± 10 ppm

Generated by
graphing the intensity
of a specific m/z range
over time

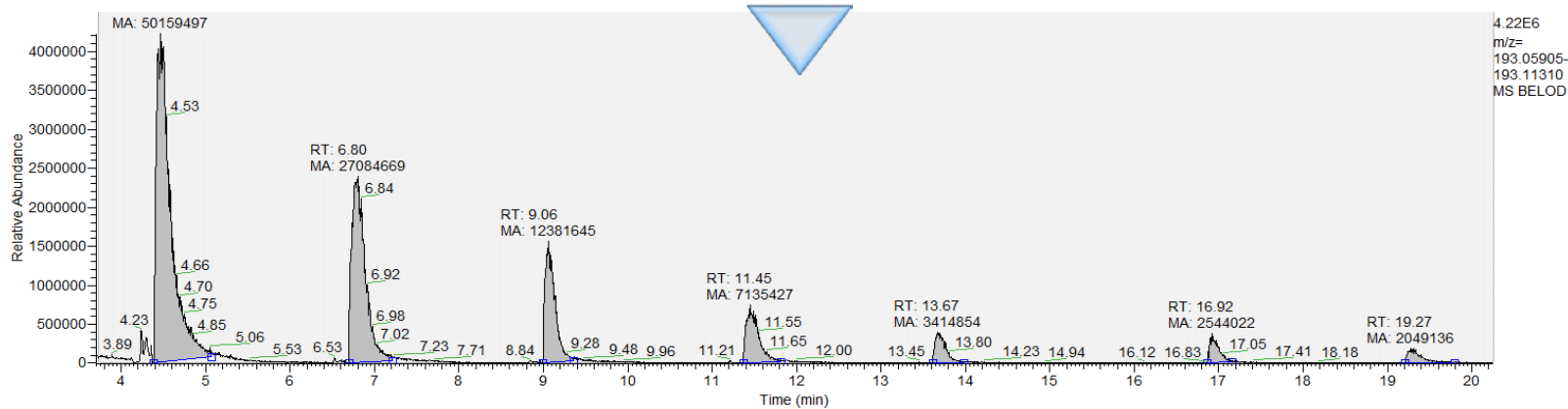
HPTLC-HRMS (Q Exactive plus)

TIC

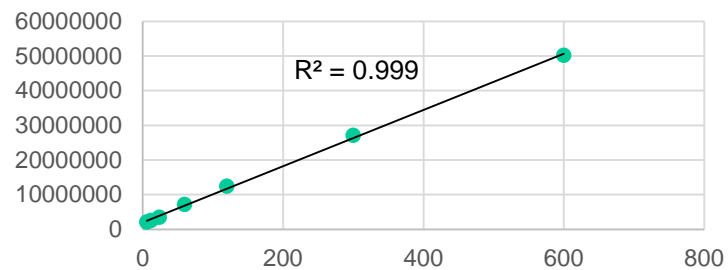
m/z 100-400



EIC

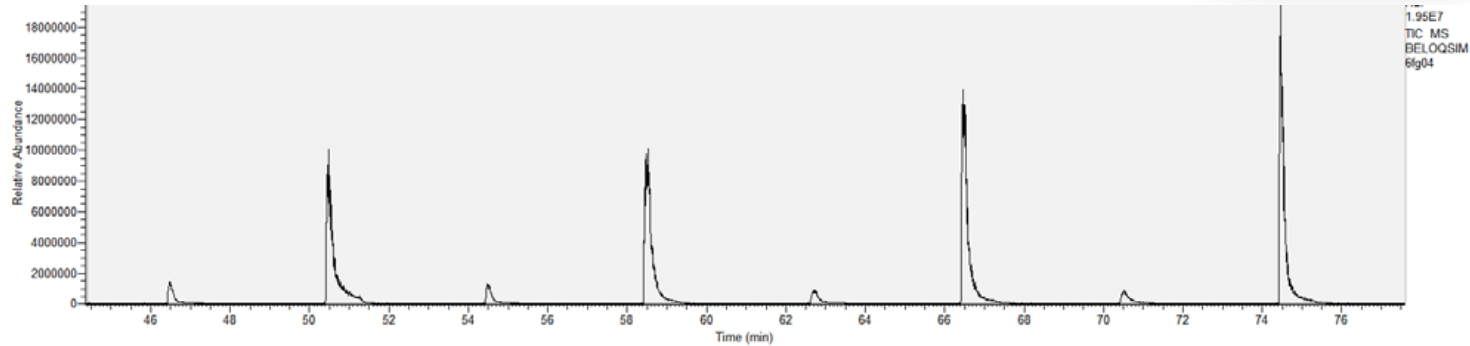


600 - 6 pg/band

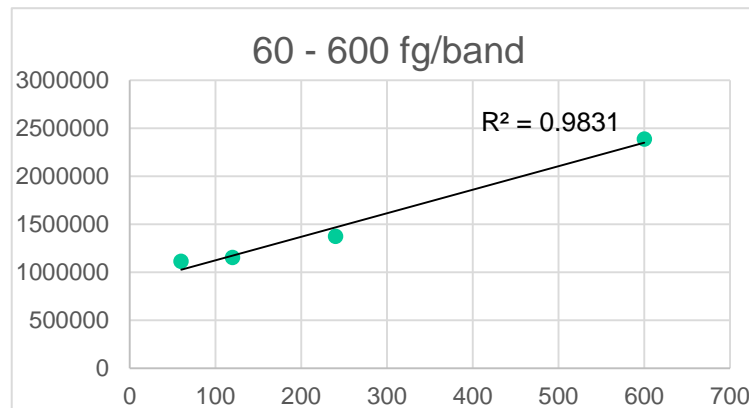
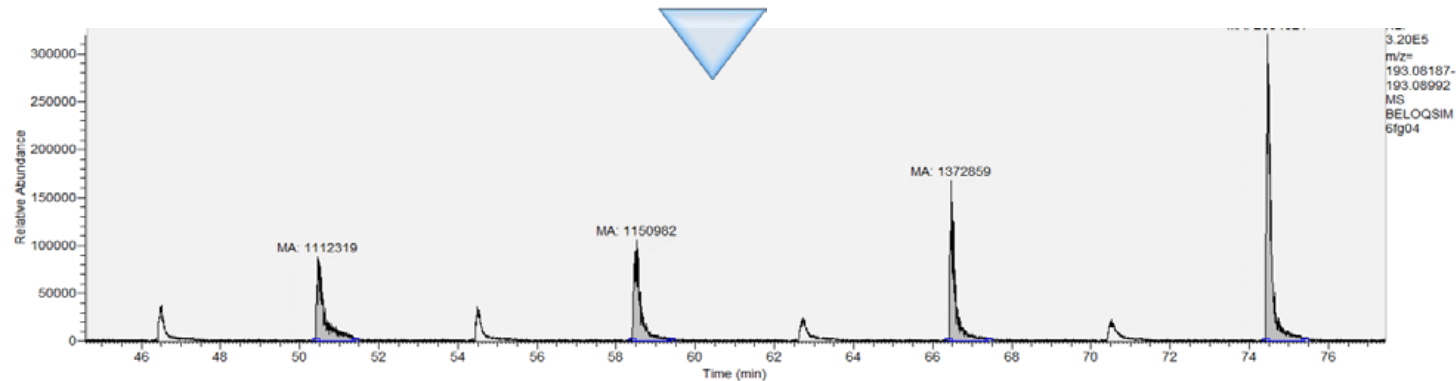


HPTLC-HRMS (Q Exactive plus)

SIM
 m/z 193.0861
 $\pm m/z$ 1.0



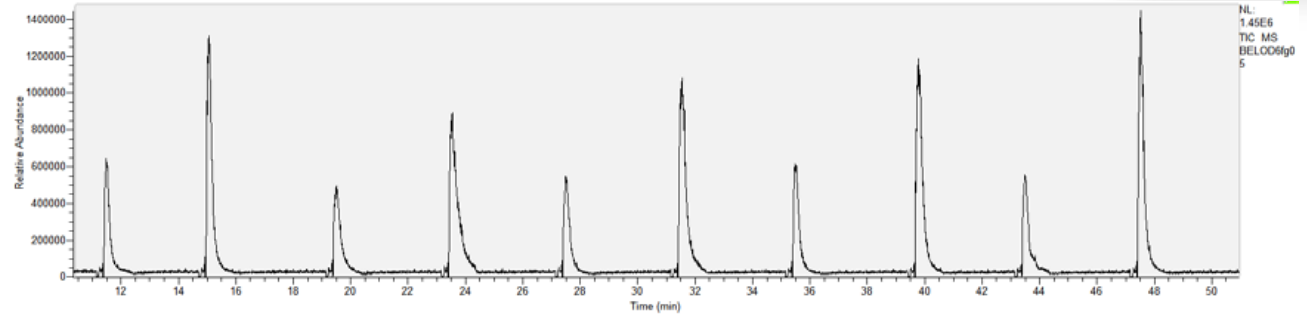
EIC
 193.08187
 - 193.08992



HPTLC-HRMS (Q Exactive plus)

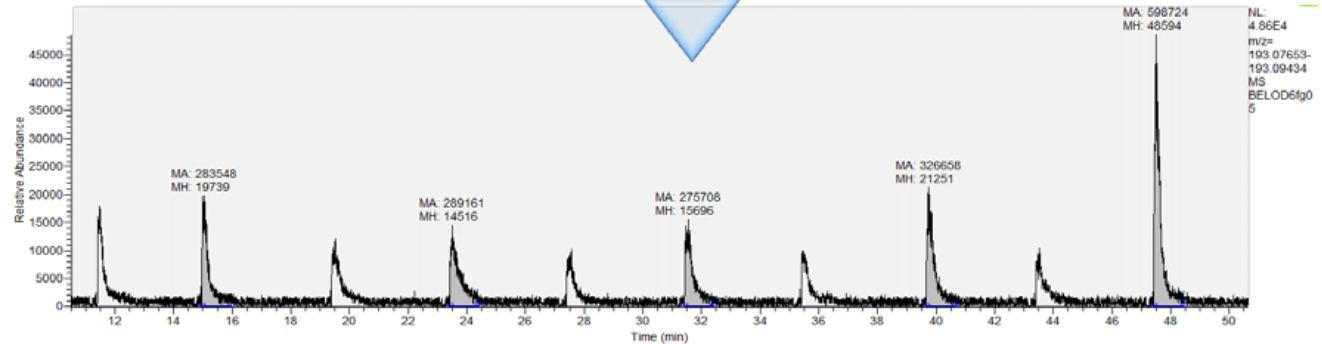
SIM

m/z 193.0861
 $\pm m/z$ 1.0



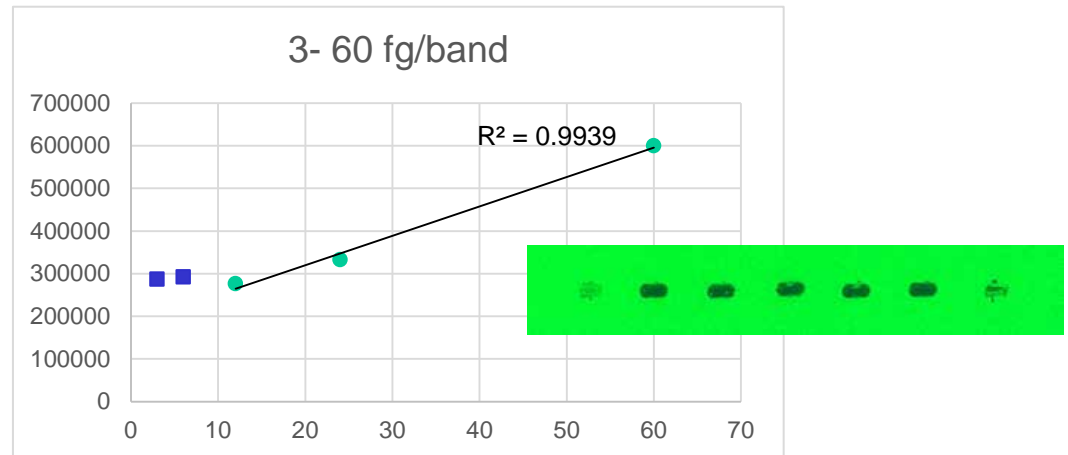
EIC

193.076
- 193.096



LOD of 24 fg/band
for butyl paraben

If 100 μ L sample
volume applied:
→ LOD of 0.24 ng/L



HPTLC-MS

Can we just compare figures
like limit of detection (LOD)?

LOD 100 pg/band?

On what does LOD depend on?

Application volume, MS analyzer, zone shape

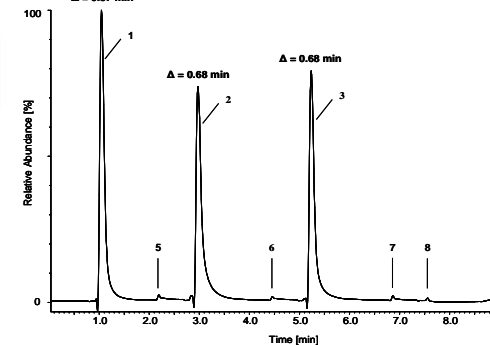
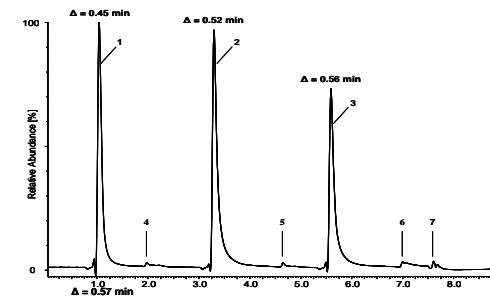
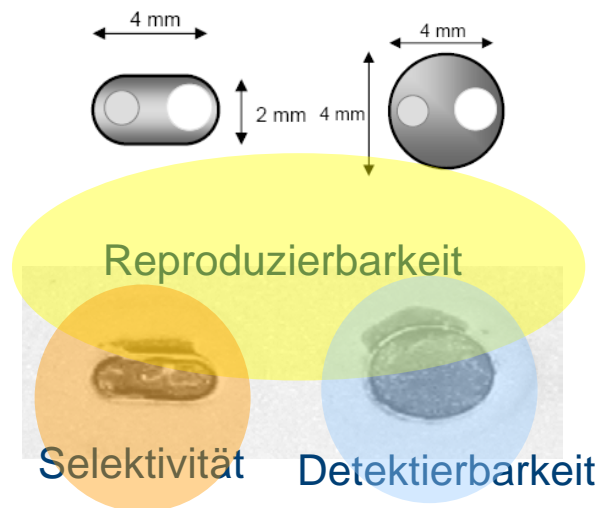
Elution head – cutting edge

Höhe

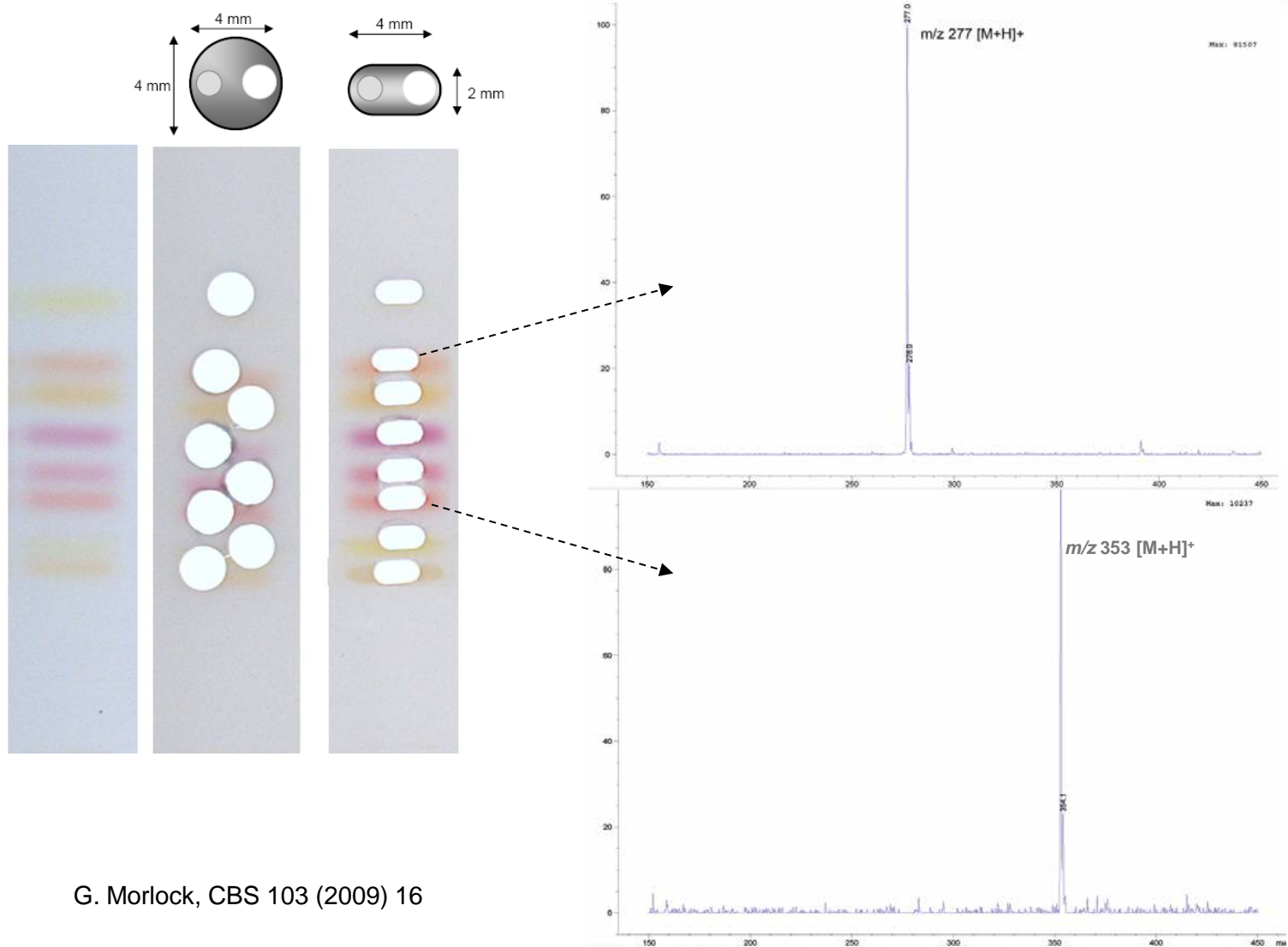
- 0.2 mm für Standardschichten → G. Morlock, W. Schwack, *Anal Bioanal Chem* 385 (2006) 586 - 595
- 0.1 mm für extra dünne Schichten → U. Jautz, G. Morlock, *Anal Bioanal Chem* 387 (2007) 1083 - 1093
- 0.5 mm für preparative Schichten → E. Dytkiewitz, G. Morlock, *J AOAC Int* 91 (2008) 1237 - 1244

Geometrie

Circular versus oval → U. Jautz, G. Morlock, *J Planar Chromatogr* 21 (2008) 367 - 371

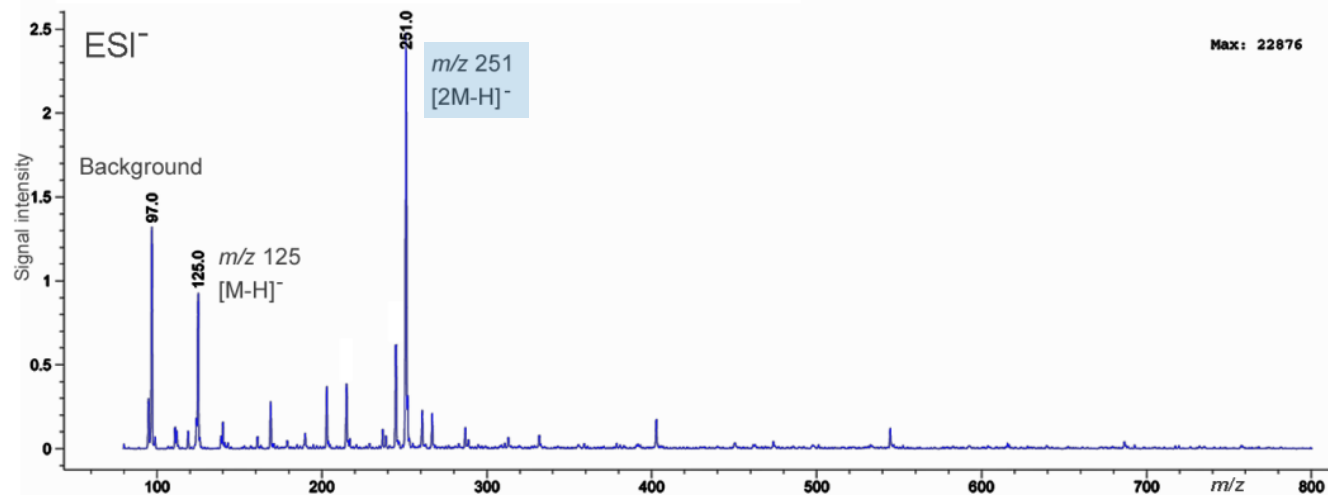
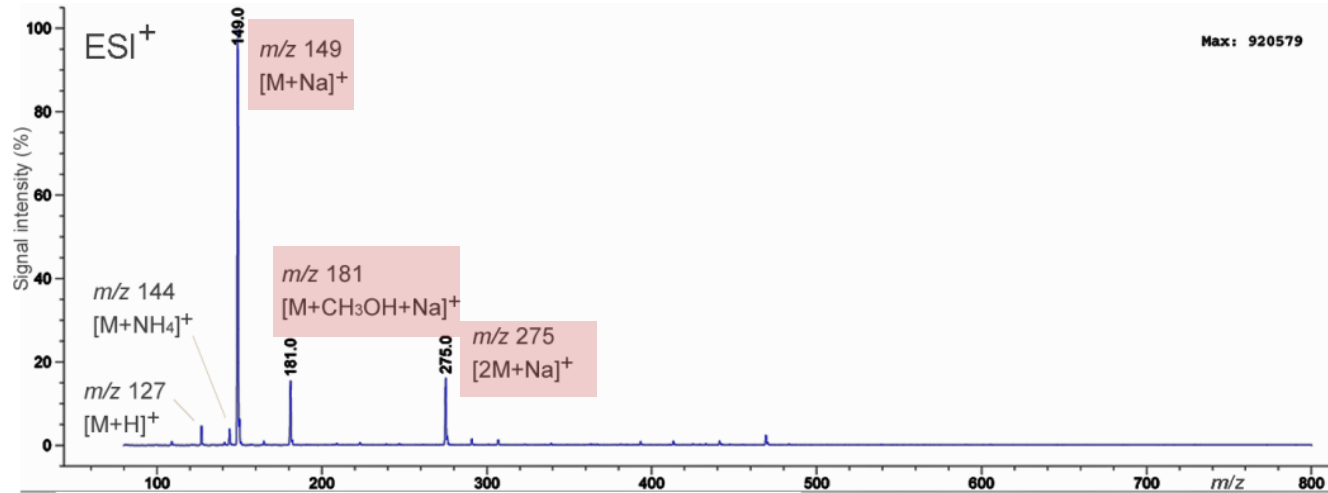


Elution head – cutting edge

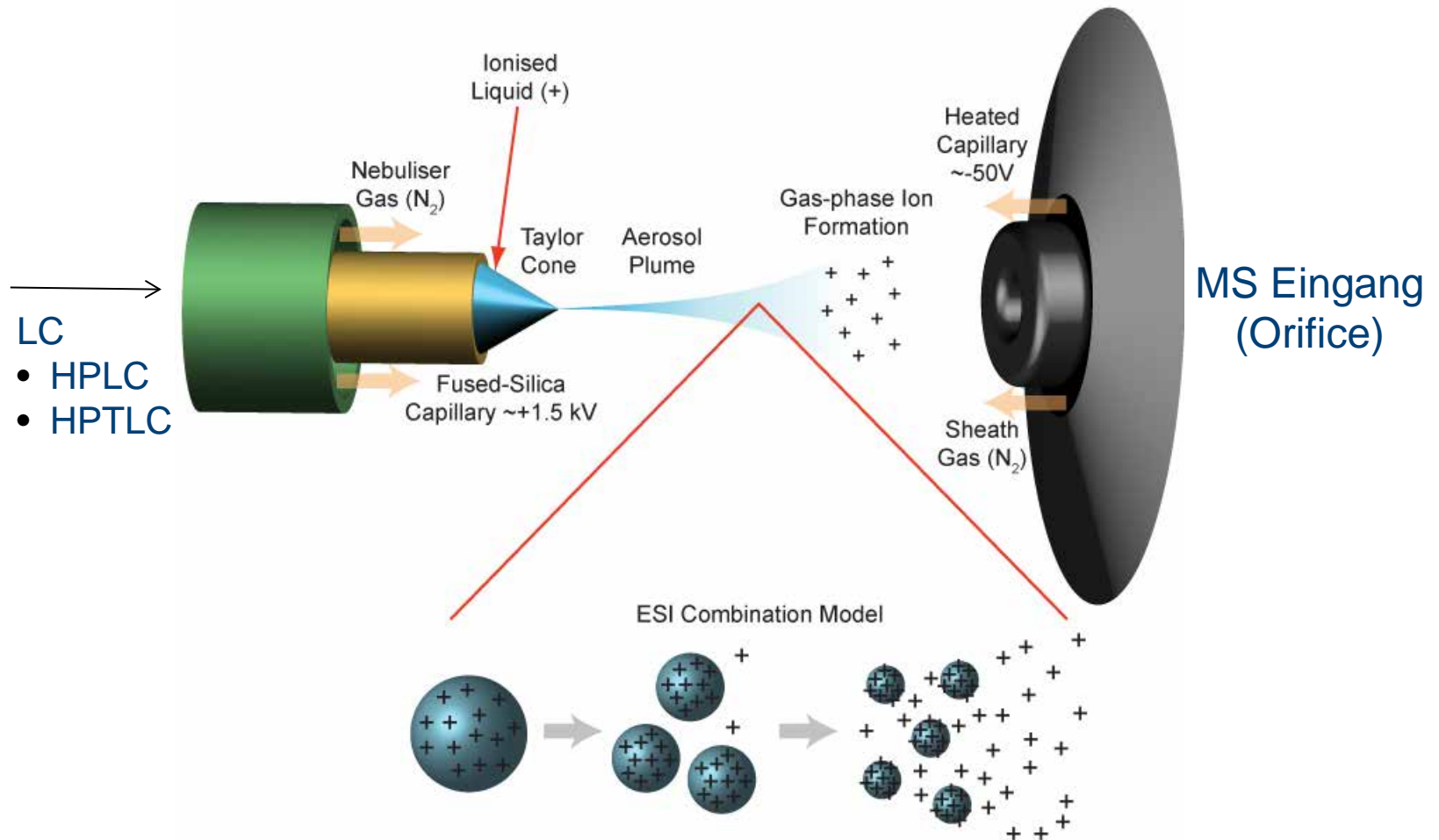


G. Morlock, CBS 103 (2009) 16

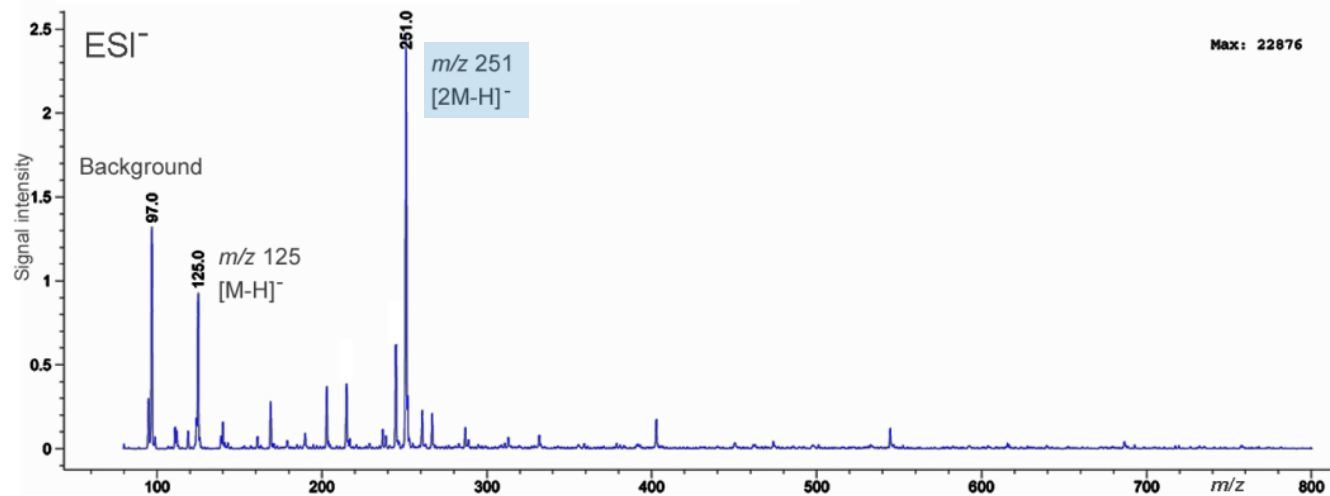
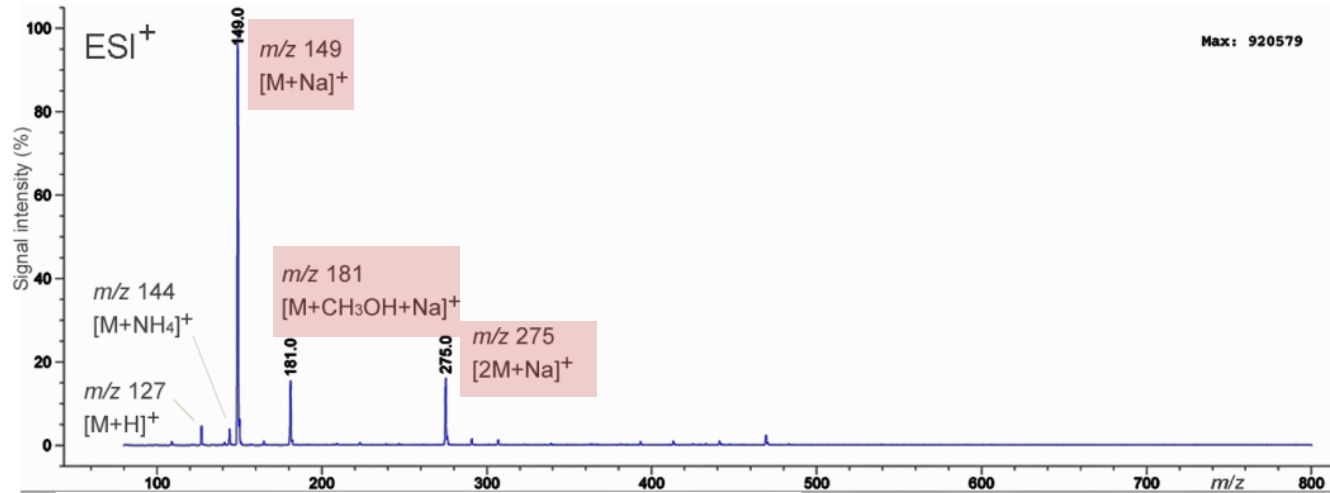
Adducts



Electrospray ionization (ESI)



Adducts



Adducts in ESI⁺

Difference of 5 Da? M + 23 Da Na [M+Na-H₂O]⁺
 M - 18 Da H₂O

No difference in Da? M + 18 Da NH₄ [M+NH₄-H₂O]⁺
 M - 18 Da H₂O

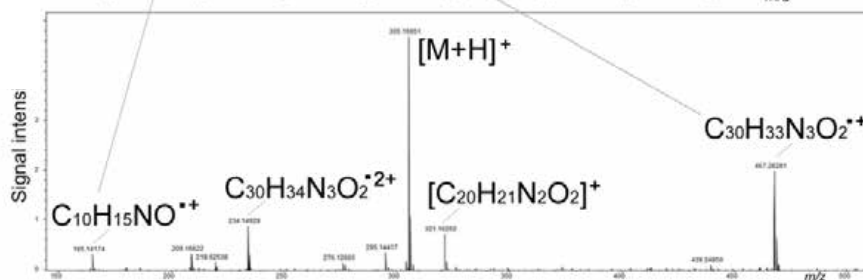
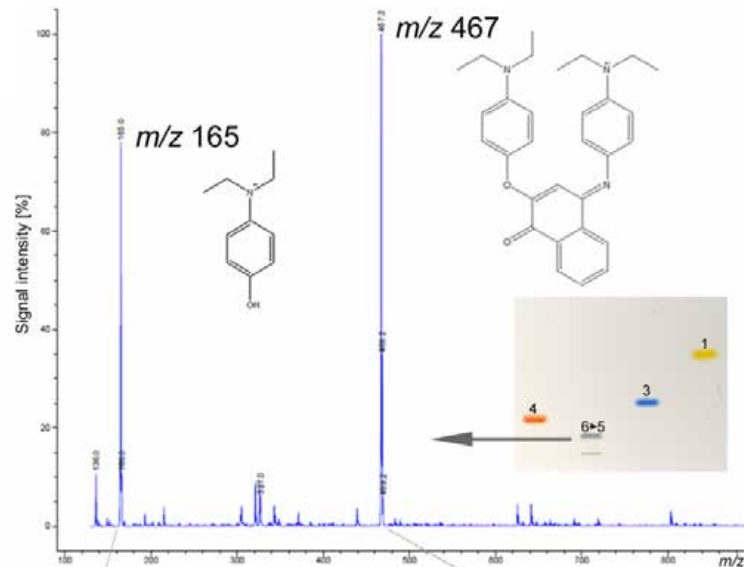
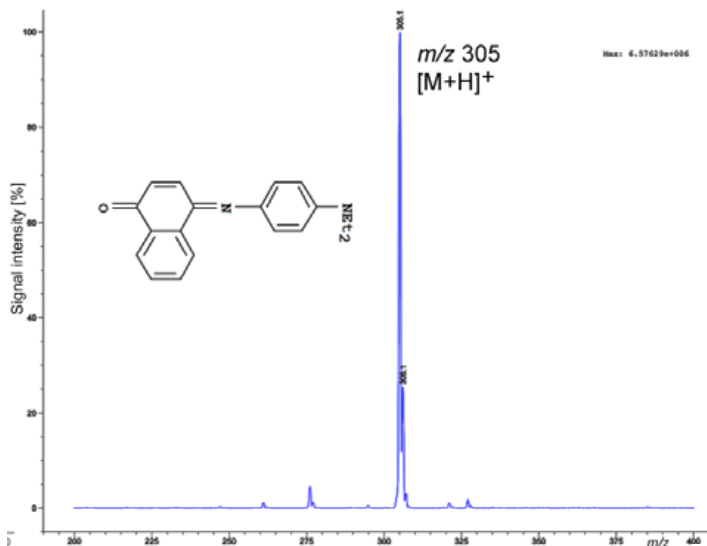
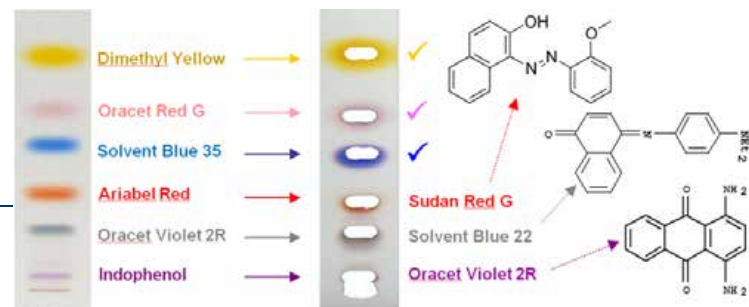
Difference of 17 Da? M + 1 Da H [M+H-H₂O]⁺
 M - 18 Da H₂O

Difference of 7 Da? [M+Li]⁺

Difference of 39 Da? [M+K]⁺

Difference of 45 Da? M + 46 Da 2 Na [M+2Na-H]⁺
 M - 1 Da H

Photooxidation effects?

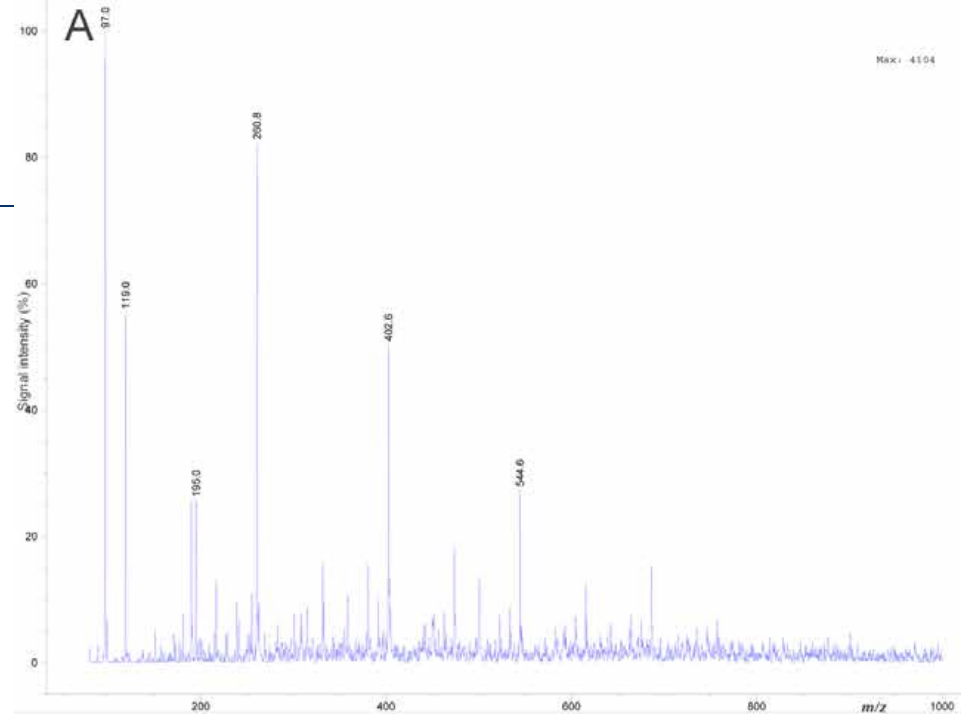


HPTLC-MS

Other signals?

Fluorescence indicator

with F₂₅₄



without F₂₅₄

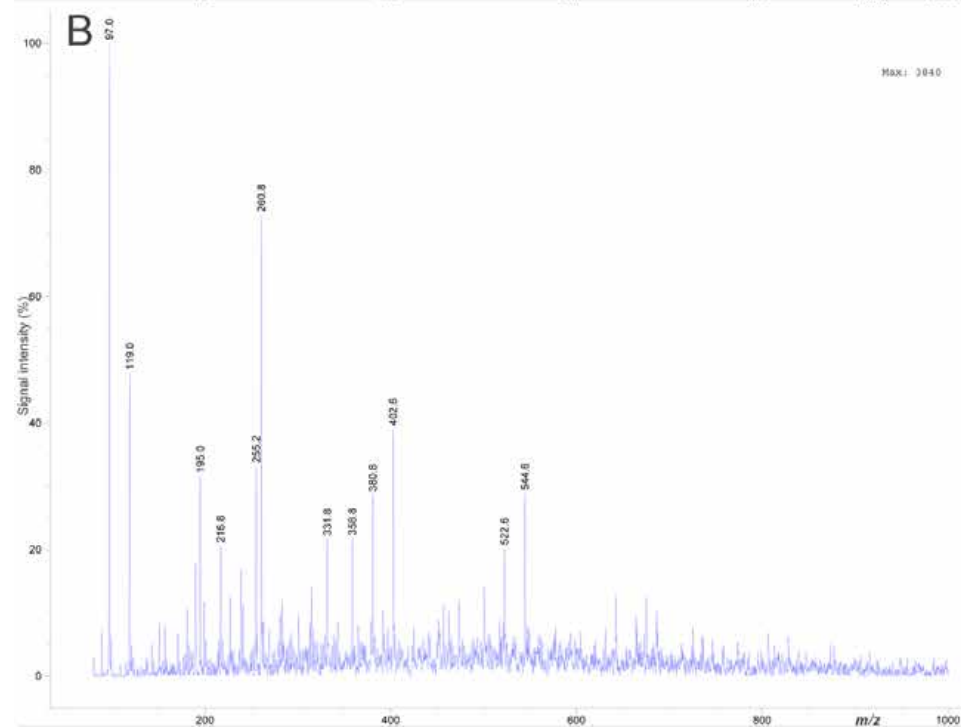


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1-Ethyl-3-methylimidazolium		111M ⁺
Trifluoroacetic acid or formate dimer	113 [M - H] ⁻ or [2M + Na-2H] ⁻	
Plate used directly	97.0 and cluster with $\Delta m/z$ 142: 119.0, 260.8 (5094), 402.8, 544.6	111.2, 391.2, 413.2 (52303), 419.2, 441.2
Plate pre-washed with neutral solvents and solvent mixtures (all v/v)		
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MeOH	97.0 and cluster with $\Delta m/z$ 142: 119.0, 260.8 (5943), 402.6, 544.6	111.2 (65390)
MeOH - H ₂ O 1:1	Very low: 255.0 (747)	413.2 (88052), 441.2
MeOH - H ₂ O 1:3	Very low: 97.0, 119.0, 123.0, 255.2, 281.2 (554), 501.0	391.2, 413.2 (64202)
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Pre-washing

directly used

methanol

methanol-water 3:1

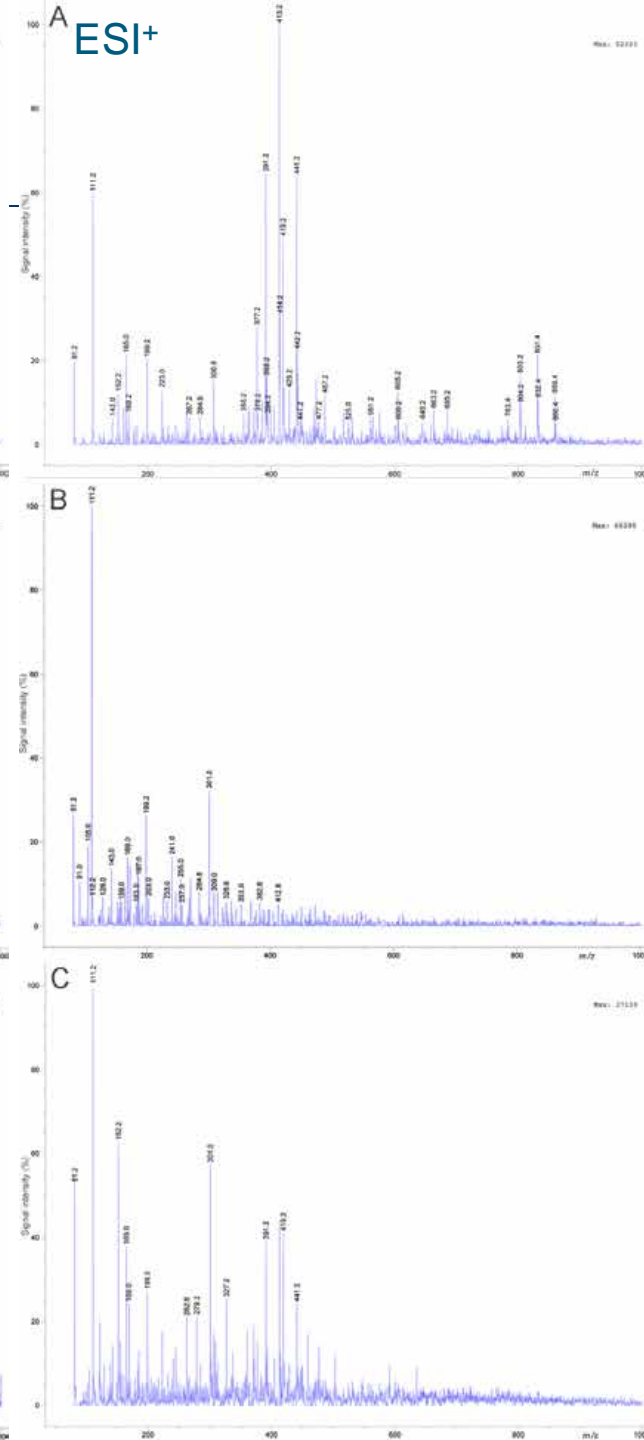
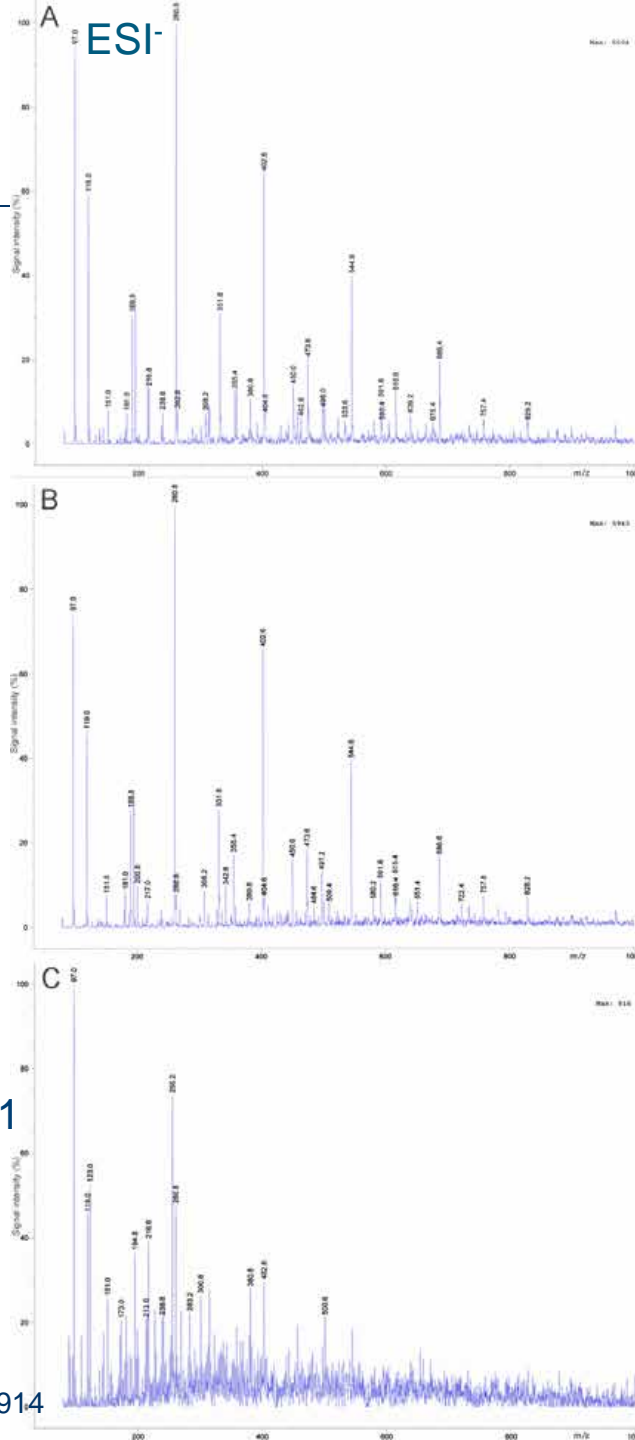
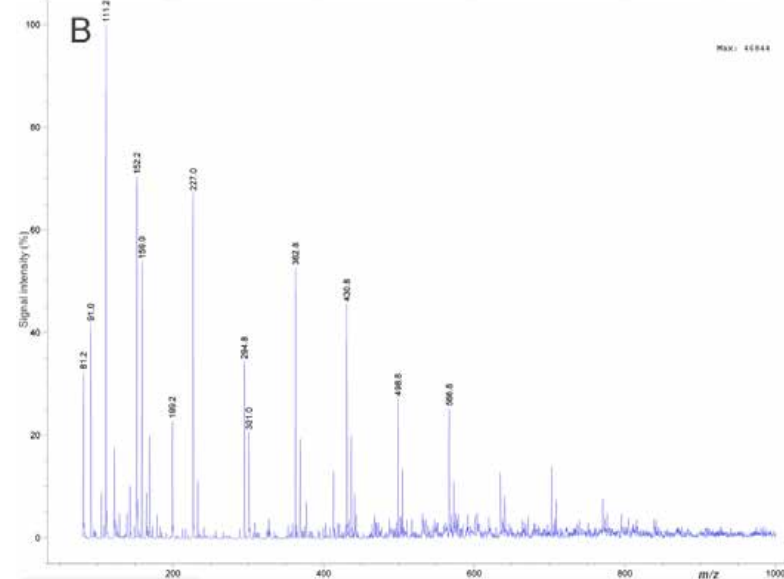
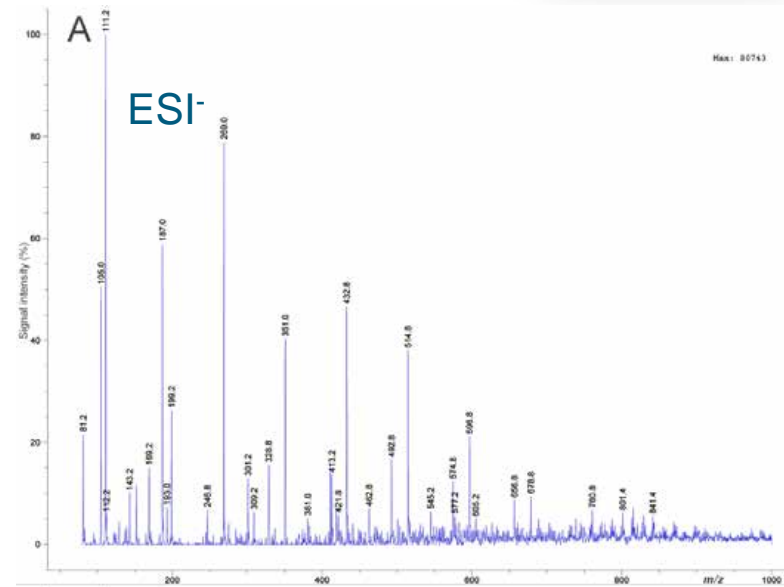
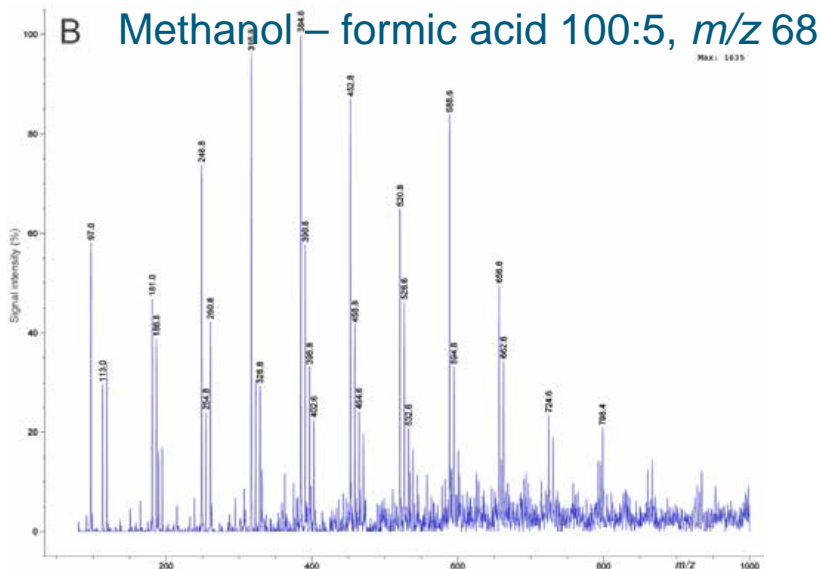
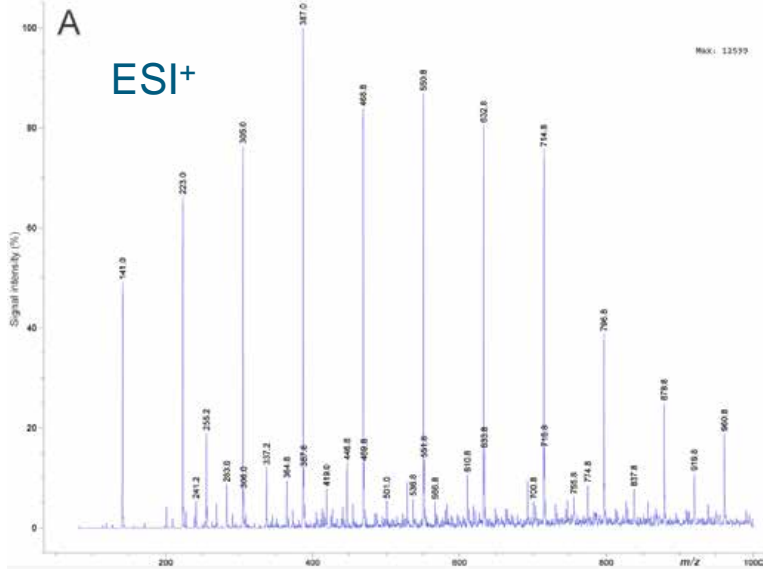


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Acidic solvents

Methanol – acetic acid 100:1, m/z 82



Background subtraction

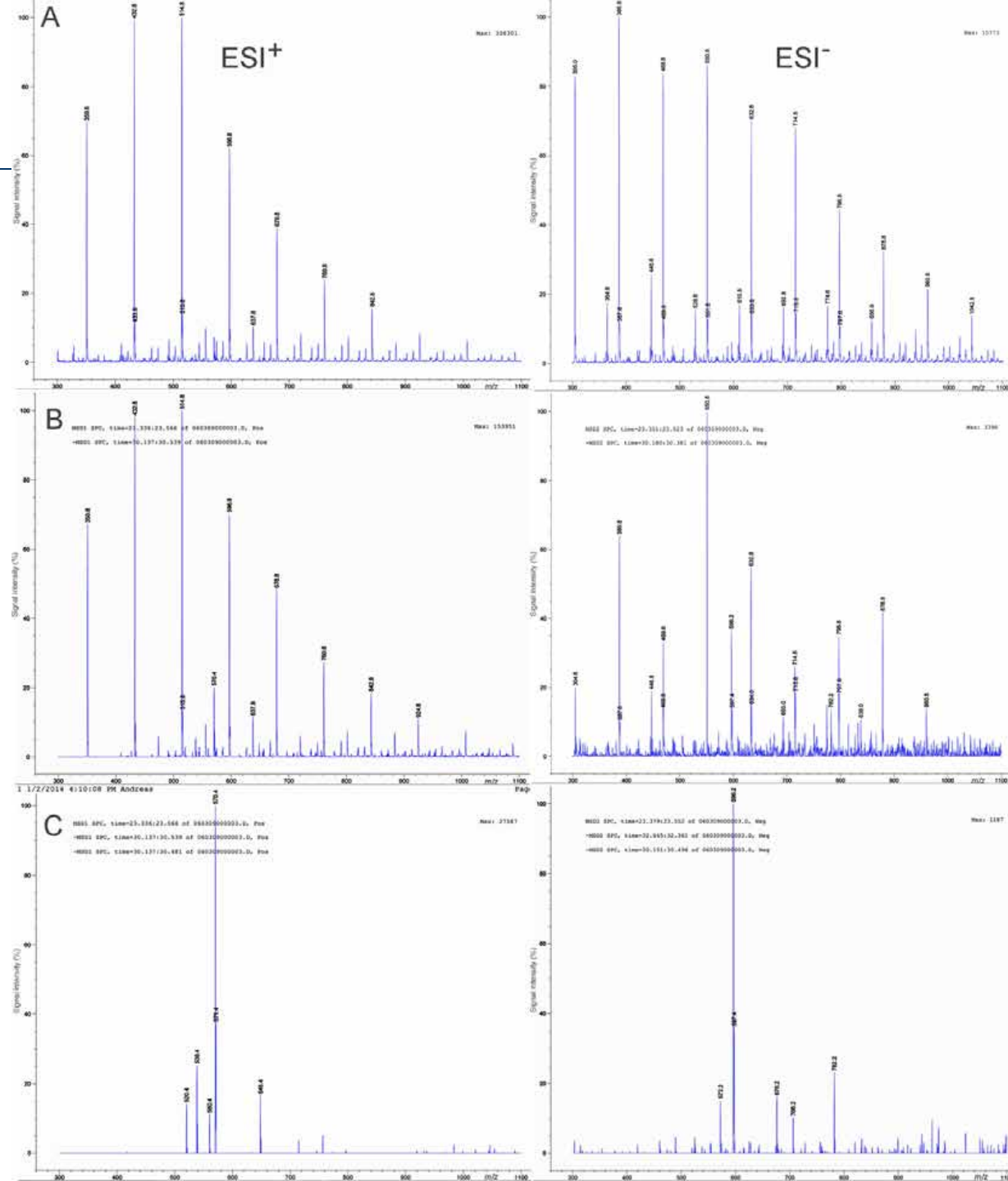
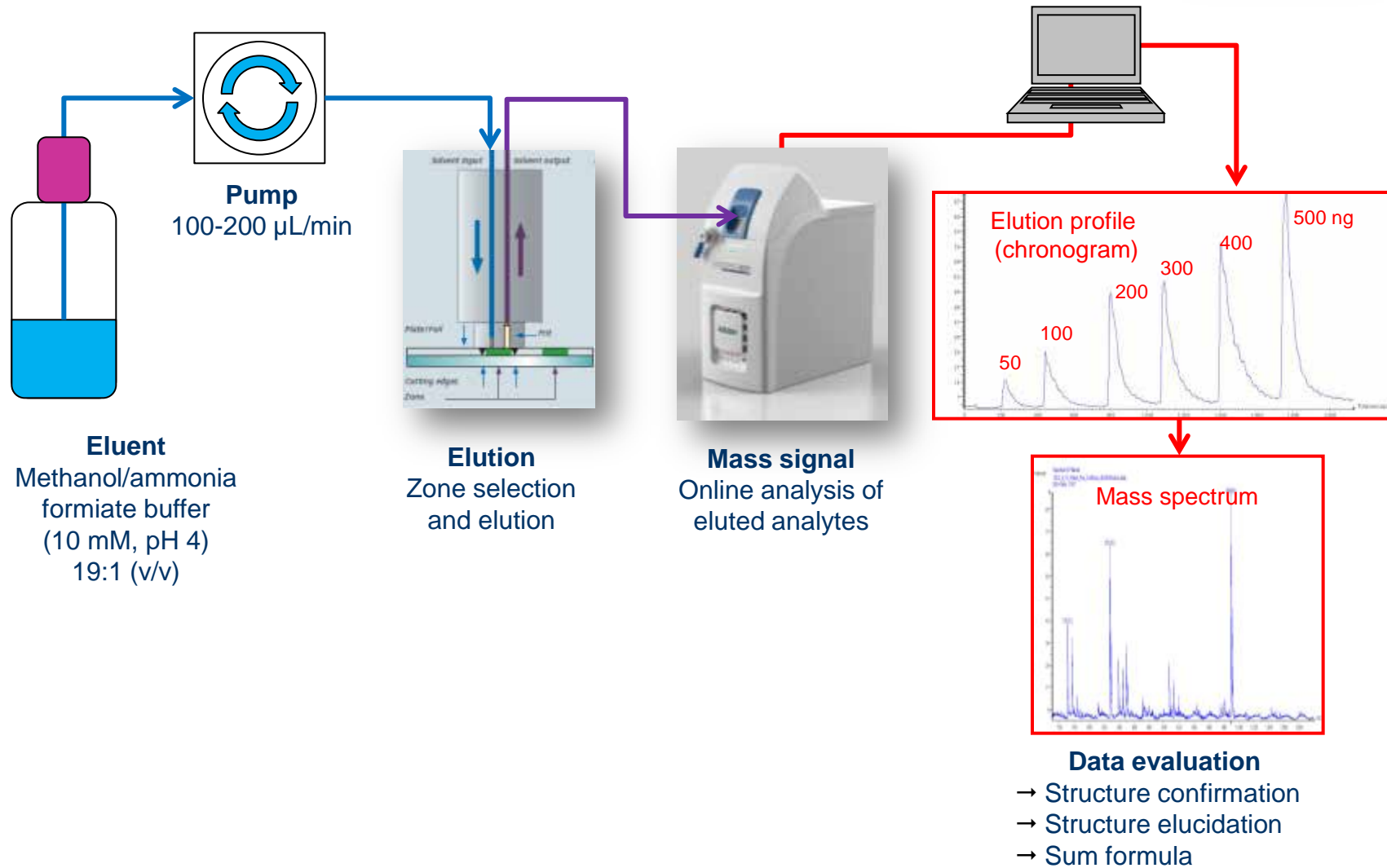


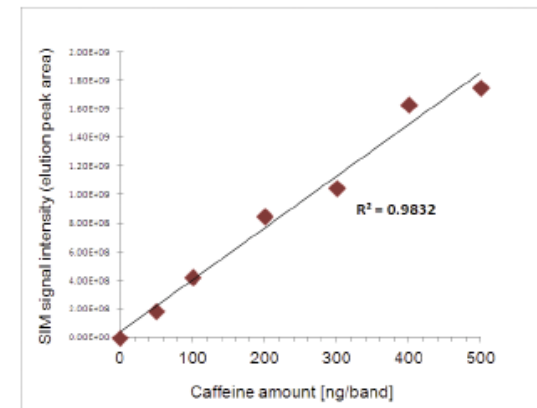
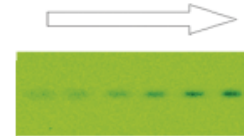
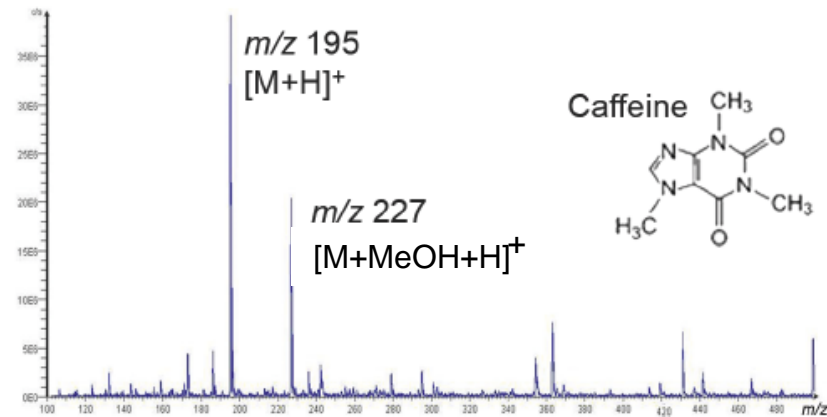
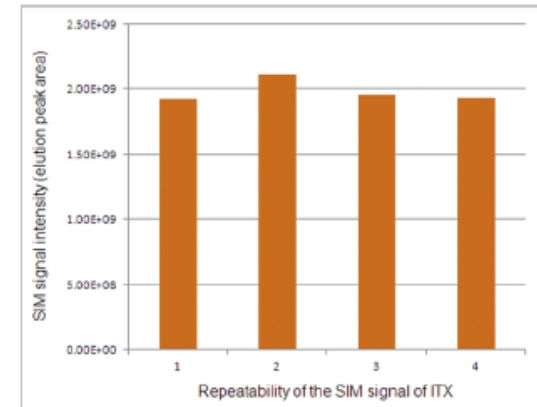
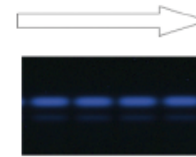
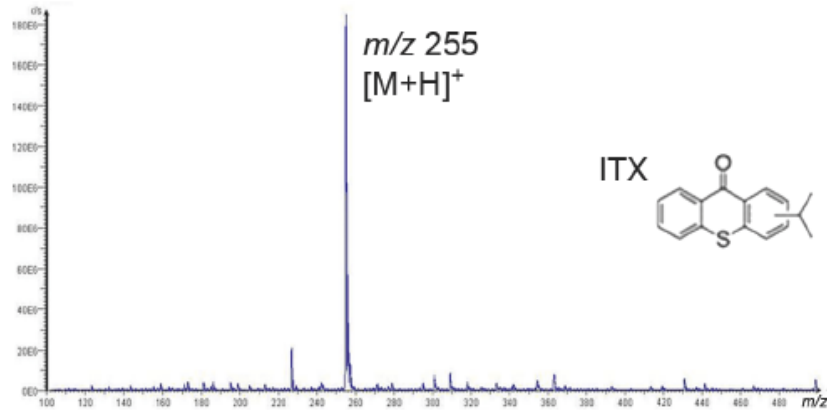
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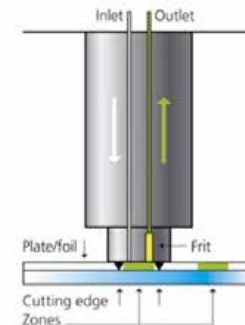
Workflow



Performance



Performance data → TLC-MS Interface

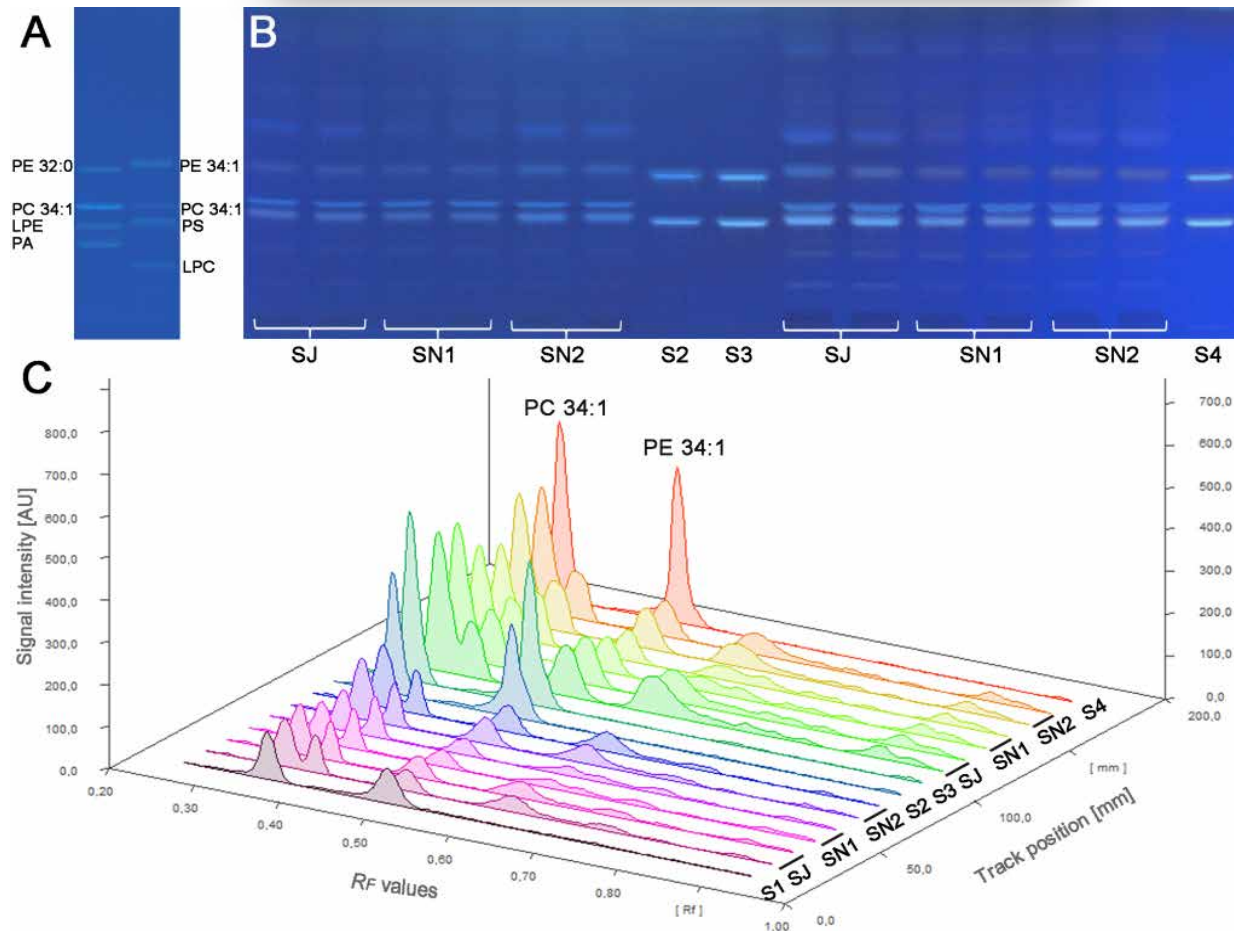


- highly reliable hyphenation
- highly targeted

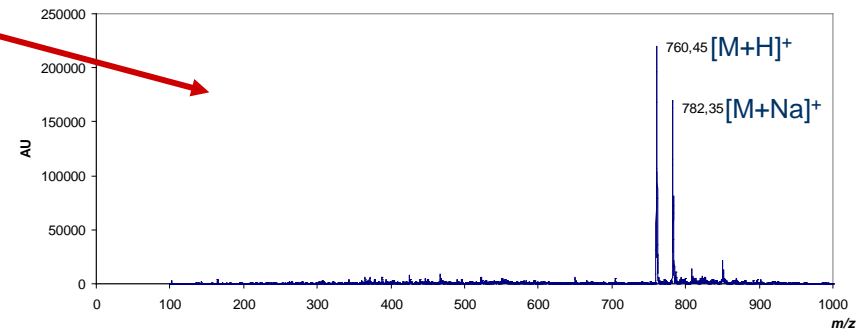
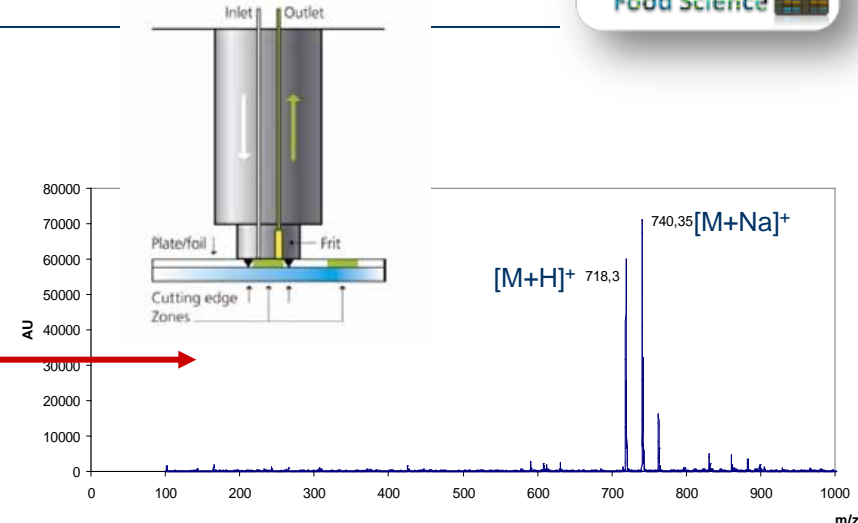
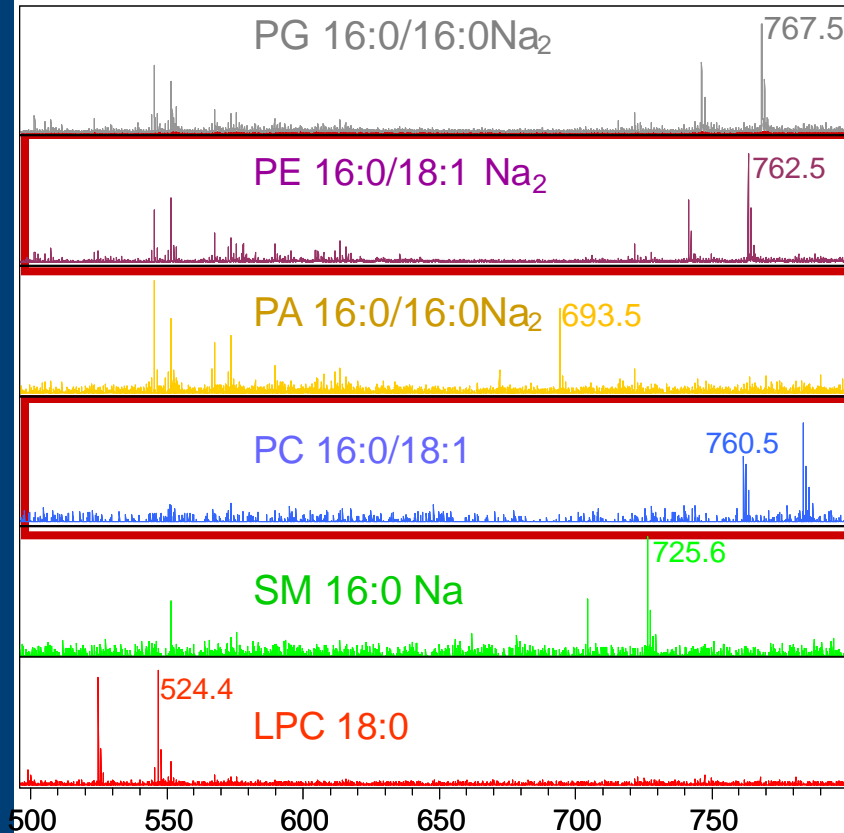


HPTLC-ESI-MS (SIM, peak area)		Linearity		Precision	
Dyes	hR_F - value	Calibration range (ng/band)	Determination coefficient	Conc. (ng/band)	%RSD, n = 5
Dimethyl Yellow	65	12 – 234	0.9943	1125	8.1
Oracet Red G	50	2 – 39	0.9950	189	11.0
Solvent Blue 35	41	10 – 52	0.9931	750	4.6
Sudan Red G	27	6 – 117	0.9984	564	8.8
Solvent Blue 22	17	21 – 78	0.9976	750	3.8
Oracet Violet 2R	4	8 – 156	0.9752	1500	11.6
Mean			0.9923		8.0

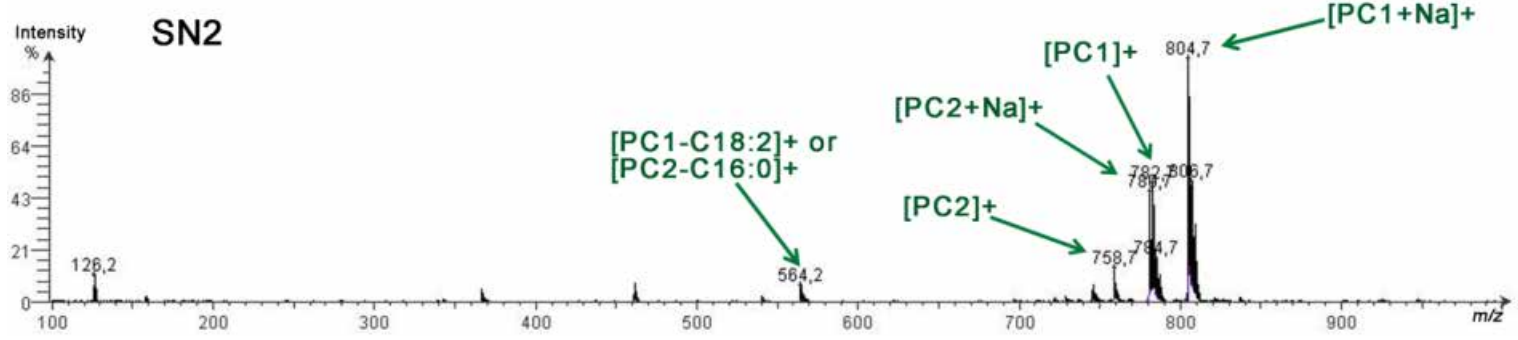
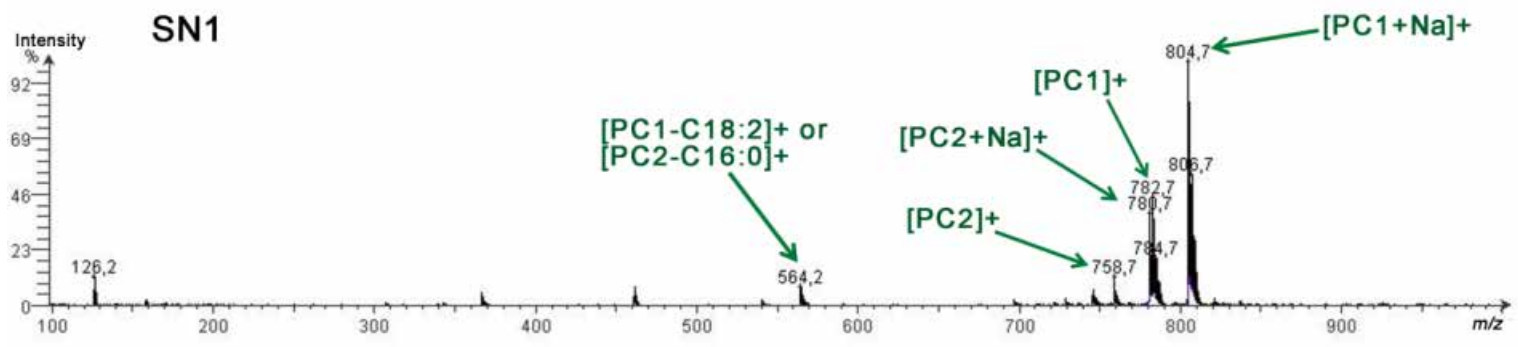
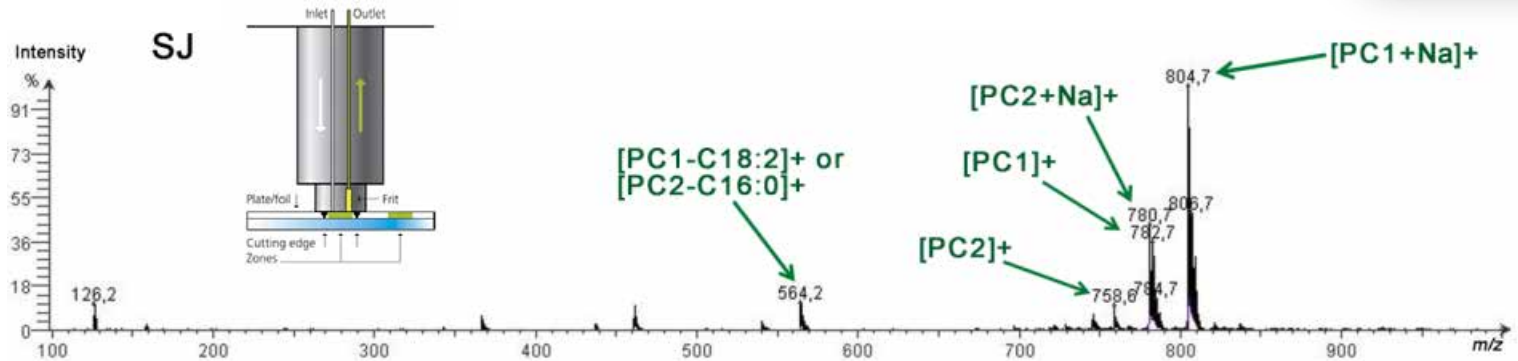
Analysis of phospholipids in lecithins



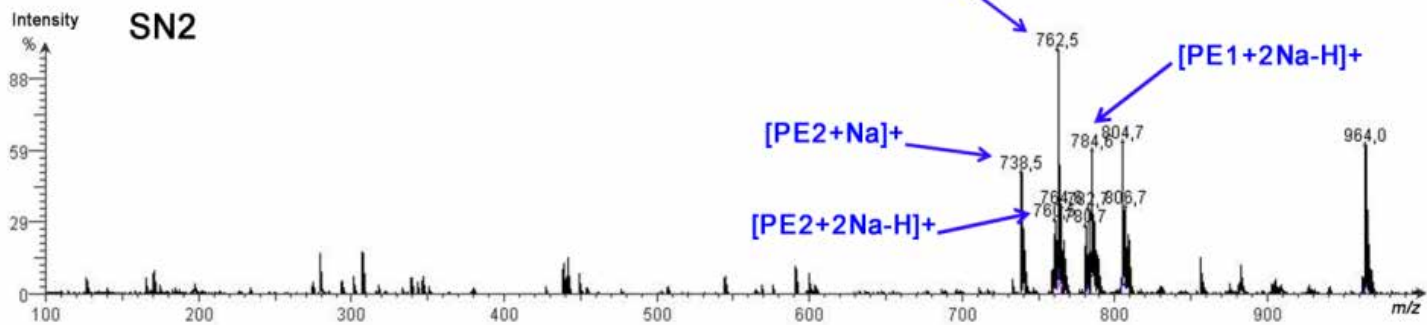
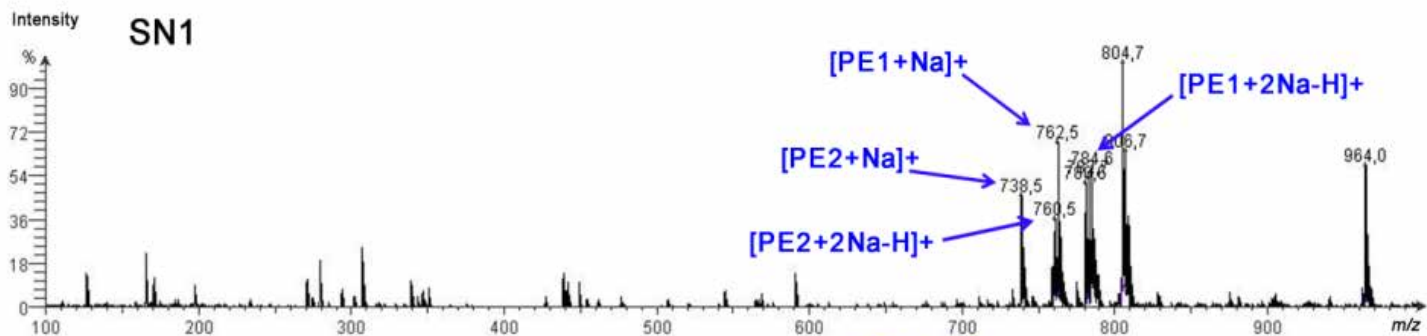
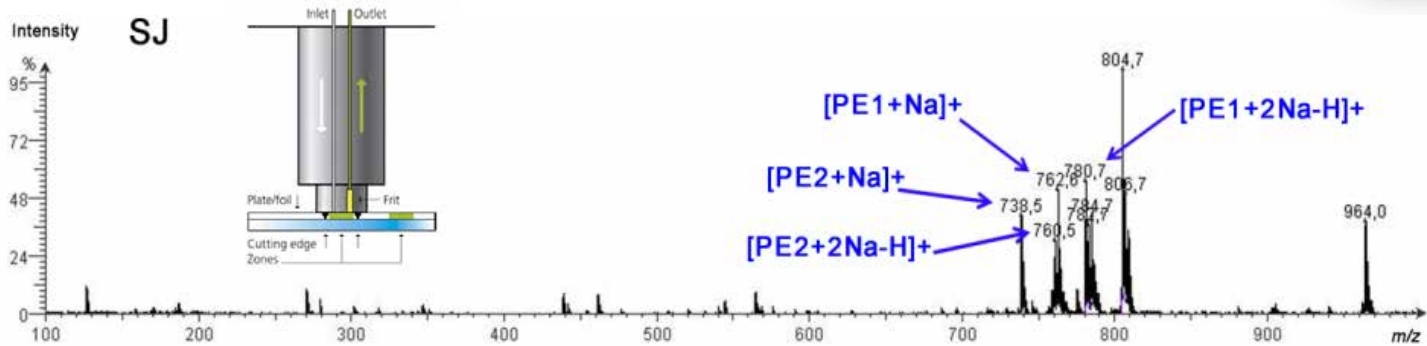
Comparison of mass spectra



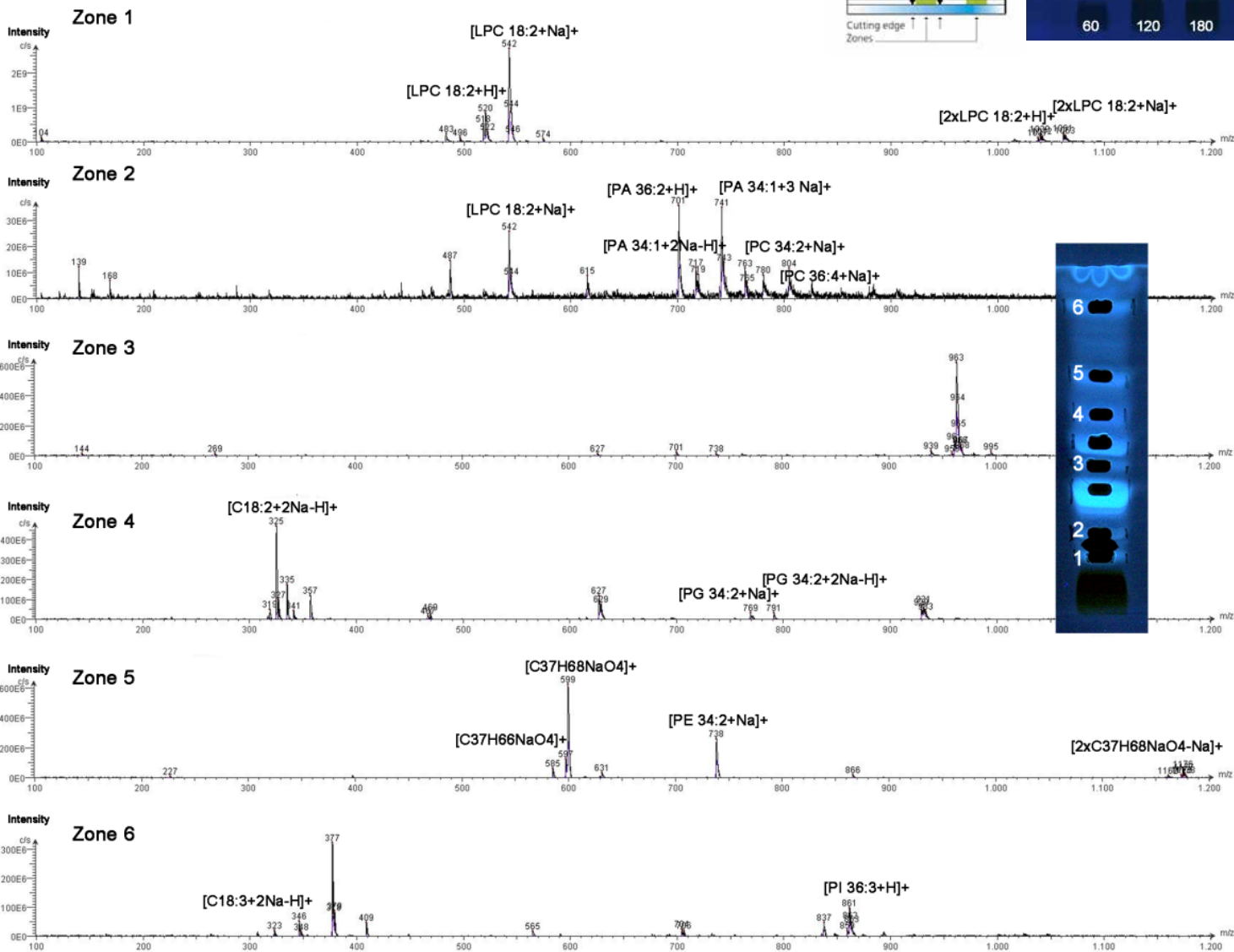
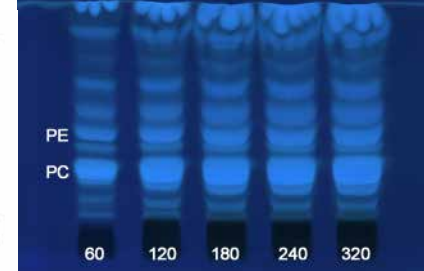
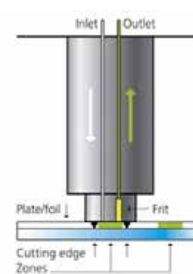
Characterization: soy bean vs. sunflower lecithin



Characterization: soy bean vs. sunflower lecithin

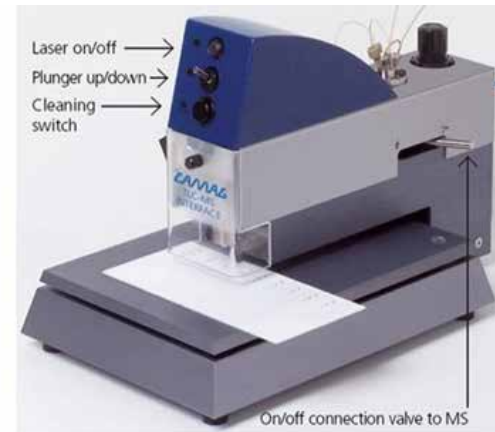
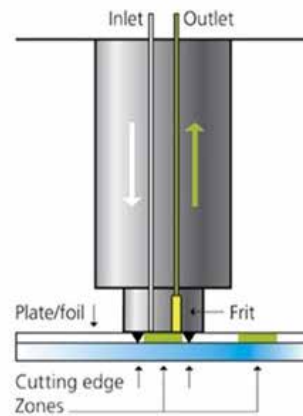


Minor phospholipids?



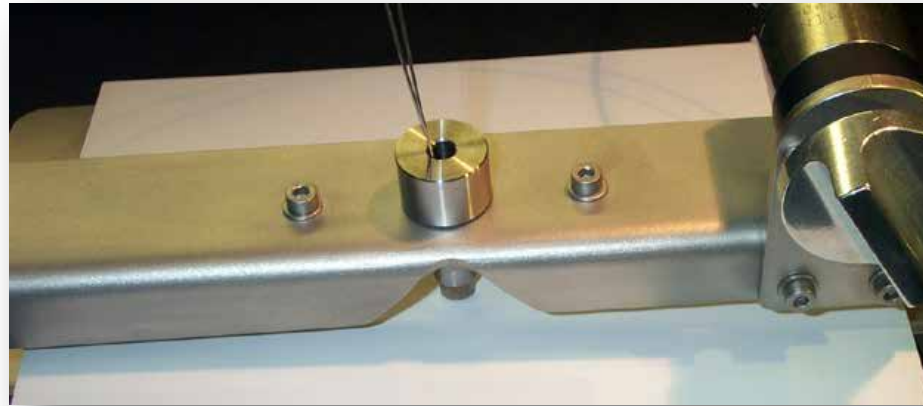
Pressure increase

Integrated online filter



- Substance amount too high: the solubility balance can be reached and nonsoluble, solid particles can block the filter
 - Forward sequence and backward sequence let forget the intermediate cleaning step
- Full automatization is the next step

ChromeXtractor



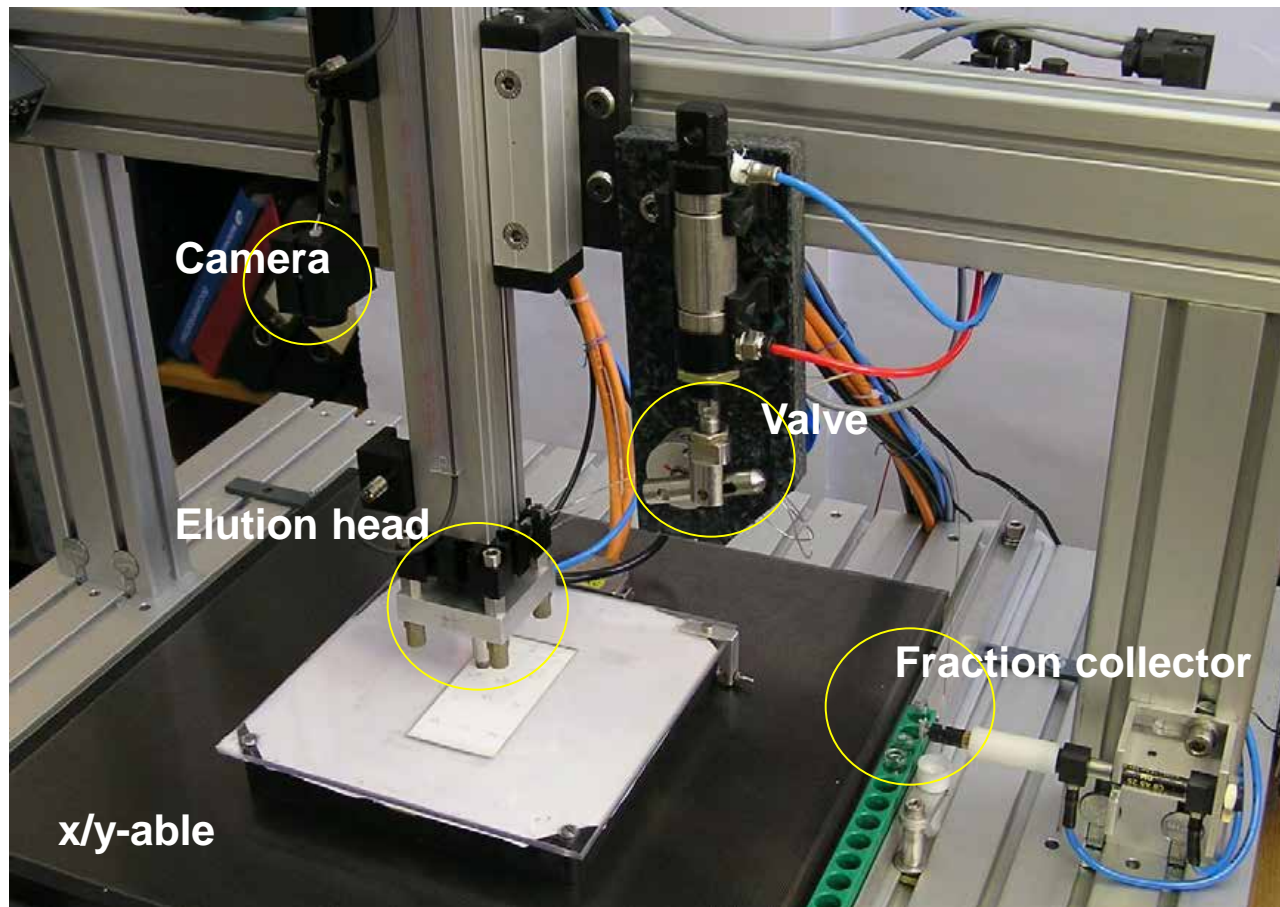
H. Luftmann, Anal Bioanal Chem 378 (2004) 964-968

→ Modification of the elution head for its use on glass plates

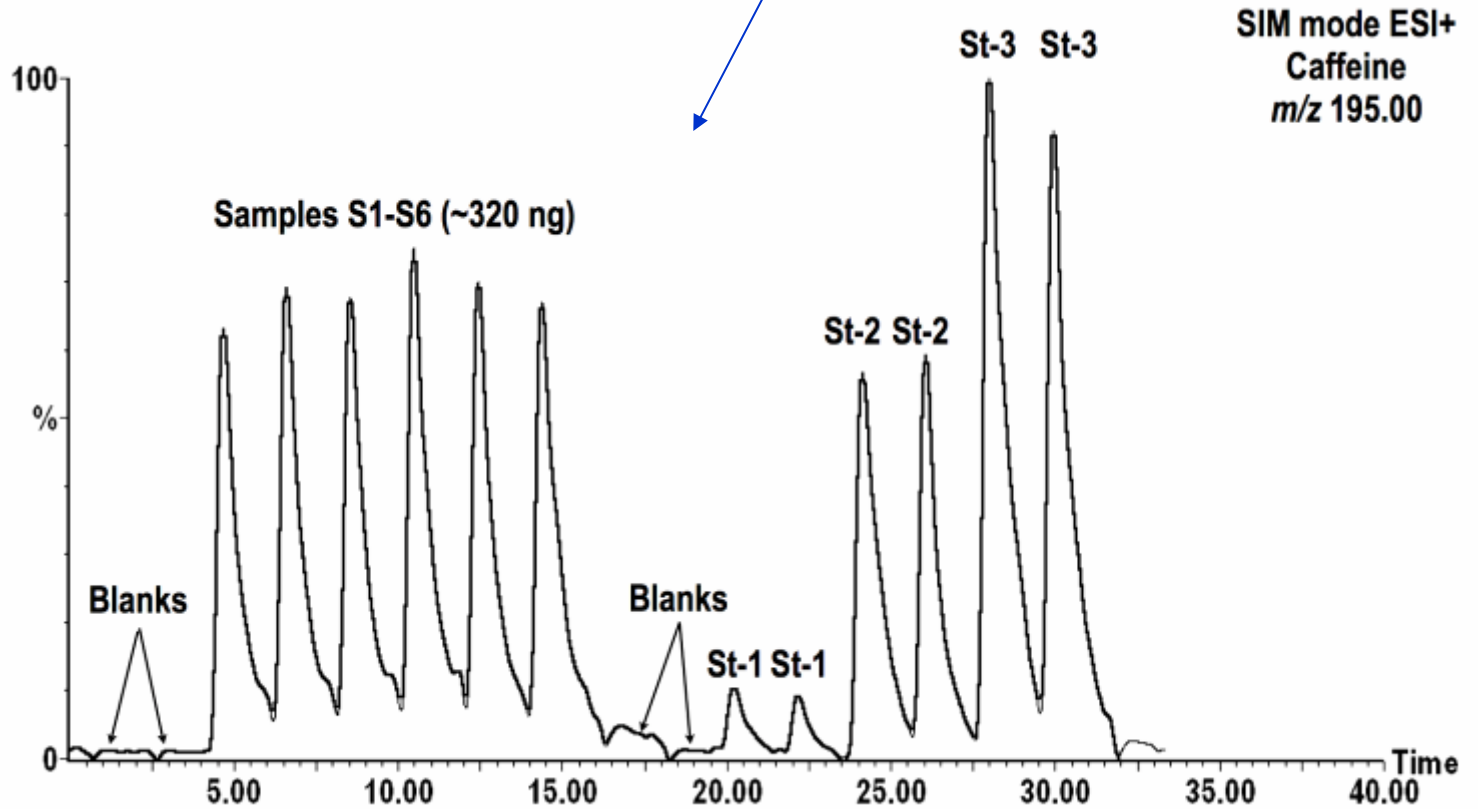
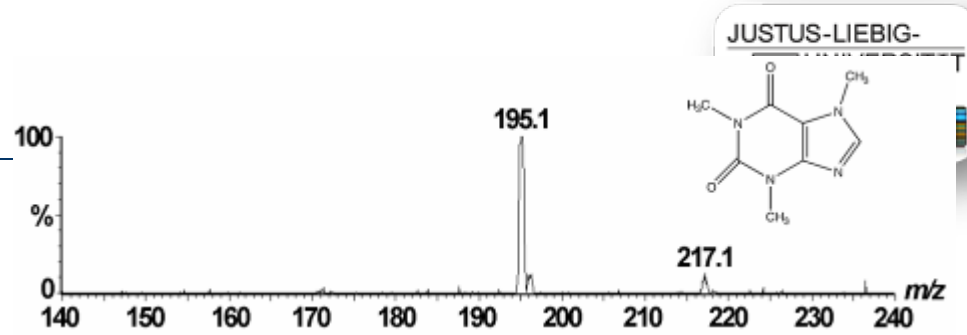


A. Alpmann, G. Morlock, Anal Bioanal Chem 386 (2006) 1543-1551

Automated elution head-based interface

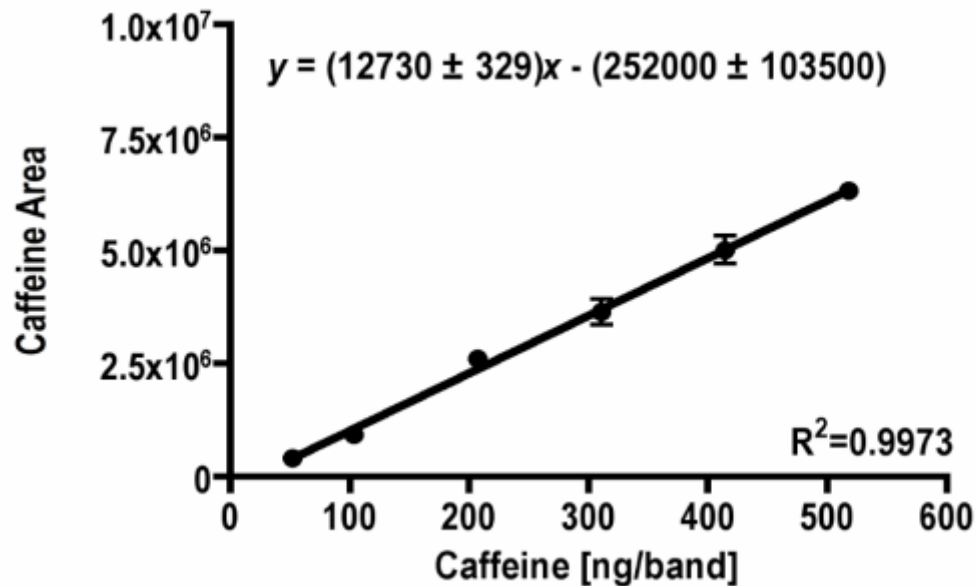


Elution profiles



Data of validation without IS

- Repeatability (%RSD, $n = 6$) in matrix: 5.6 %
- Linearity R^2 : 0.9973



H. Luftmann, M. Aranda, G. Morlock, Rapid Commun Mass Spectrom 21 (2007) 3772-3776

Analysis of samples containing caffeine

Sample	Pharmaceutical mean \pm SD (mg/tablet)	Energy drink mean \pm SD (mg/100 mL)
HPTLC/ESI-MS RSD (% , n = 6)	102.09 \pm 5.76 (5.6)	32.91 \pm 1.60 (4.9)
HPTLC/UV RSD (% , n = 5)	101.98 \pm 2.30 (2.3)	33.71 \pm 0.96 (2.8)
Label	100	32

→ Comparable findings to validated HPTLC/UV methods (F-test, t-test)

Comparison of automated interfaces

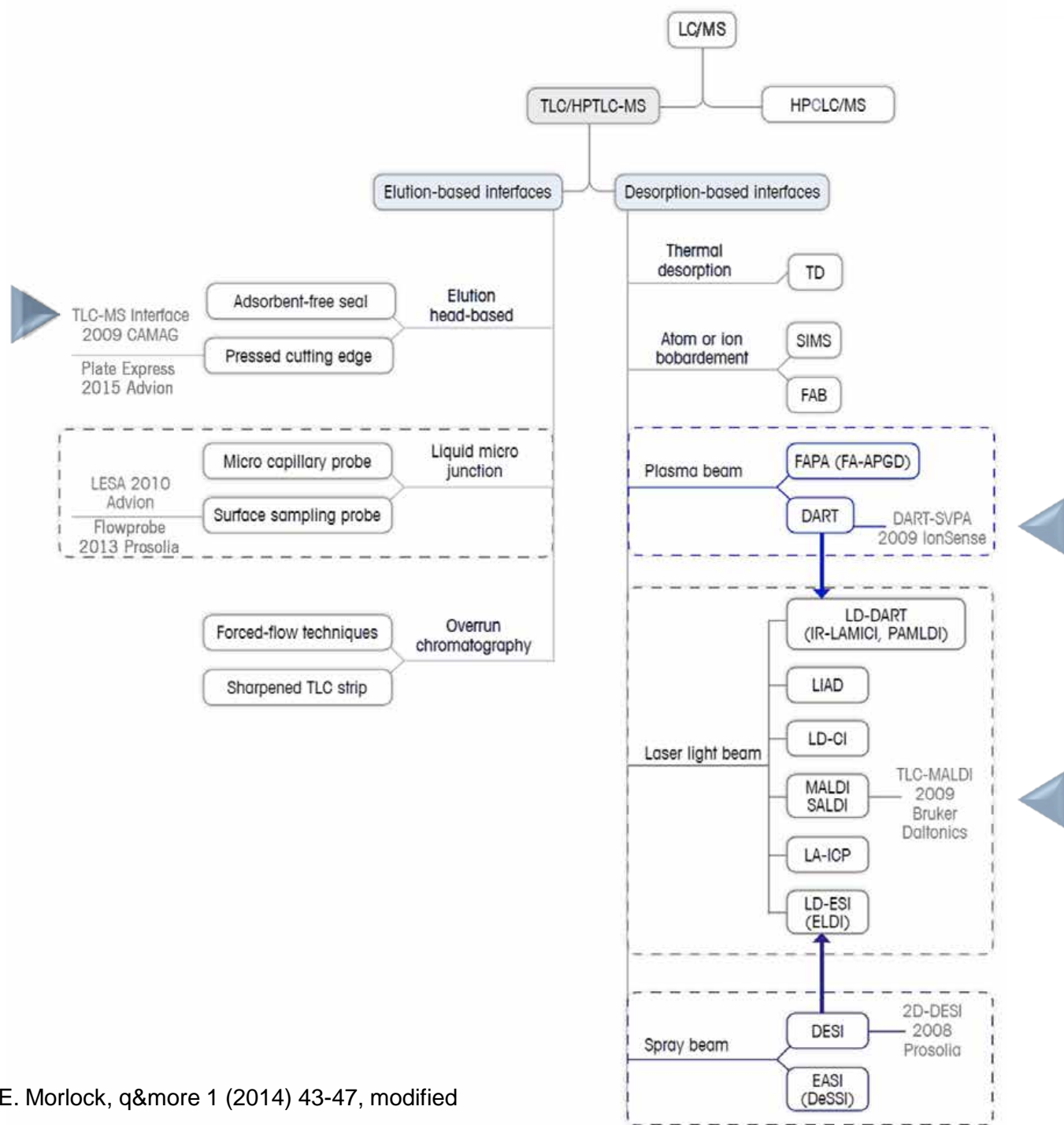
Parameter	Precision %RSD	Linear Response r^2
-----------	-------------------	--------------------------

Quantification **without** internal standard

▶ Elution head (autom.)	≤ 5.6 %	0.9973
DESI	≤ 16.8 %	0.95 - 0.98
MALDI	10 %	-
LA-ICP	17 – 41 %	≥ 0.90

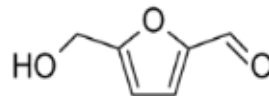
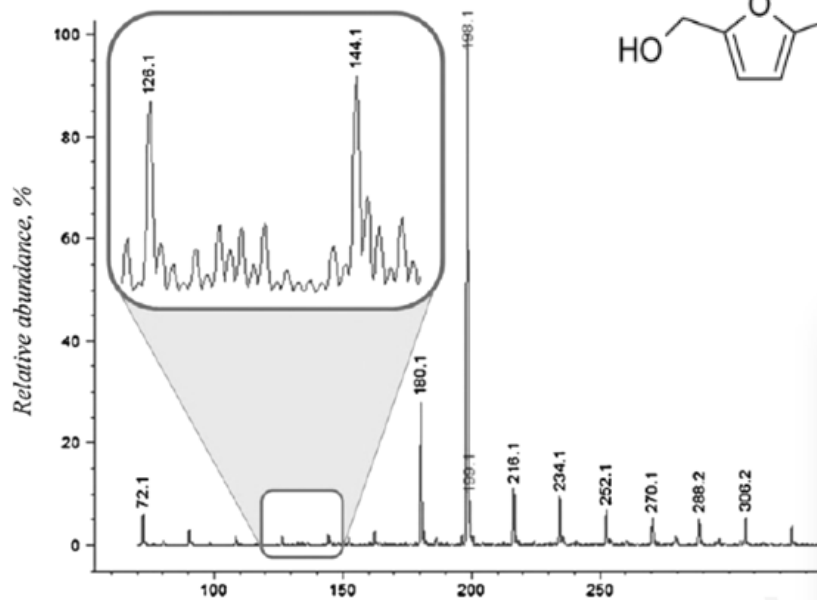
Quantification **with** internal standard

Micro-junction ESI	≤ 4.4 %	0.9999
SALDI/APCI	7 %	0.9991
MALDI	≤ 8.9 %	0.9969
LA-ICP	3 – 40 %	≥ 0.98



DIP-it[®]-DART-MS

Direct Analysis in Real Time Mass Spectrometry



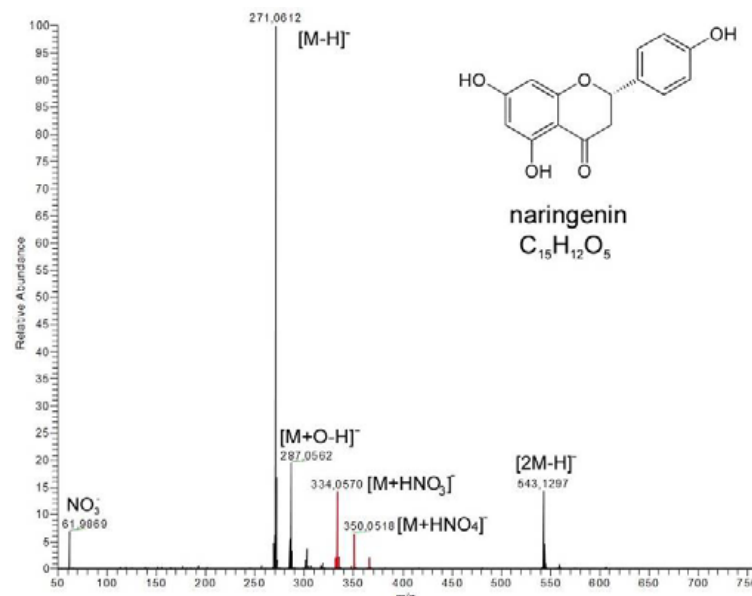
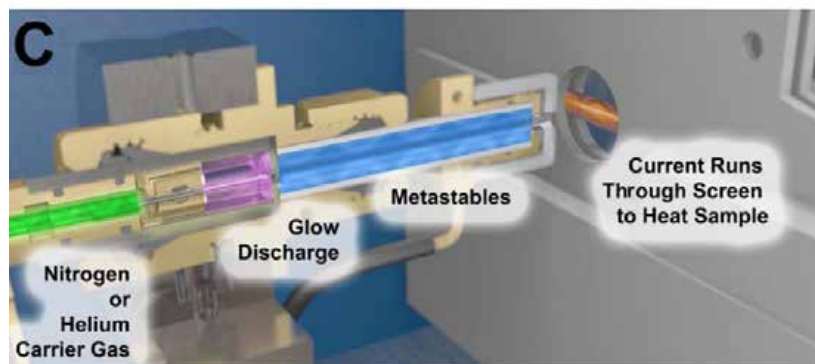
ID-CUBE-DART-MS



→ Phenolic compounds of *Bergenia crassifolia* leaves



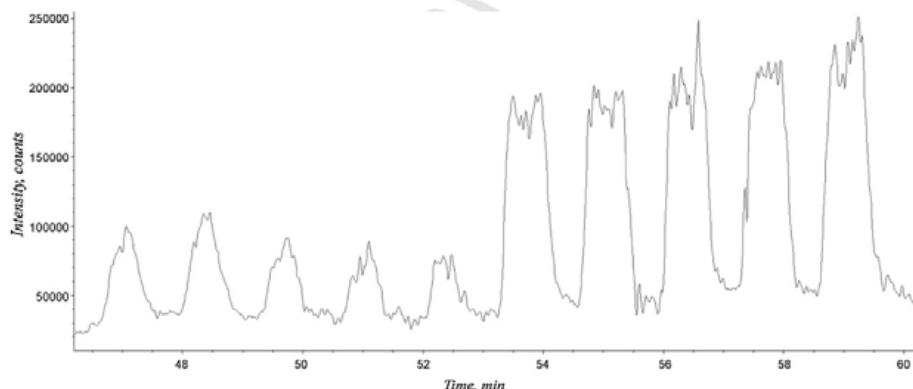
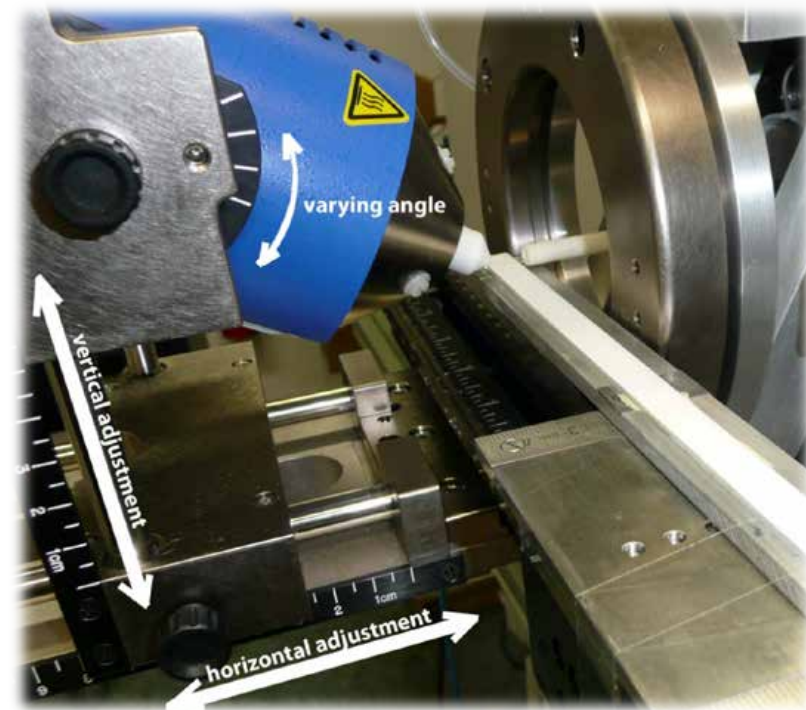
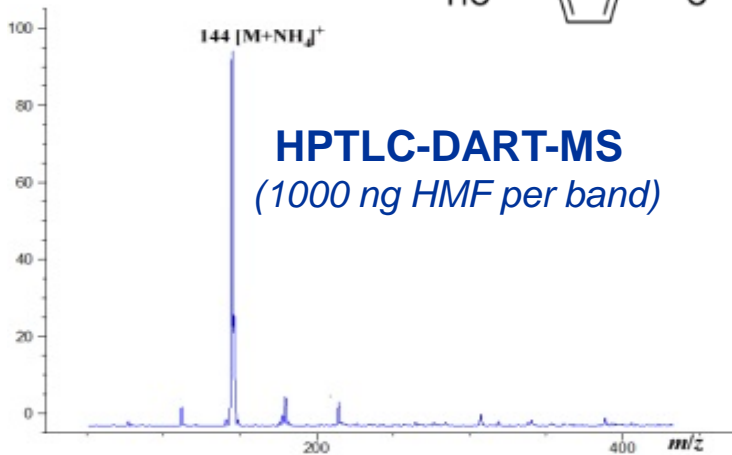
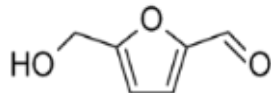
#	$m/z_{exp.}$	δm , mmu	elemental formula, ion	ion composition	supposed compound	number of citations in literature for presence in herbal extracts
1	115.0024	-0.2	C ₄ H ₃ O ₄	[M-H] ⁻	fumaric acid	43
2	125.023	-0.3	C ₆ H ₅ O ₃	[M-H] ⁻	pyrogallol	20
3	133.0128	-0.3	C ₄ H ₅ O ₅	[M-H] ⁻	malic acid	108
4	191.0551	0.2	C ₇ H ₁₁ O ₆	[M-H] ⁻	quinic acid	38
5	193.0133	0.2	C ₉ H ₅ O ₅	[M-H] ⁻	trihydroxycoumarin	2



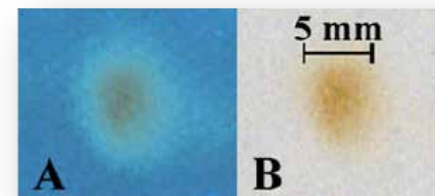
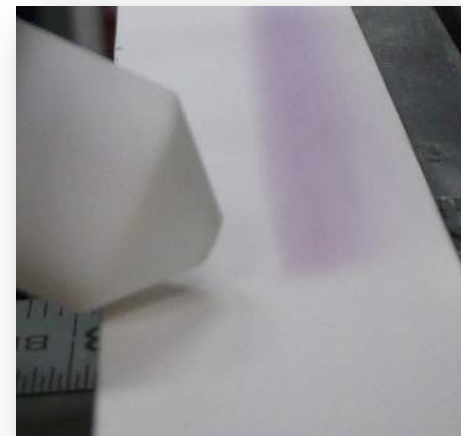
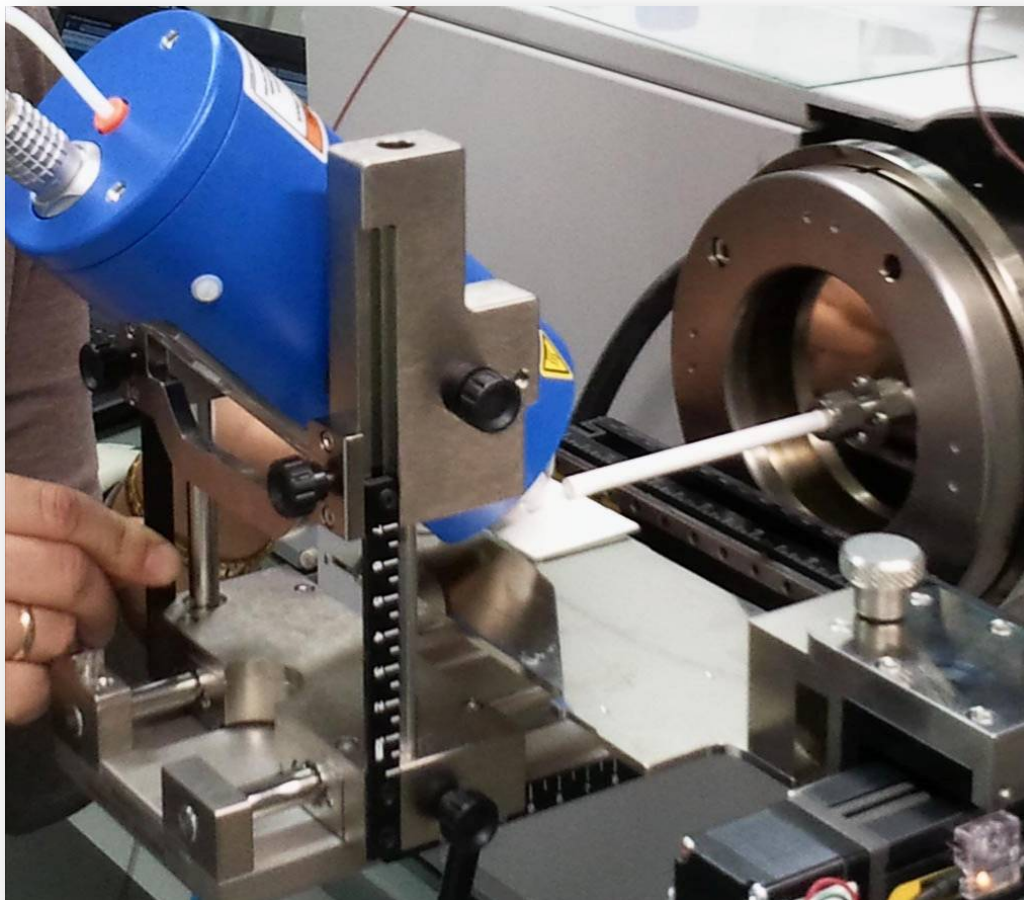
HPTLC-DART-SVPA-MS



2006 ↔ 2011

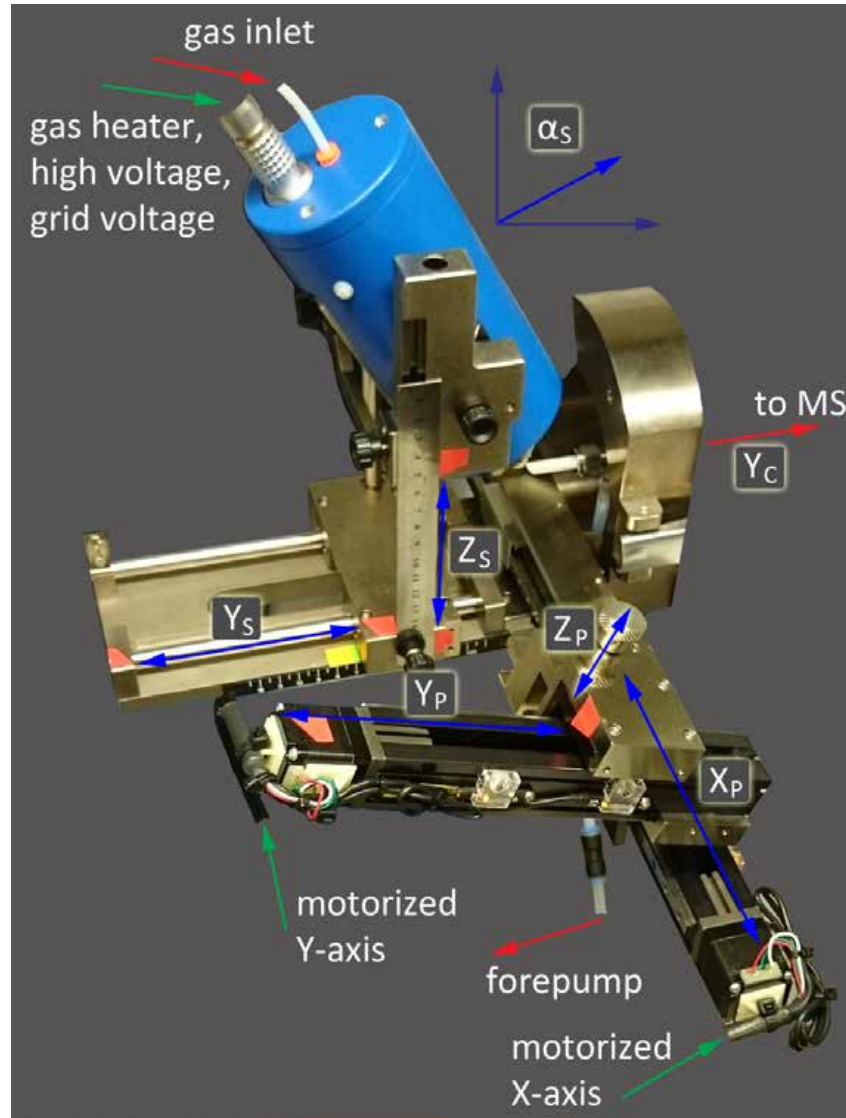


HPTLC-DART-SVPA-MS

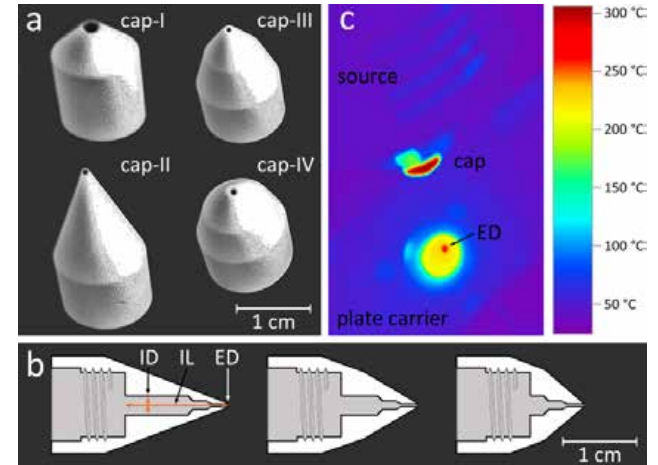
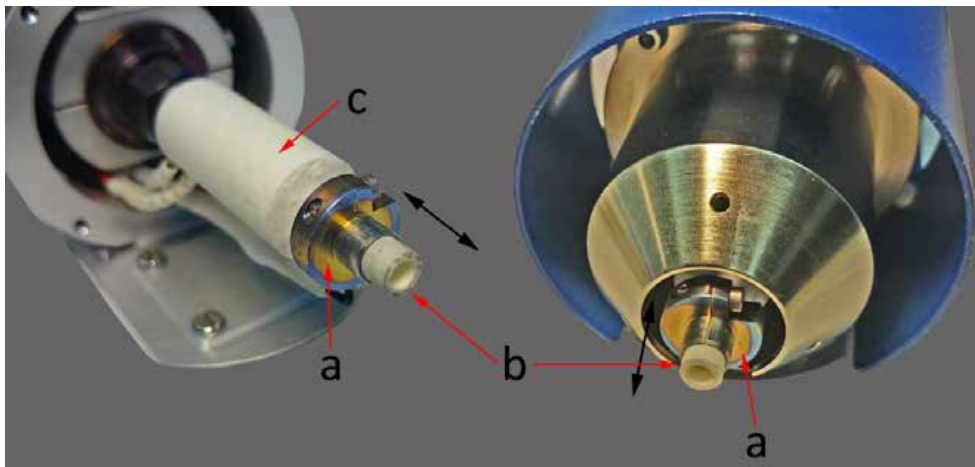
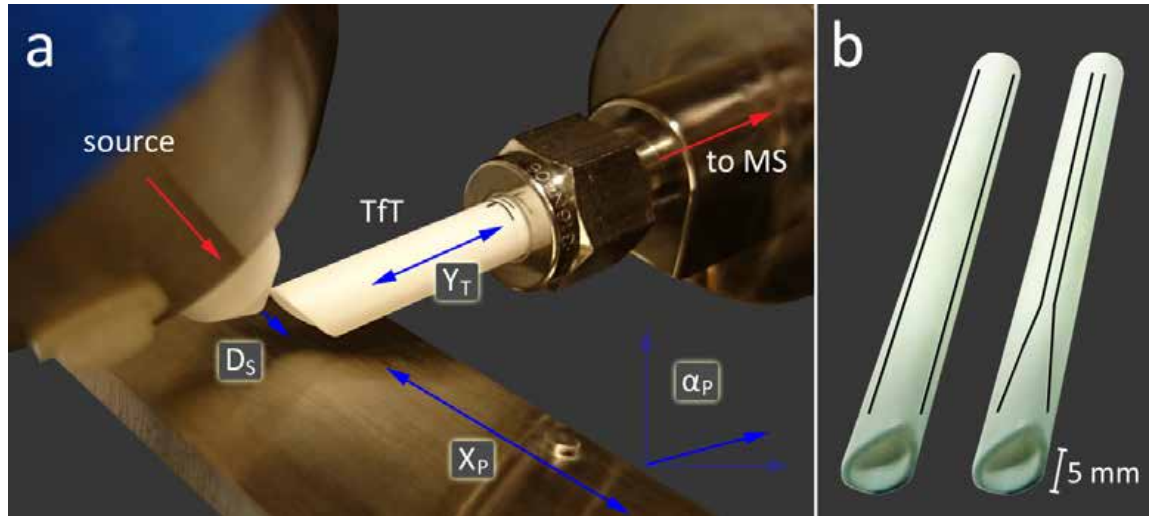
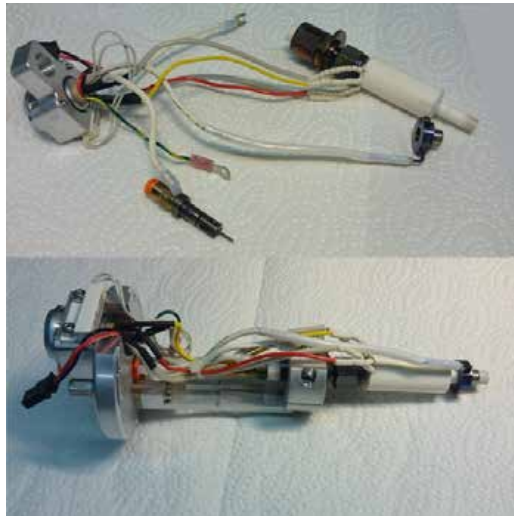


E. Chernetsova, A. Revelsky, G. Morlock, Rapid Commun Mass Spectrom 25 (2011) 2275-2282

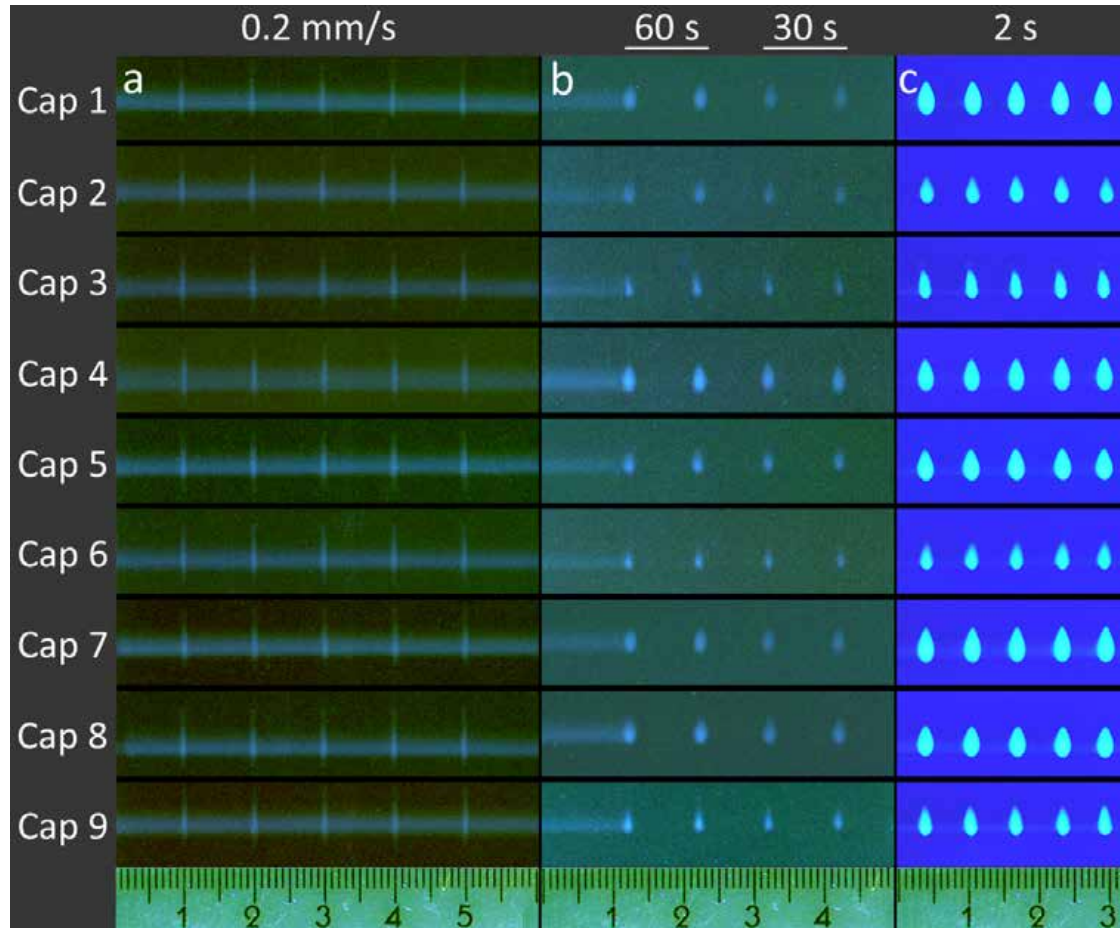
Optimization of HPTLC-DART-SVPA-MS



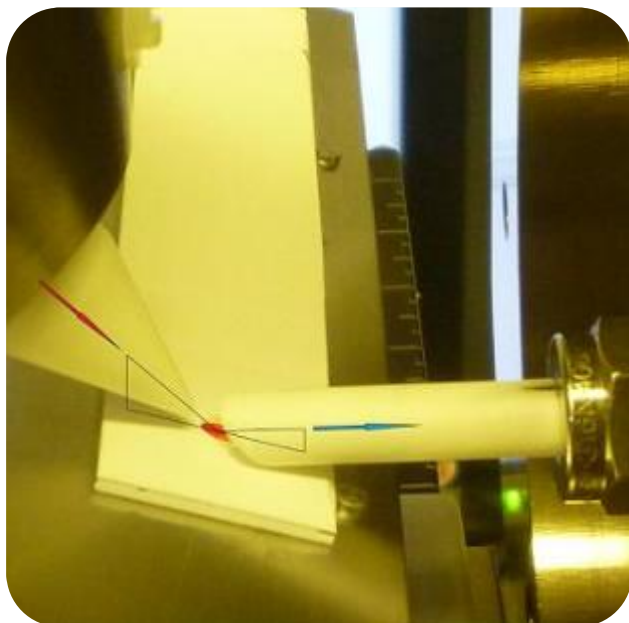
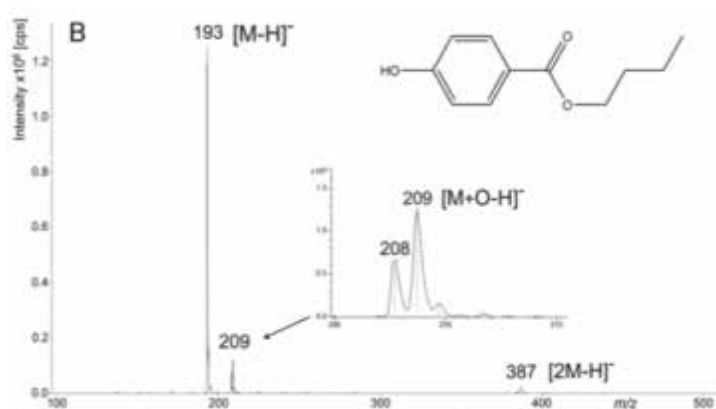
Optimization of HPTLC-DART-SVPA-MS



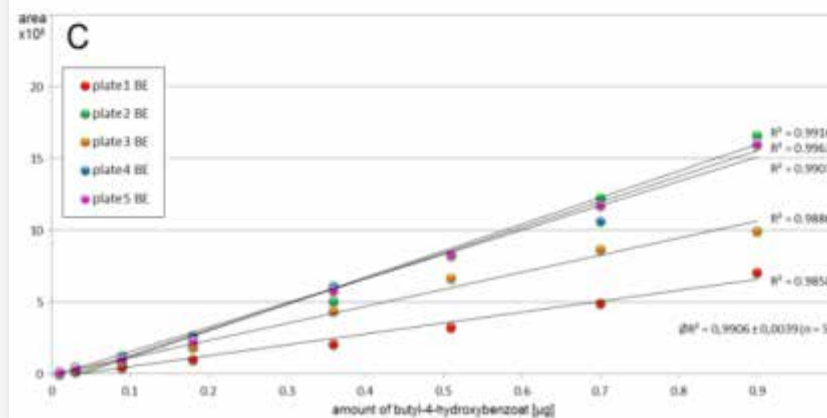
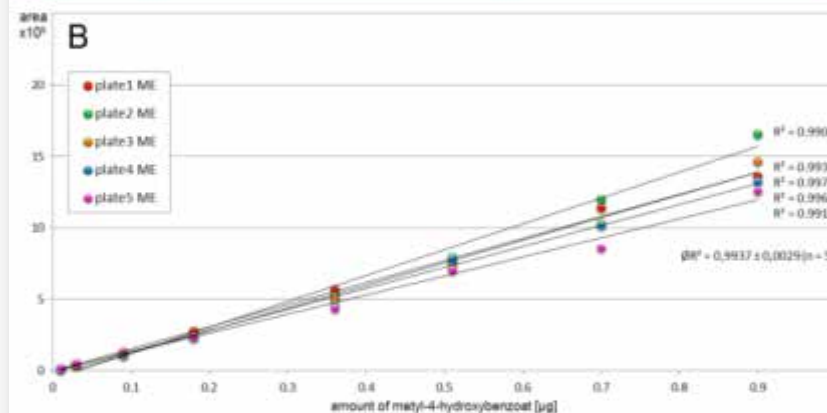
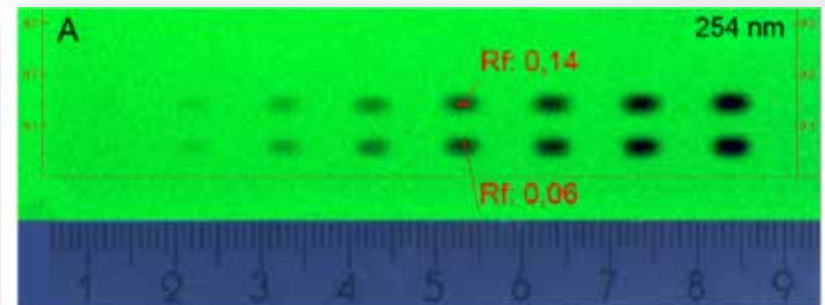
Optimization of HPTLC-DART-SVPA-MS



HPTLC-DART-SVPA-MS of preservatives

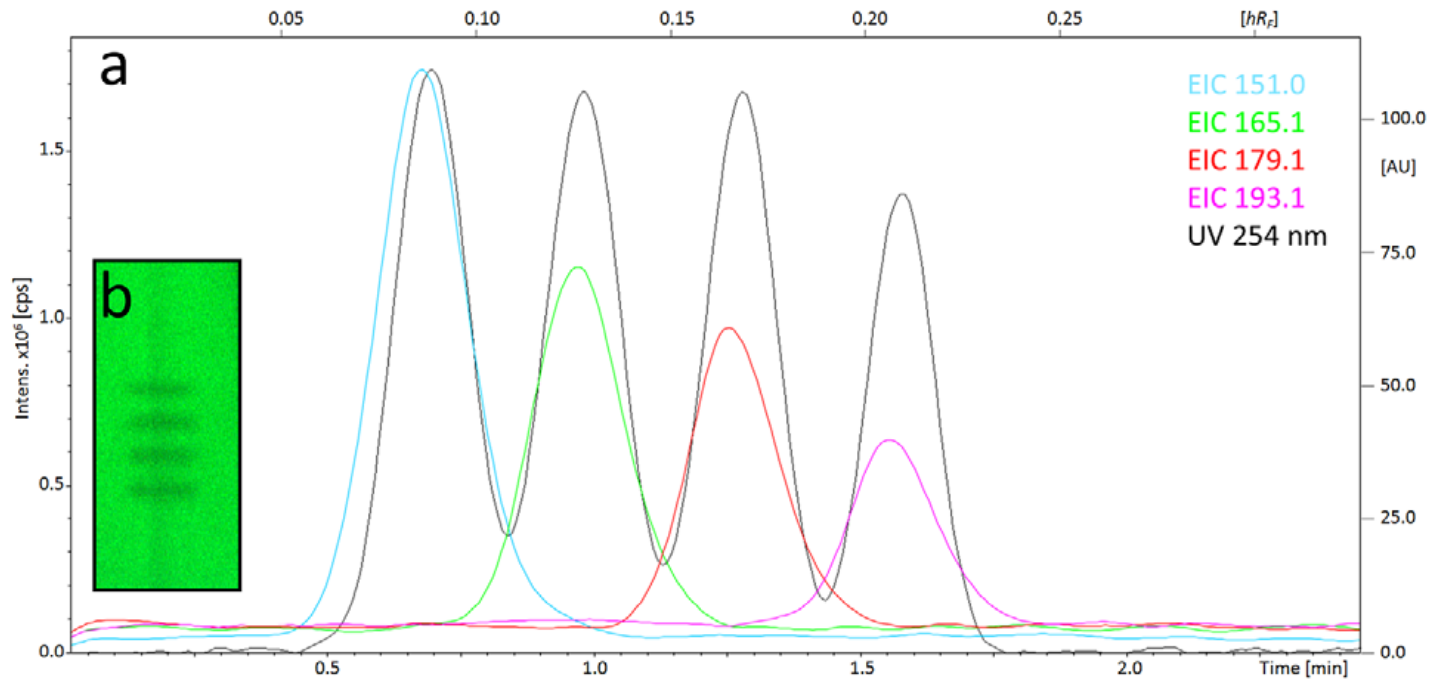


T. Häbe, G. Morlock, Rapid Commun Mass Spectrom 29 (2015) 474–484



HPTLC-UV *versus* scanning HPTLC-DART-MS

Four separated parabens (each 120 ng/band) detected via densitometry and DART-MS



T. Häbe, G. Morlock, in preparation

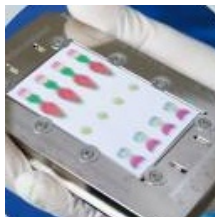
Comparison of the approaches

DART/APGD



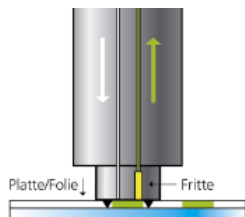
- dry desorption technique ↔ DESI
- no plate preparation etc. ↔ SALDI, MALDI
- ambient conditions, no high voltage ↔ micro junction
- simple spectra ↔ MALDI, SIMS
- **quantitativ *with* internal standard** → **scan function**

MALDI



- ✓ strict protocol for plate preparation
- ✓ complex spectra
- ✓ quantitativ *with* internal standard → scan function

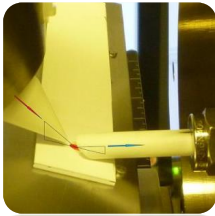
Elution-head based Interface



- ✓ *universally* connectable to any LC-MS system given
- ✓ plug & play interface (without adjustments or modifications)
- ✓ whole plate (no cut)
- ✓ all carriers and all layers ↔ micro junction
- ✓ whole zone incl. depth profile → high detectabilities
- ✓ quantitativ *without* internal standard ↔ desorption techniques
- ✓ targeted recording → cost-effective, but *no* scan function

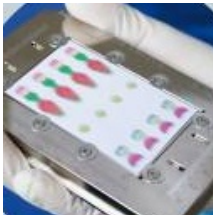
Comparison of the approaches

DART/FAPA



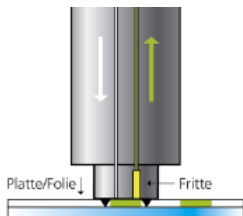
- dry desorption technique ↔ DESI
- no plate preparation etc. ↔ SALDI, MALDI
- ambient conditions, no high voltage ↔ micro junction
- simple spectra ↔ MALDI, SIMS
- **quantitativ** → **scanning MS..... discriminative MS**

MALDI



- ✓ strict protocol for plate preparation
- ✓ complex spectra
- ✓ quantitativ *with* internal standard → scan function

Elution-head
based
Interface



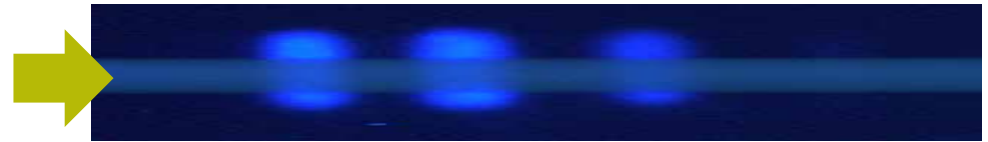
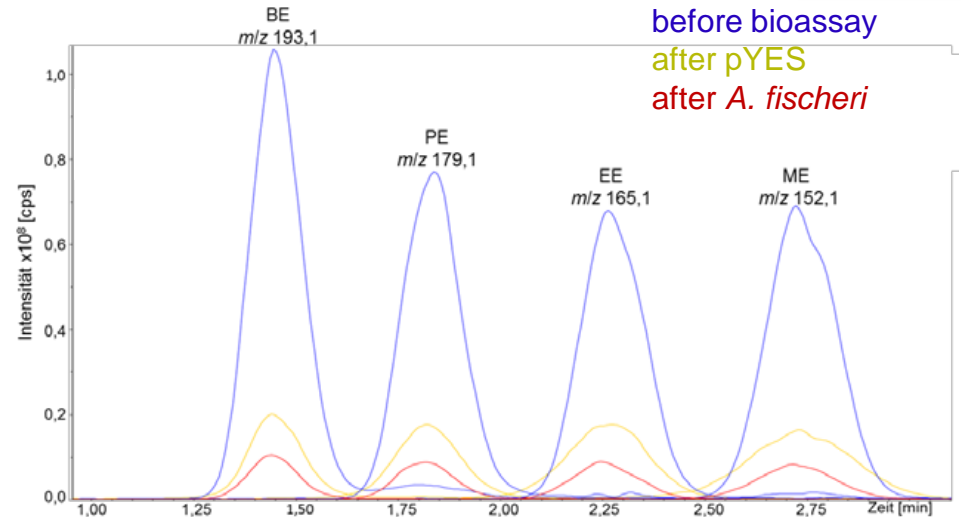
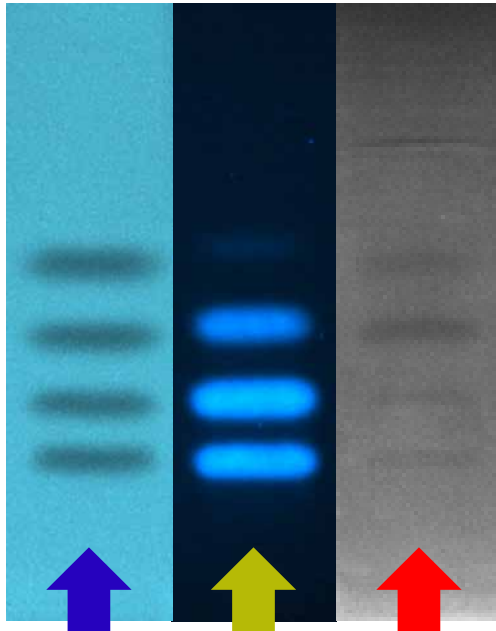
- ✓ *universally* connectable to any LC-MS system given
- ✓ plug & play interface (without adjustments or modifications)
- ✓ whole plate (no cut)
- ✓ all carriers and all layers ↔ micro junction
- ✓ whole zone incl. depth profile → high detectabilities
- ✓ quantitativ *without* internal standard ↔ desorption techniques
- ✓ targeted recording → cost-effective, but *no* scan function

HPTLC-DART-MS

Can we apply DART-MS
directly after the bioassay?

Still on the same plate?

Direct Bioautography hyphenated to DART-MS

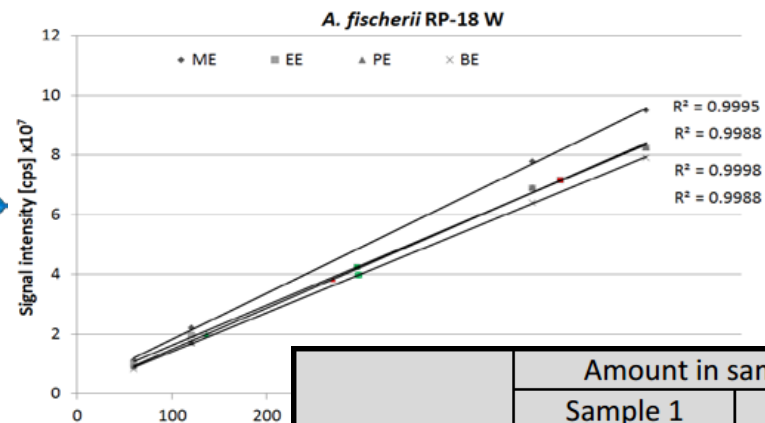
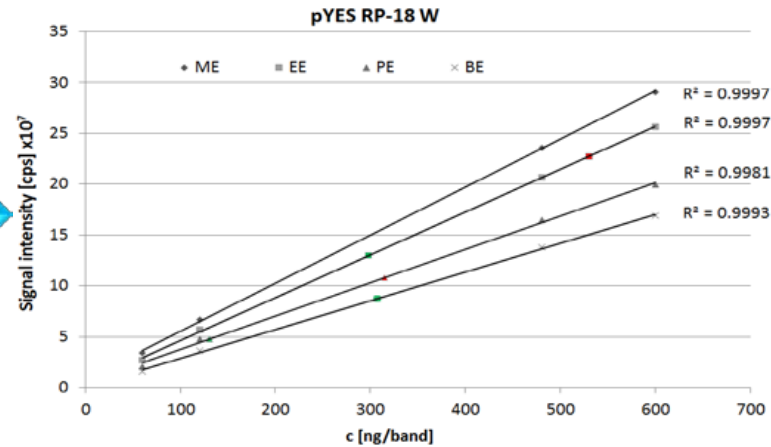
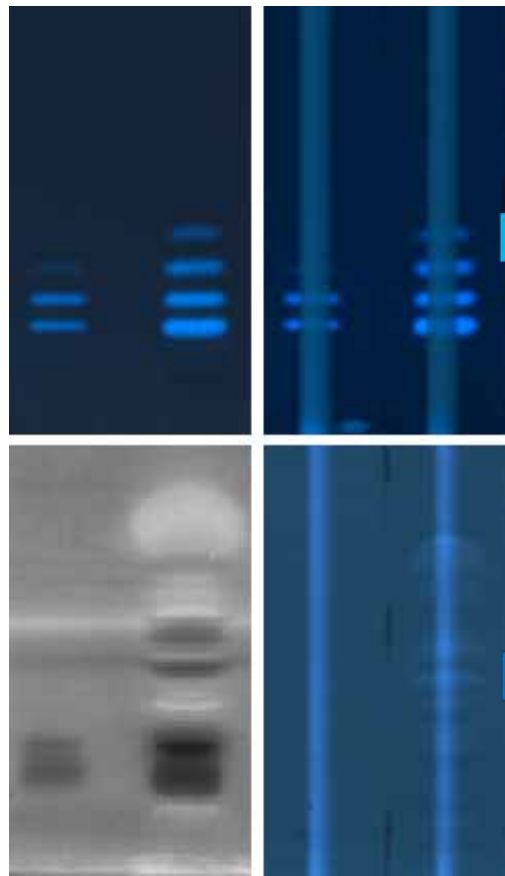


EICs of 4 separated parabens (each 600 ng/band)

- Signal decay *ca.* 90% for *A. fischeri* and 65-81% for pYES
- Sensitivity still sufficient for quantitation

	Signal decay [%]	
	<i>A. fischeri</i>	pYES
ME	88	65
EE	89	67
PE	90	76
BE	91	81

Sample quantitation after direct bioautography



- Mean determination coefficients of 0.9992
- Mean RSD of 4.6% between both methods.
- Reliable quantitation was possible after direct bioautography on normal and reversed phase layers

		Amount in sample [mg/100g]						
		Sample 1			Sample 2			
		ME	EE	PE	ME	EE	PE	BE
without	NP	103	56	30	165	75	37	65
BioAssay	RP	97	59	34	147	69	30	67
<i>A. fischeri</i>	NP	96	51	27	173	69	24	53
	RP	101	51	27	157	59	27	59
pYES	RP	111	53	31	170	60	26	62

T. Häbe, G. Morlock, in preparation

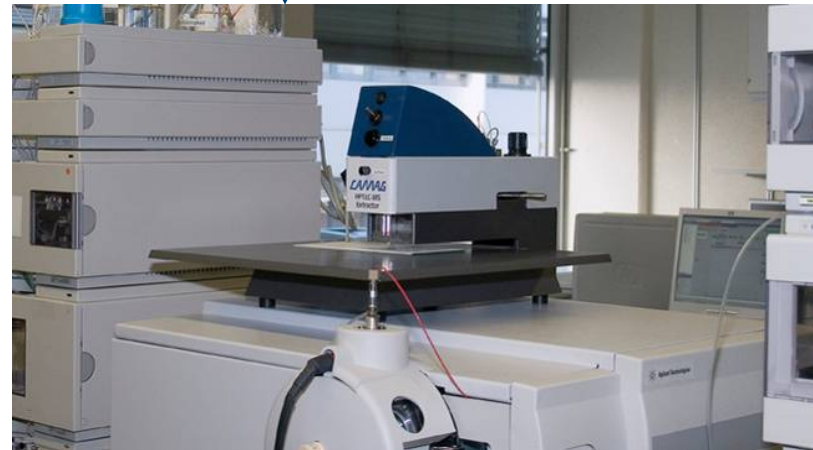
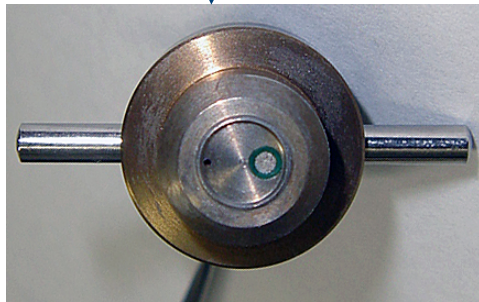
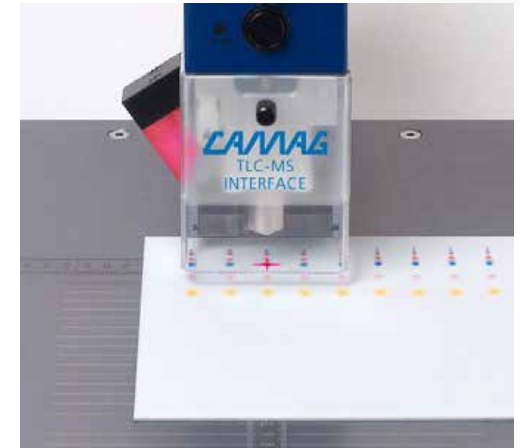
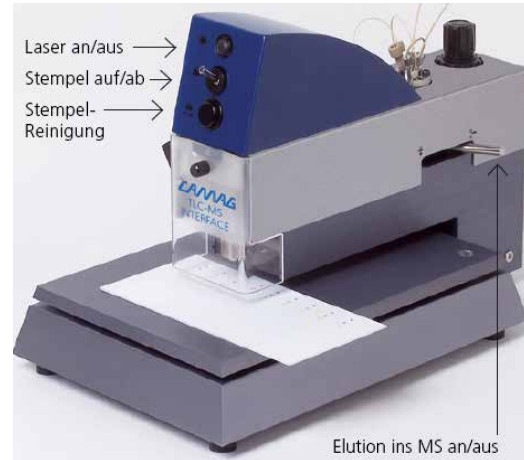
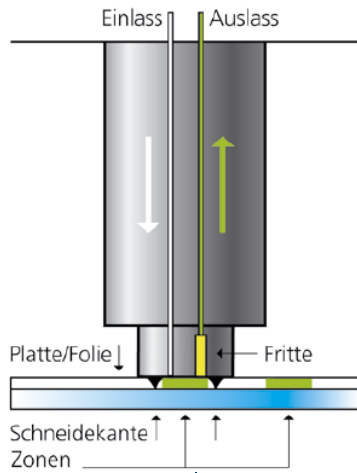
HPTLC-DART-MS

Can we apply DART-MS
directly after the bioassay?

Still on the same plate?

Yes, seems to work.

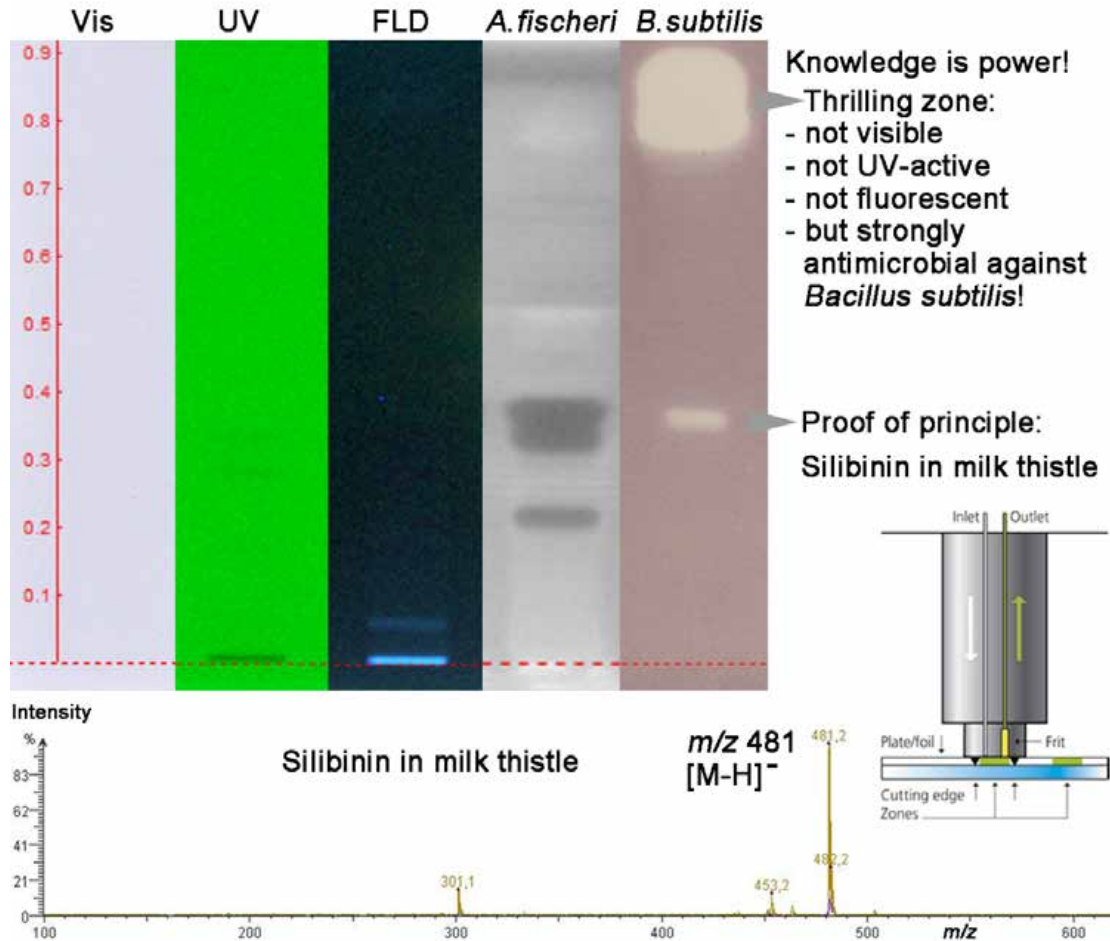
... and for elution head-based HPTLC-MS?



H. Luftmann, Anal Bioanal Chem 378 (2004) 964-968

A. Alpmann, G. Morlock, Anal Bioanal Chem 386 (2006) 1543-1551

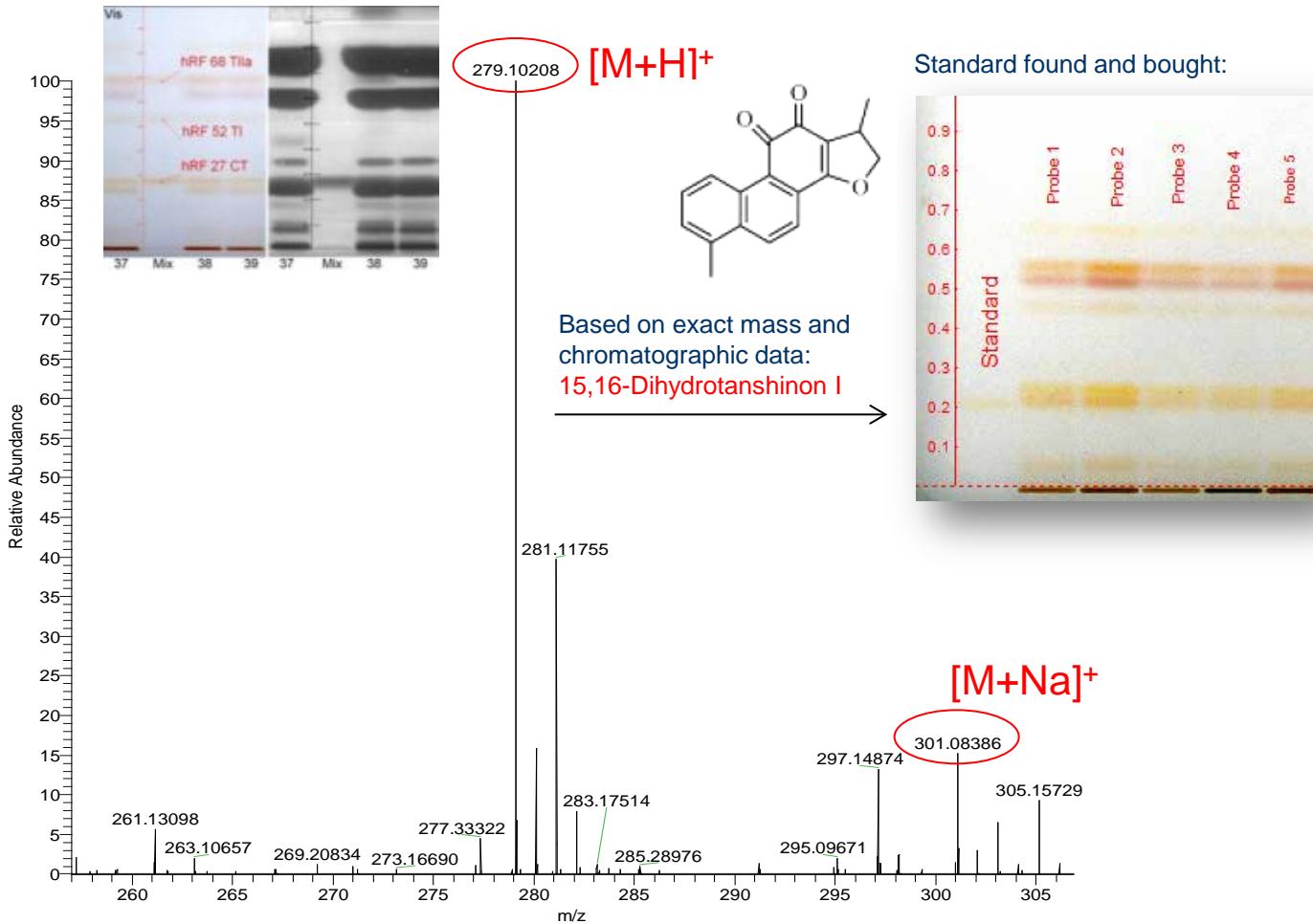
Directly from bioassay plate?



G. Morlock, The Analytical Scientist 27 (2015) 42-43

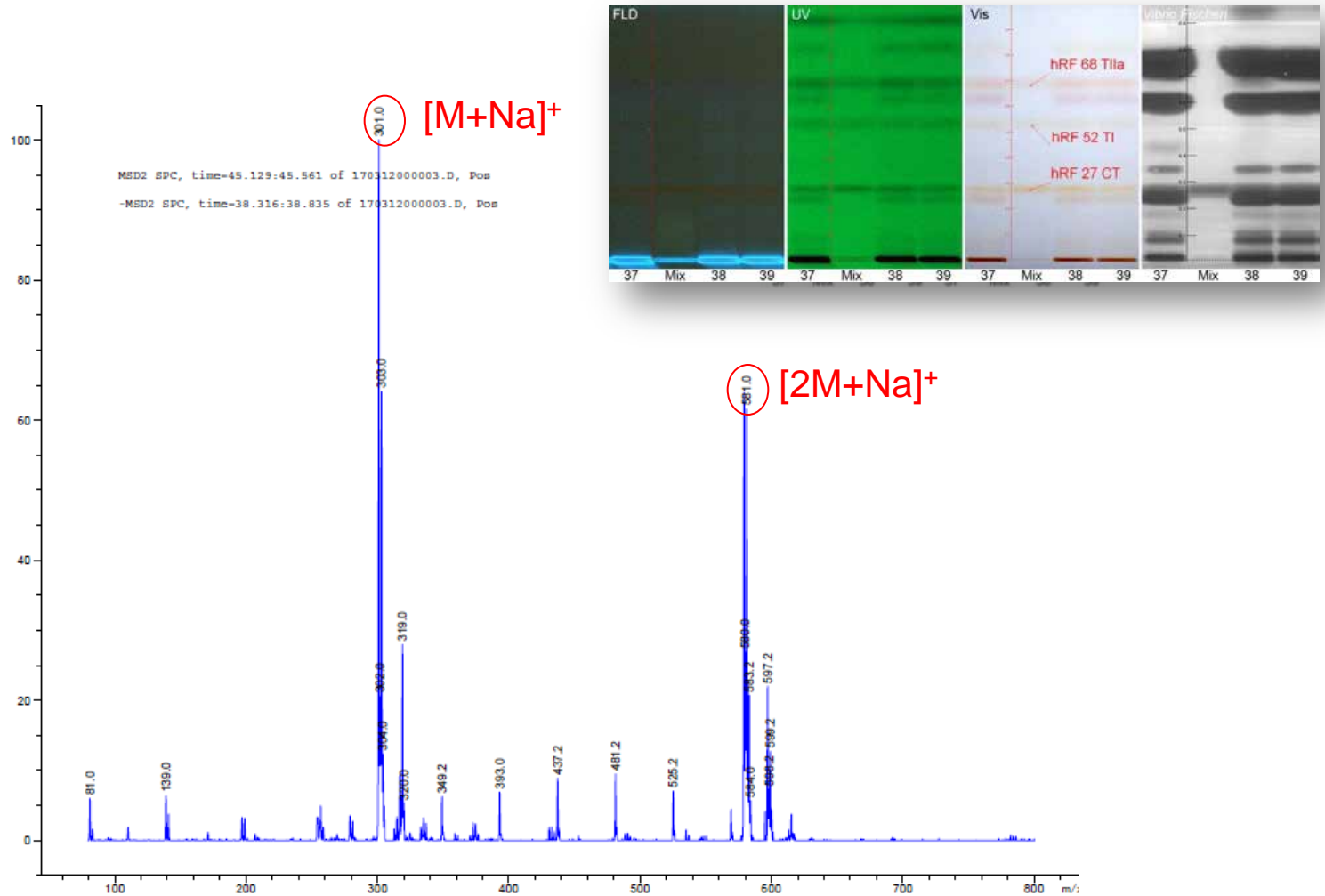
Taha, M.T., Krawinkel, M.B., Morlock, G.E., J Chromatogr A 1394 (2015) 137-147

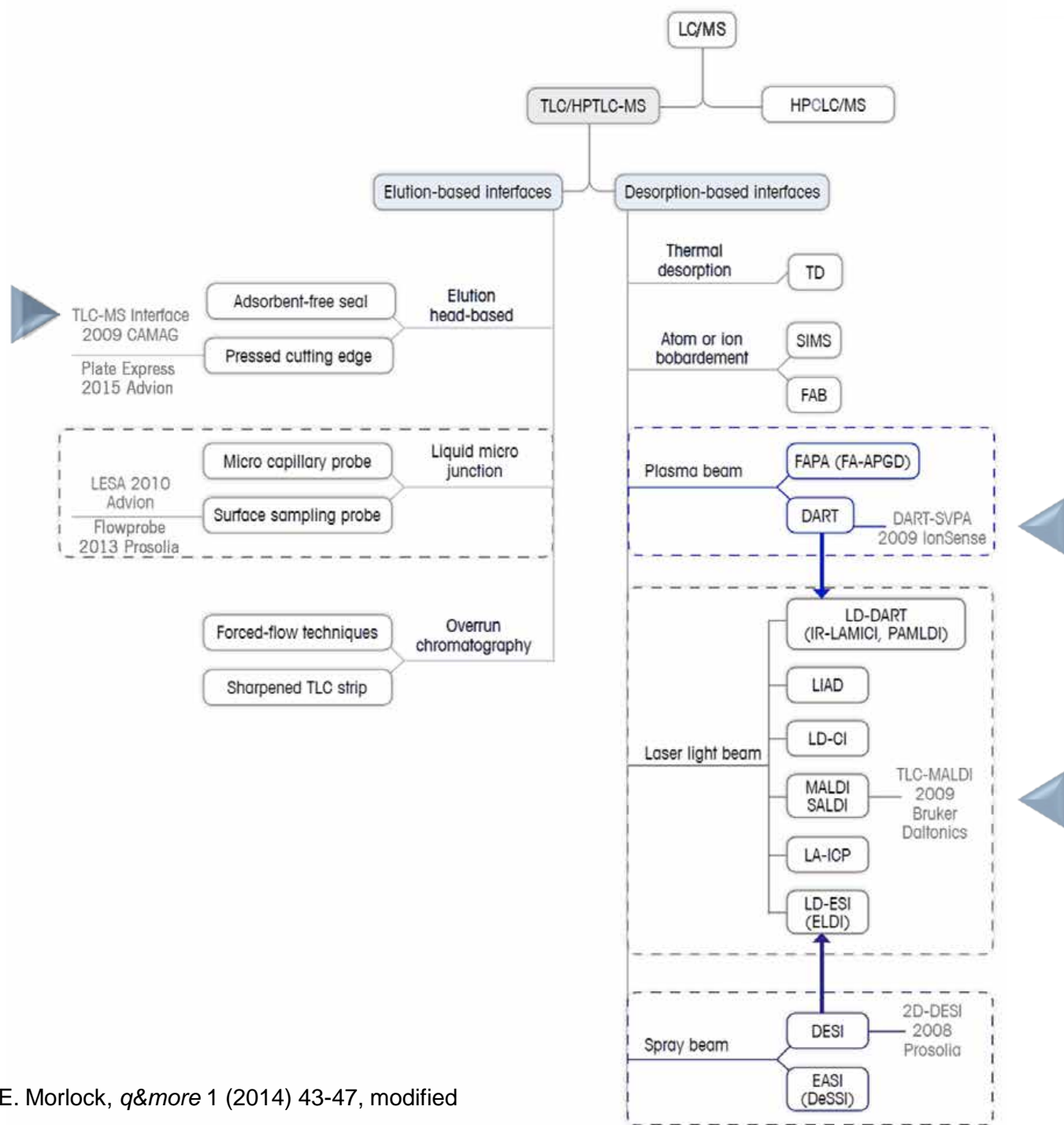
Unknown bioactive compound (below CT)



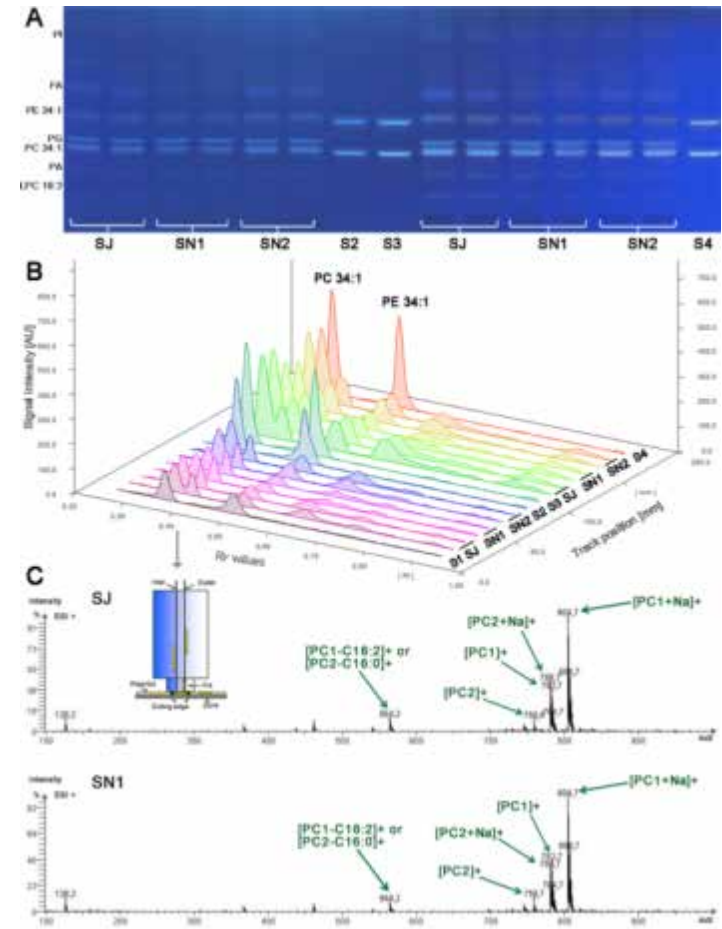
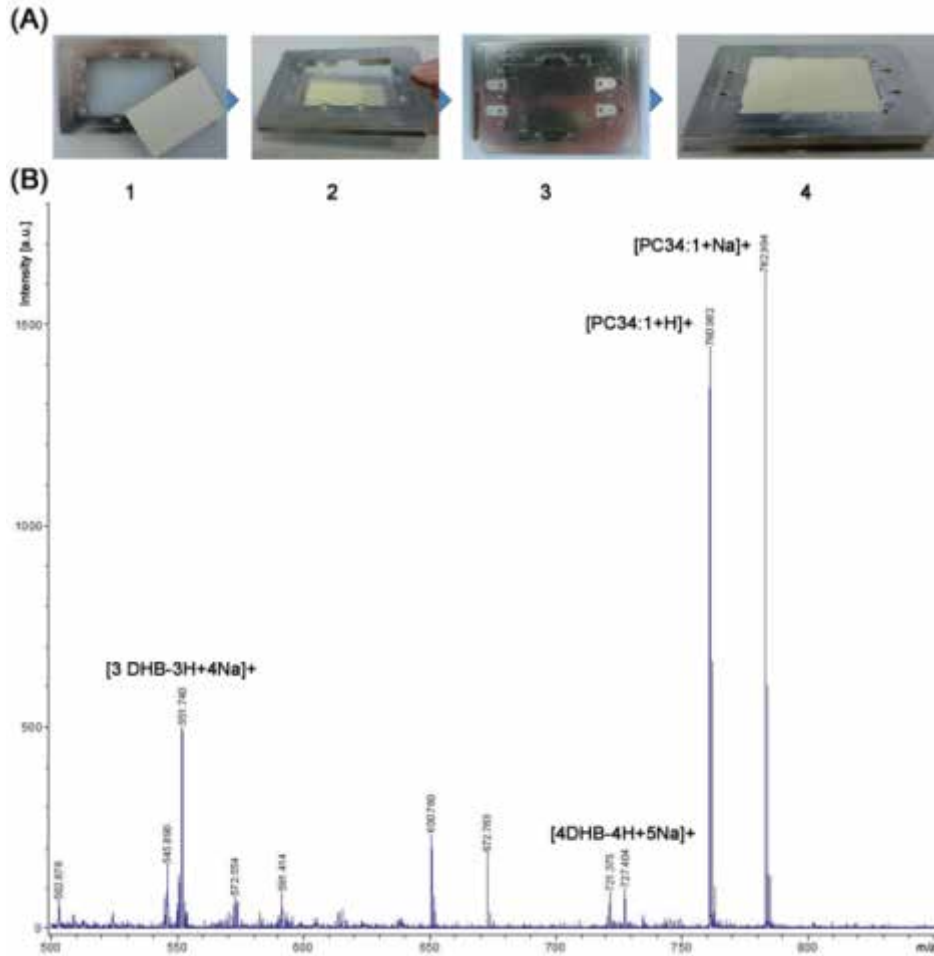
HPTLC-bioassay-ESI-MS

Mass spectra recorded after detection with bioassay → salt adducts are pronounced!

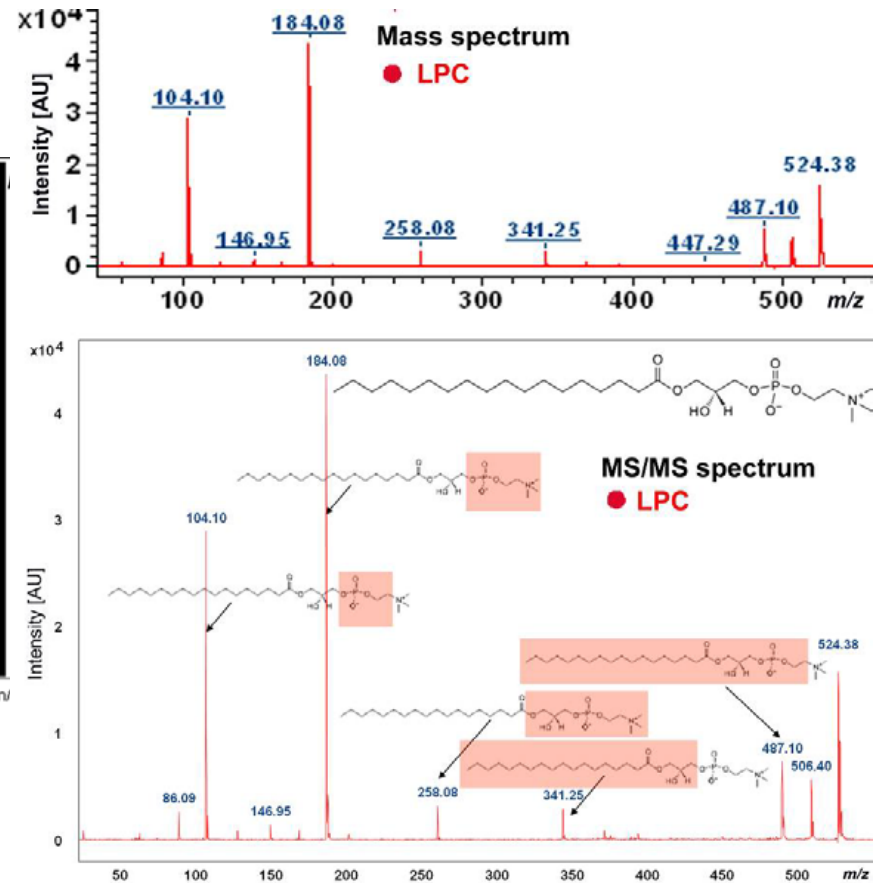
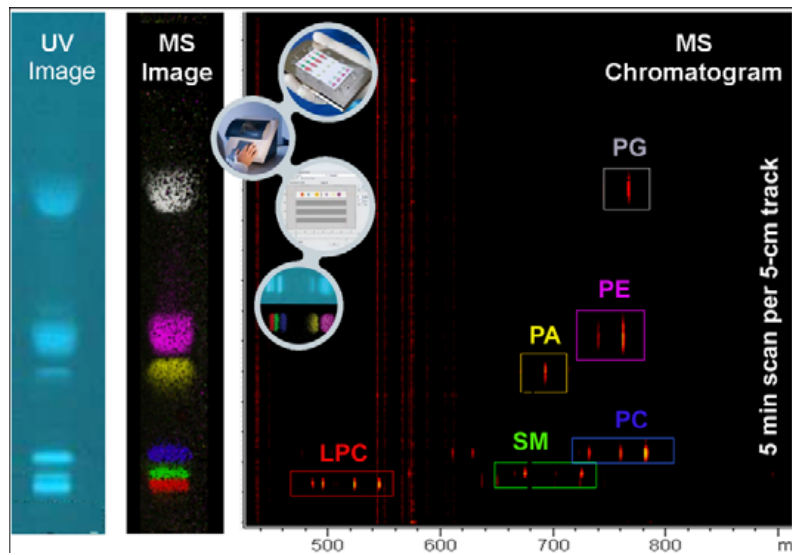




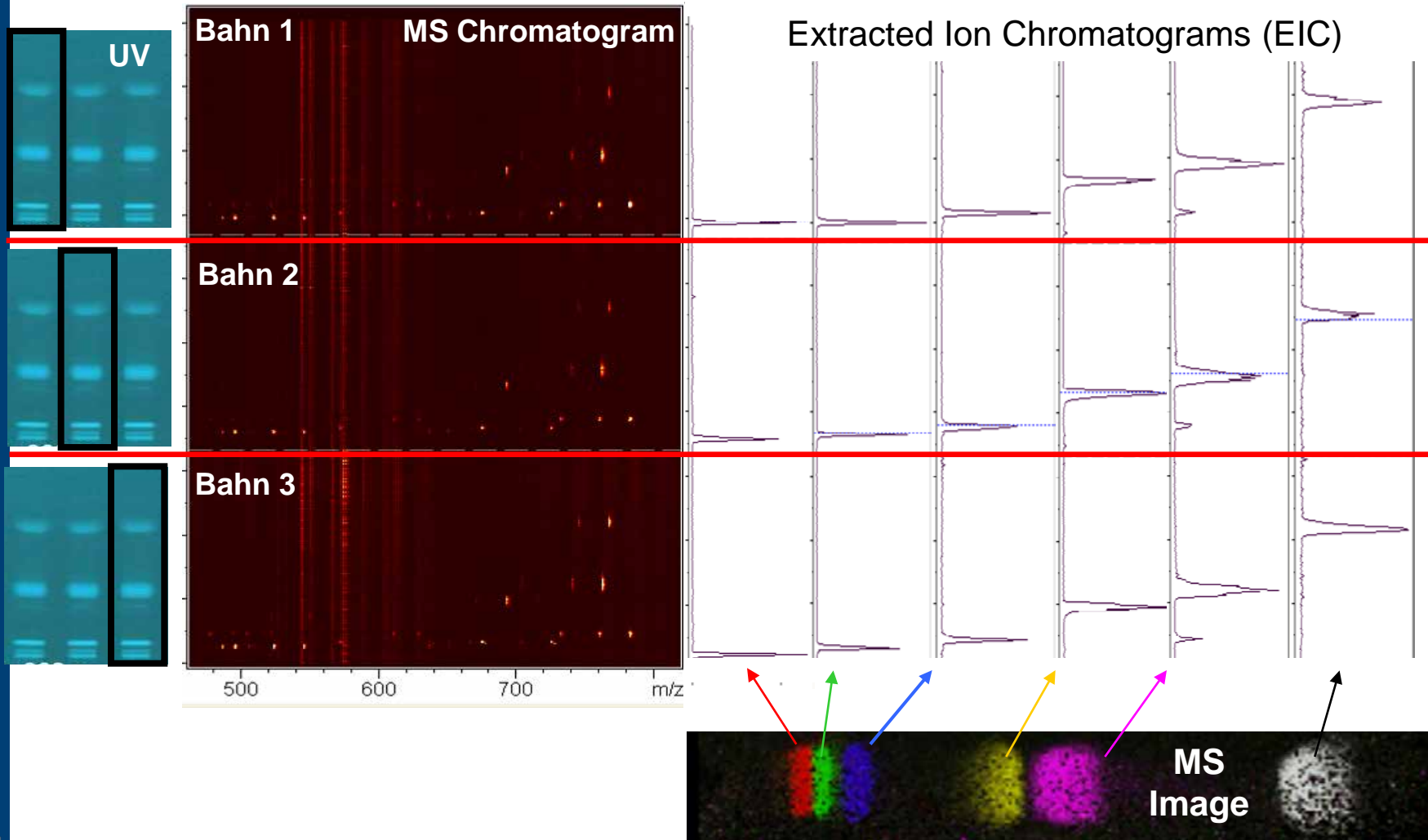
HPTLC-MALDI-TOFMS of phospholipids



HPTLC-FLD-MALDI-TOF MS

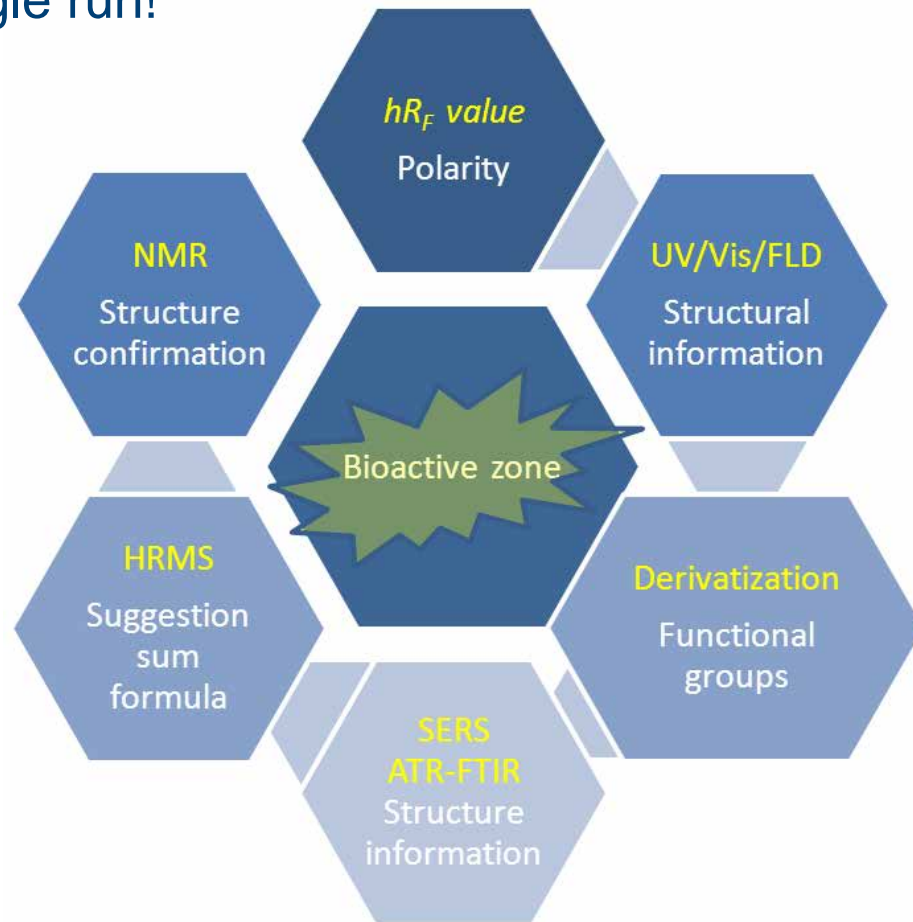


Quantification?



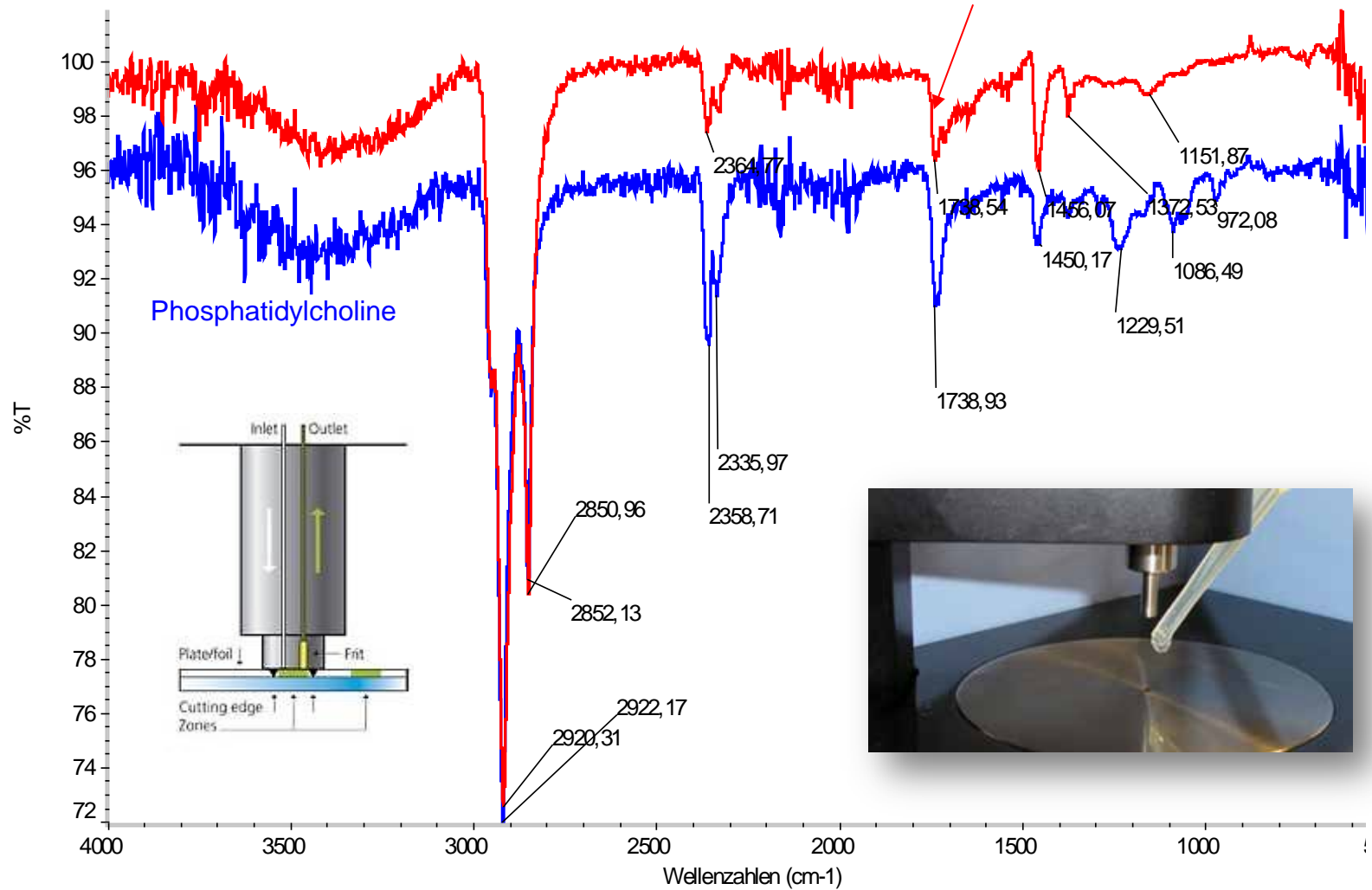
Goal: From bioactive zone to sum formula

...in a single run!

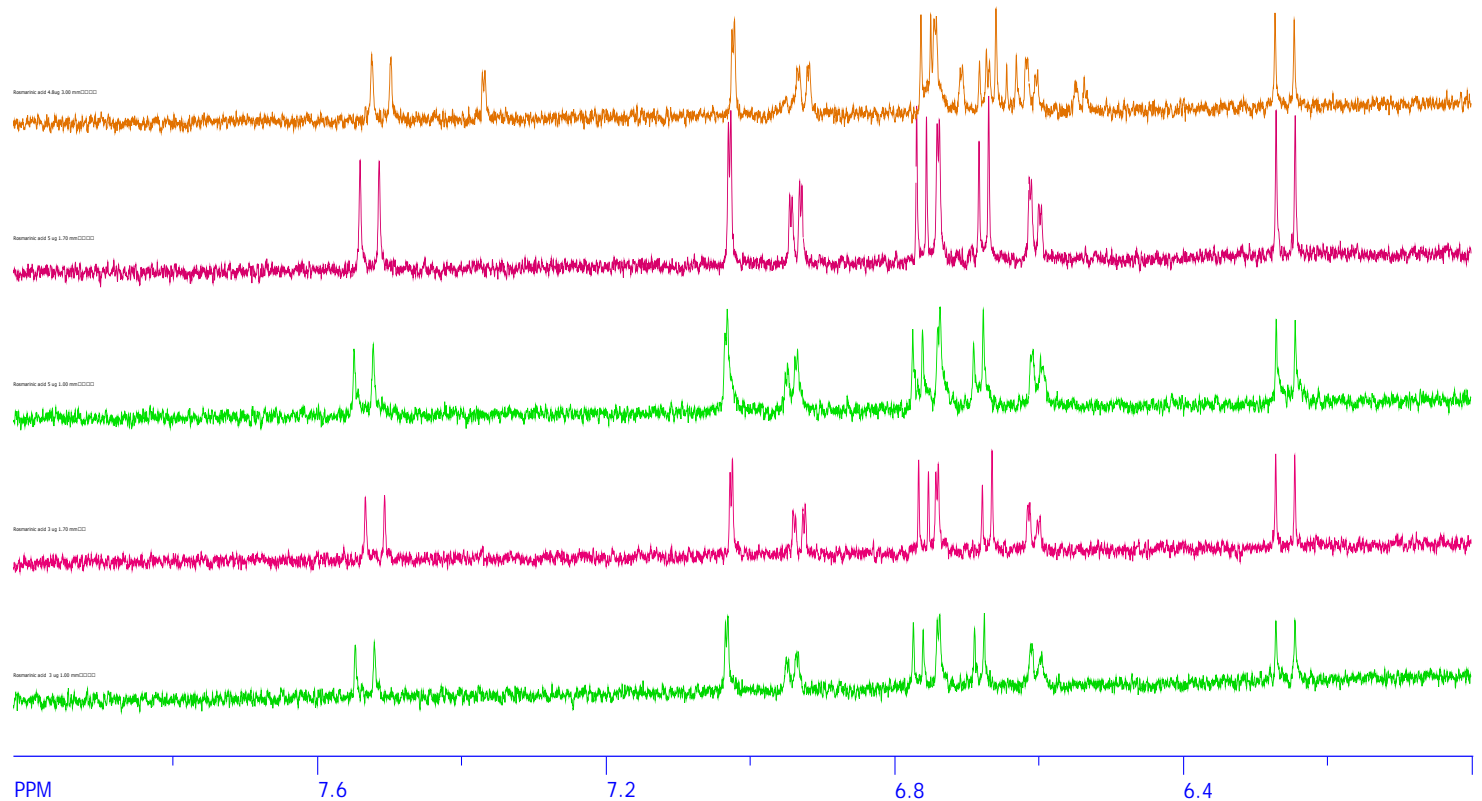
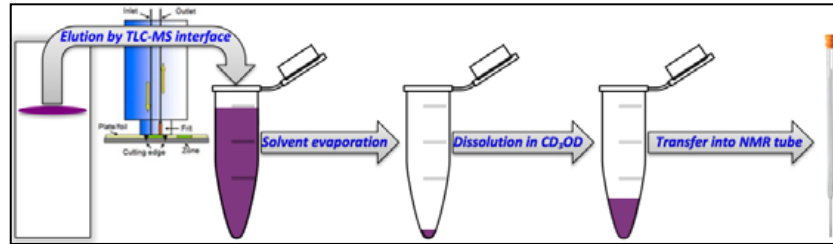


HPTLC-ATR FTIR


Anti-inflammatory compound isolated from *Lactobacillus fermentum*



HPTLC-NMR



GDCh course 335/16




GESELLSCHAFT DEUTSCHER CHEMIKER

Hyphenations in der HPTLC

HPTLC und Kopplungen
(in Zusammenarbeit mit der JLU Gießen)


Prof. Dr. Gertrud Morlock

- Kopplungstechniken
- Massenspektrometrie (MS)
- Wirkungsbezogene Analytik (Bioassays)
- ATR-FTIR und NMR
- Effektive Analytik



335/15

11. November 2015 · Gießen



Anerkannt mit 18 Punkten
(www.zfzo.org)

Zentrum für
Lebensmittelchemie

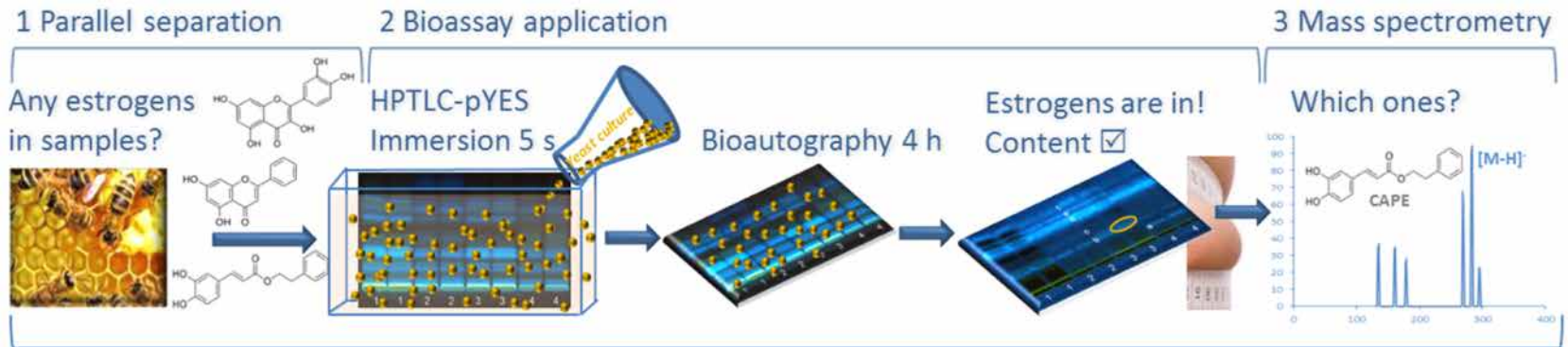
ANALYTISCHE CHEMIE

PROGRAMM

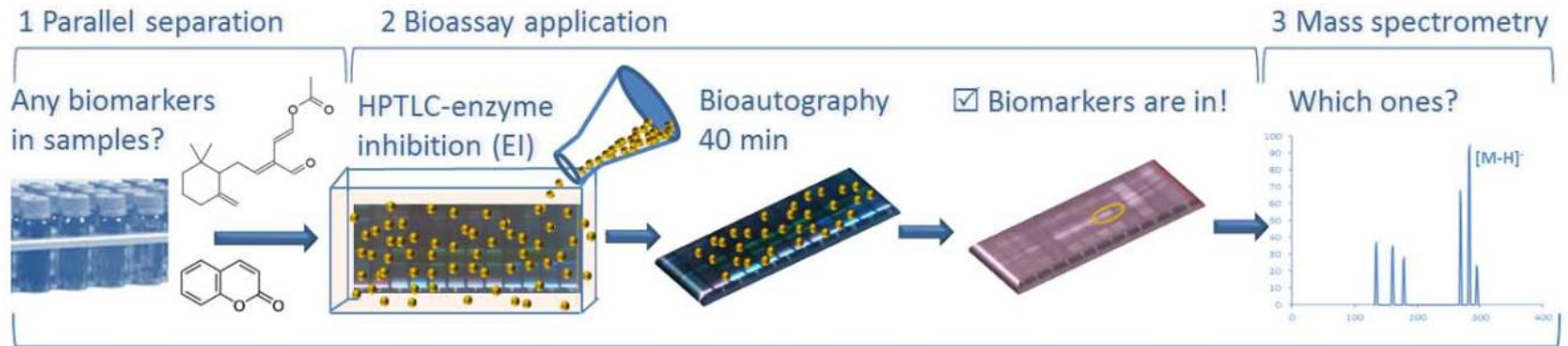
Mittwoch, 11. November 2015

- 9.00 Begrüßung und Einführung in die HPTLC (Morlock)
- 9.45 HPTLC erfahren – Experimente (Häbe, Klingelhöfer)
- 10.45 Kaffeepause
- 11.00 Hyphenations in der Planar-Chromatographie – Teil 1 (Morlock, Schwack)
 - 11.45 Gruppe 1: Experiment DC-HPLC/DAD-ESI MS (Oellig, Schwack)
 - Gruppe 2: Experiment HPTLC-UV/Vis/FLD-MALDI-TOF MS/MS (Lochnit, Krüger)
- 12.30 Gruppe 1: Experiment HPTLC-UV/Vis/FLD-MALDI-TOF MS/MS (Lochnit, Krüger)
- Gruppe 2: Experiment DC-HPLC/DAD-ESI MS (Oellig, Schwack)
- 13.15 Mittagspause
- 13.45 Hyphenations in der Planar-Chromatographie – Teil 2 (Morlock)
- 14.00 Gruppe 1: Experiment HPTLC-UV/Vis/FLD-ATR FTIR (Klingelhöfer, Gerbig)
- Gruppe 2: Experiment HPTLC-UV/Vis/FLD-Bioassay-ESI MS (Krüger, Kirchert)
- 14.45 Gruppe 1: Experiment HPTLC-UV/Vis/FLD-Bioassay-ESI MS (Krüger, Kirchert)
- Gruppe 2: Experiment HPTLC-UV/Vis/FLD-ATR FTIR (Klingelhöfer, Gerbig)
- 15.30 Kaffeepause
- 15.45 Hyphenations in der Planar-Chromatographie – Teil 3 (Morlock)
- 16.00 Gruppe 1: Experiment HPTLC-UV/Vis/FLD-DART-MS (Häbe, Krüger)
- Gruppe 2: Experiment HPTLC-UV/Vis/FLD-DESI-MS (Kirchert, Stiefel)
- 16.15 Gruppe 1: Experiment HPTLC-UV/Vis/FLD-DESI-MS (Kirchert, Stiefel)
- Gruppe 2: Experiment HPTLC-UV/Vis/FLD-DART-MS (Häbe, Krüger)
- 16.30 Diskussion (Morlock)
- 17.00 Voraussichtliches Ende der Veranstaltung

HPTLC-(bio)assay-MS



→ LC-bioassay-MS workflow for 20 samples in parallel within 5 h (15 min per sample)



→ LC-EI-MS workflow for 20 samples in parallel within 2 h (6 min per sample)

GDCh course 338/16



Wirkungsbezogene Analytik mit HPTLC-Bioassay-HRMS

(in Zusammenarbeit mit der JLU Gießen)

Prof. Dr. Gertrud Morlock

- Direkter Link zur wirkenden Substanz
- Chromatographie verbunden mit Bioassay
- HPTLC-UV/Vis/FLD-bioassay-HRMS
- Non-target Analytik
- Effektive Analytik



338/16

12. November 2015 - Gießen



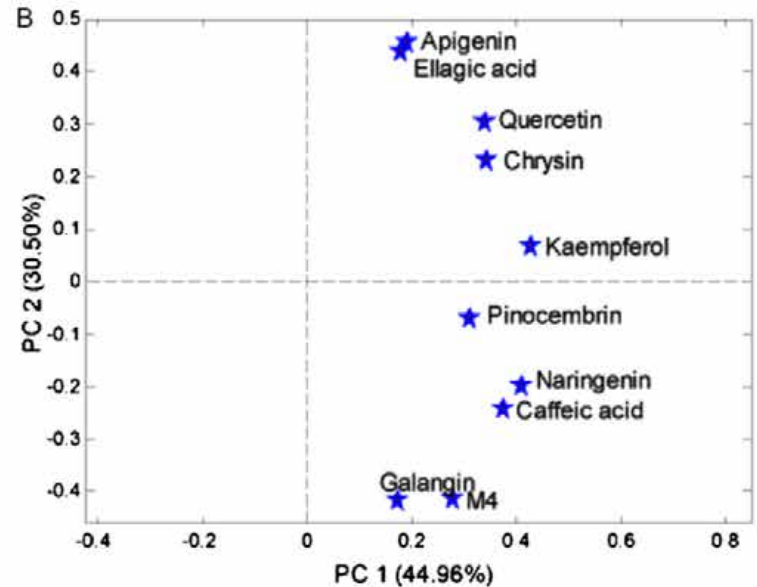
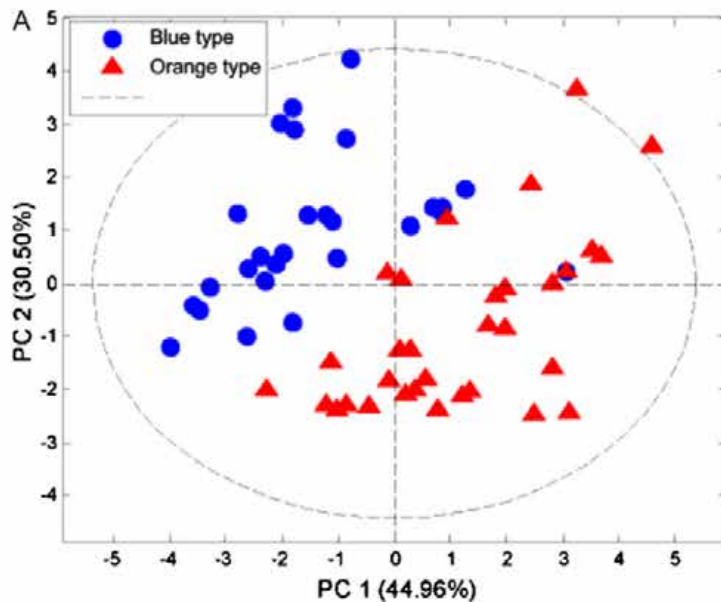
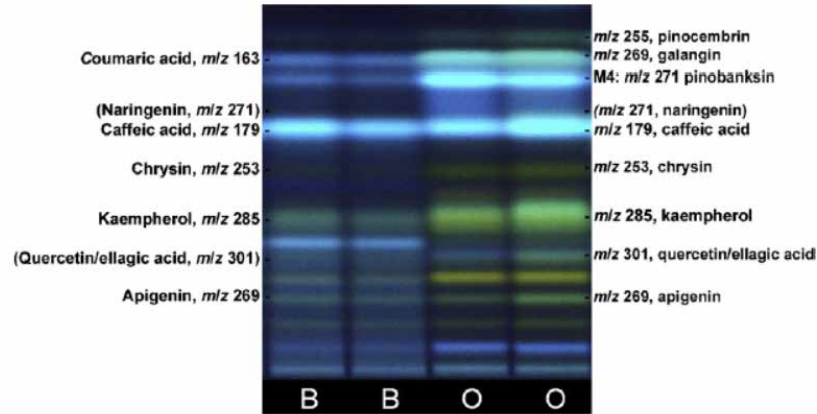
ANALYTISCHE CHEMIE

PROGRAMM

Donnerstag, 12 November 2015

- 9.00 Begrüßung und Überblick über die wirkungsbezogene Analytik (effect-directed analysis, EDA) unter besonderer Berücksichtigung der planar-chromatographischen Möglichkeiten (Morlock)
- Durchführung von Experimenten**
(in 2 Gruppen parallel à 6-8 Personen)
- 9.15 Gruppe 1: EDA von antimikrobiell-wirkenden Inhaltsstoffen: Experiment HPTLC-UV/Vis/FLD-*Bacillus subtilis*-(HPLC-)ESI-HRMS (Jamshidi-Aidj/Stiefel)
- Gruppe 2: EDA von estrogenartig-wirkenden Inhaltsstoffen mit dem planar Yeast Estrogen Screen (pYES): Experiment HPTLC-UV/Vis/FLD-pYES-(HPLC-)ESI-HRMS (Klingelhöfer)
- 10.15 Gruppe 1: EDA von α/β -Glucosidasehemmer: Experiment HPTLC-UV/Vis/FLD-Enzym-(HPLC-)ESI-HRMS (Jamshidi-Aidj/Kirchert)
- Gruppe 2: EDA von Cholinesterasehemmer: Experiment HPTLC-UV/Vis/FLD-Enzym-(HPLC-)ESI-HRMS (Häge)
- 11.00 Kaffeepause
- 11.15 Fortführung des *Bacillus subtilis*-Bioassays und der Enzymassays
- 12.00 Mittagessen
- 13.00 pYES-Fortführung
- 13.30 HPTLC-(HPLC-)ESI-HRMS von bioaktiven Verbindungen (Stiefel, Häbe)
- 14.15 pYES-Fortführung
- 14.45 Kaffeepause
- 15.00 Gruppe 1: EDA von Tyrosinase- und Xanthinoxidasehemmer: Experiment HPTLC-UV/Vis/FLD-Enzym-(HPLC-)ESI-HRMS sowie Experiment HPTLC-UV/Vis/FLD-DPPH^{*}-ESI-HRMS (Häge, Xingmei)
- Gruppe 2: EDA von bioaktiven Verbindungen (genereller Hinweis auf Bioaktivität): Experiment HPTLC-UV/Vis/FLD-*Alivibrio fischeri*-DART-HRMS (Krüger/Häbe)
- 16.15 Zusammenfassung und Diskussion der unterschiedlichen Bioassays
- 17.00 Voraussichtliches Ende der Veranstaltung

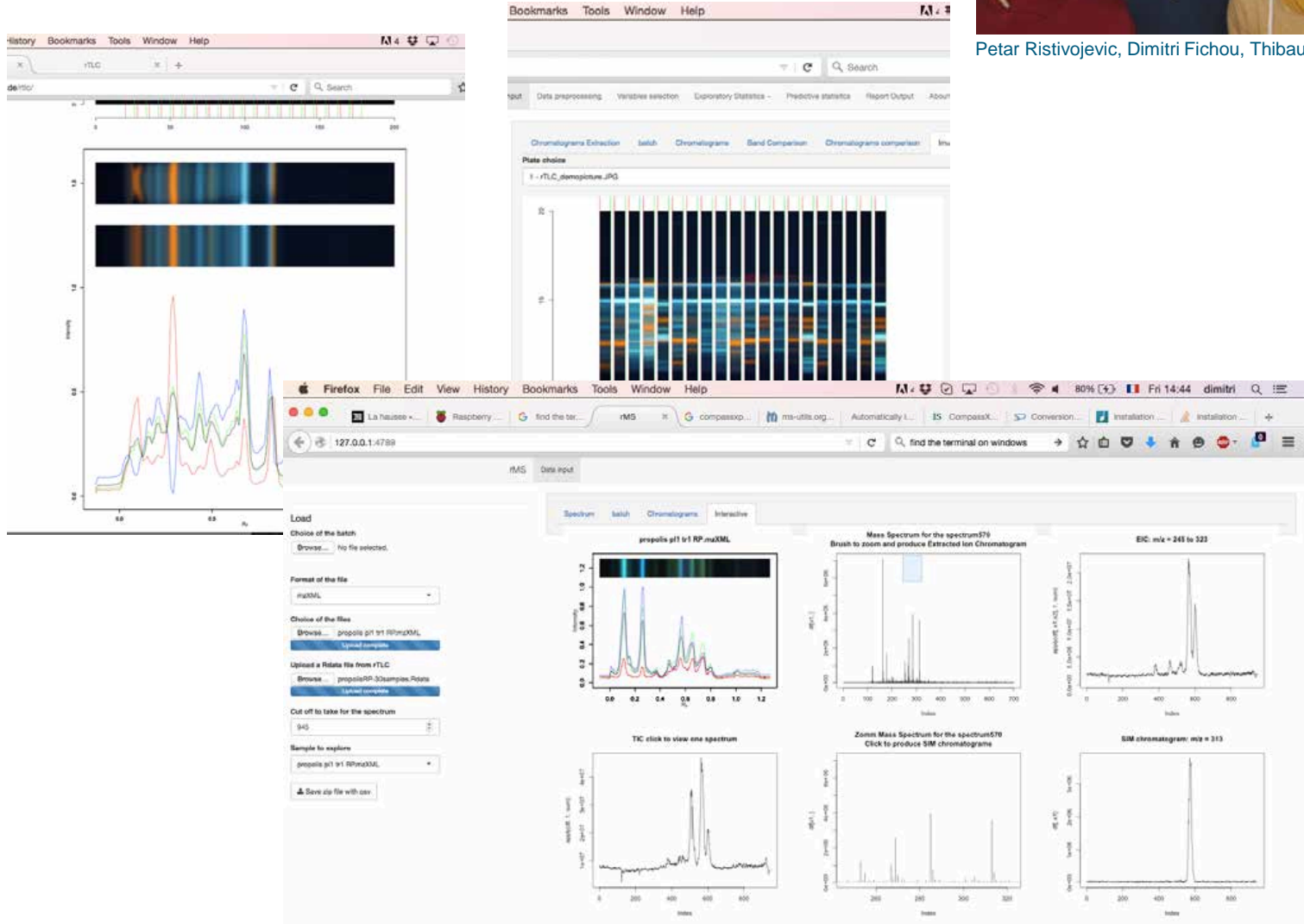
Multivariate data analysis: HPTLC and MS



Multivariate data analysis



Petar Ristivojevic, Dimitri Fichou, Thibaut Chasset



Use the best method for the given task!



Use the best method for the given task!

Selective derivatization **post**-chromatographically compensates the low separation power!

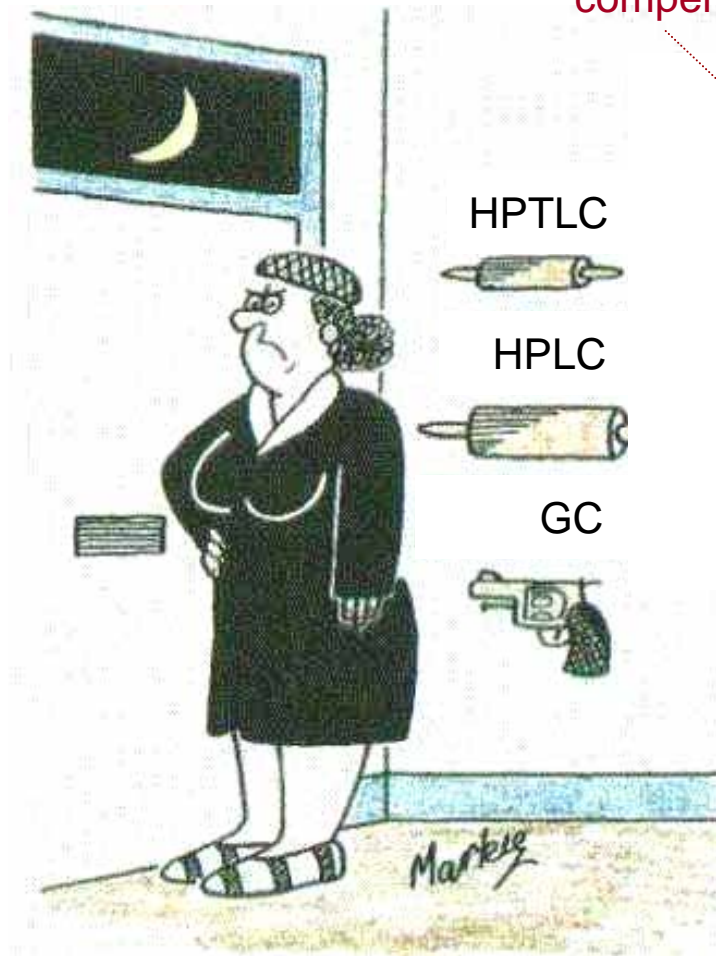


Plate number N

HPTLC

→ 8.000 ✓

HPLC

→ 18.000

180.000/m

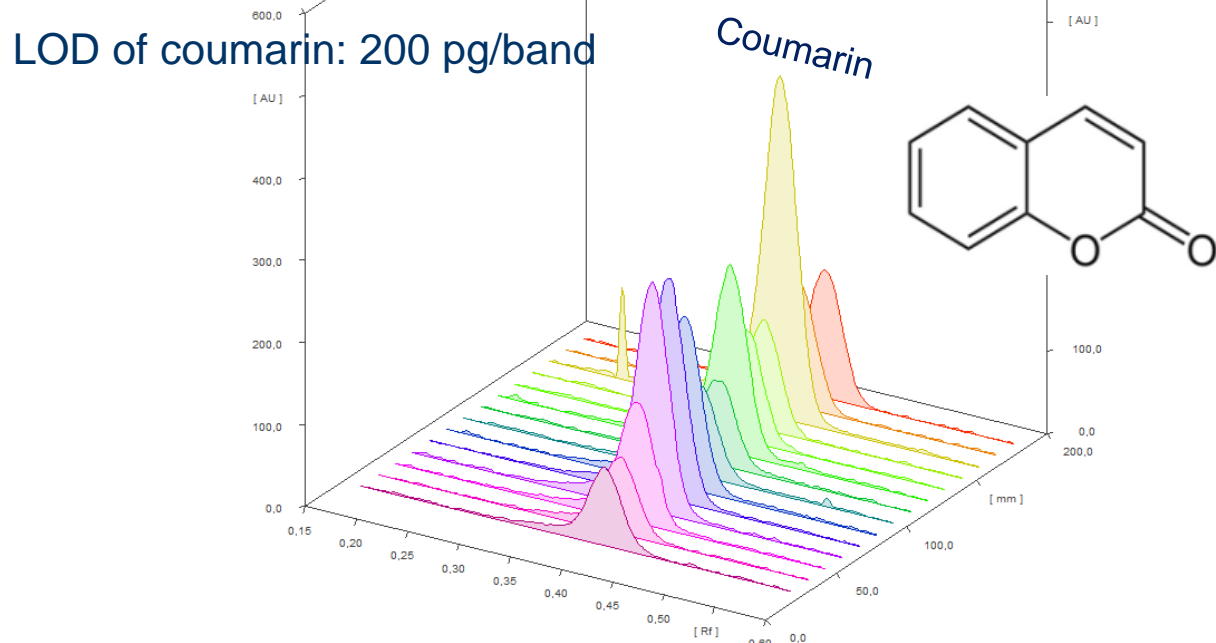
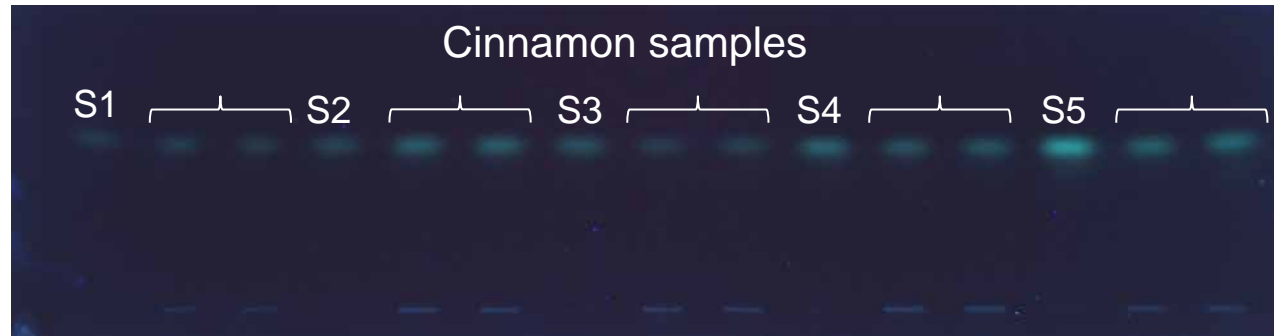
9.000/5cm

GC

→ 80.000

Analysis of coumarin

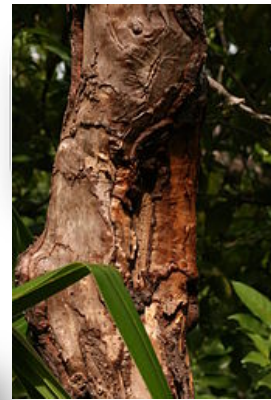
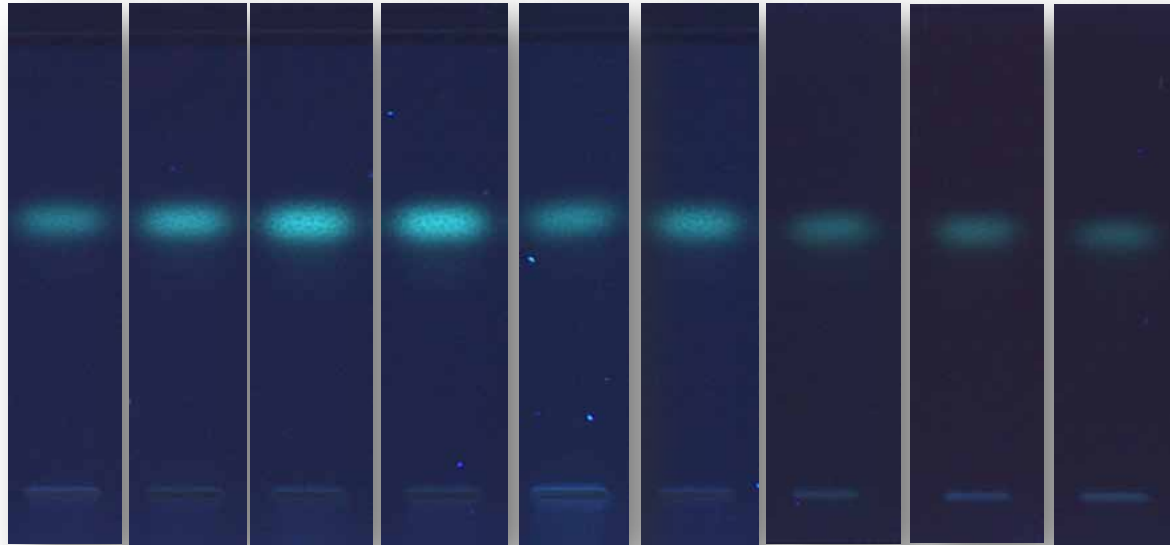
5 different cinnamon spice samples containing coumarin



L. Winheim, S. Krüger, G. Morlock, in preparation

Analysis of coumarin

9 different food samples containing coumarin



www.wikipedia.de



www.colourbox.de



www.deutsche-wirtschafts-nachrichten.de



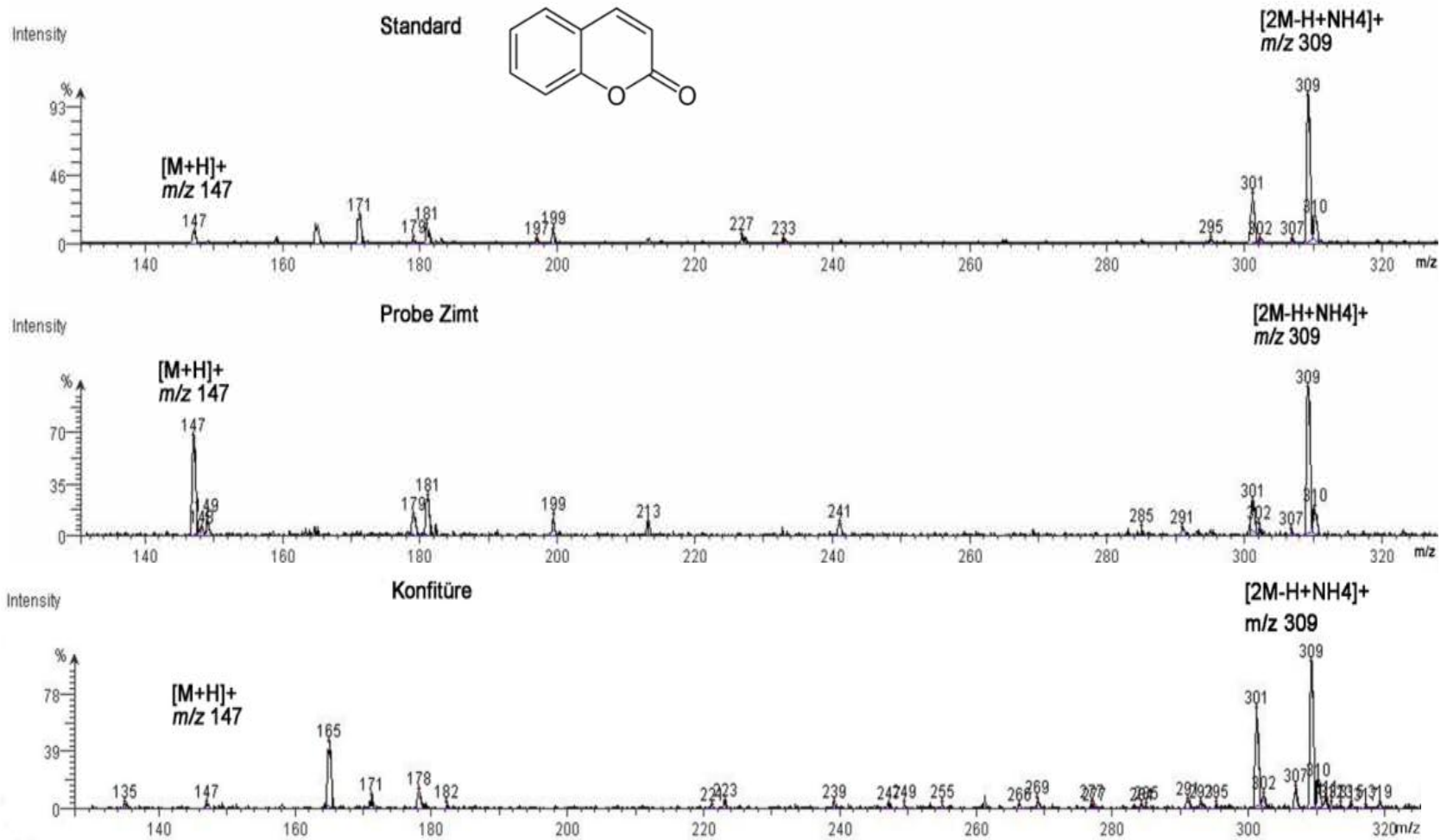
www.institut-fresenius.de

Coumarin content

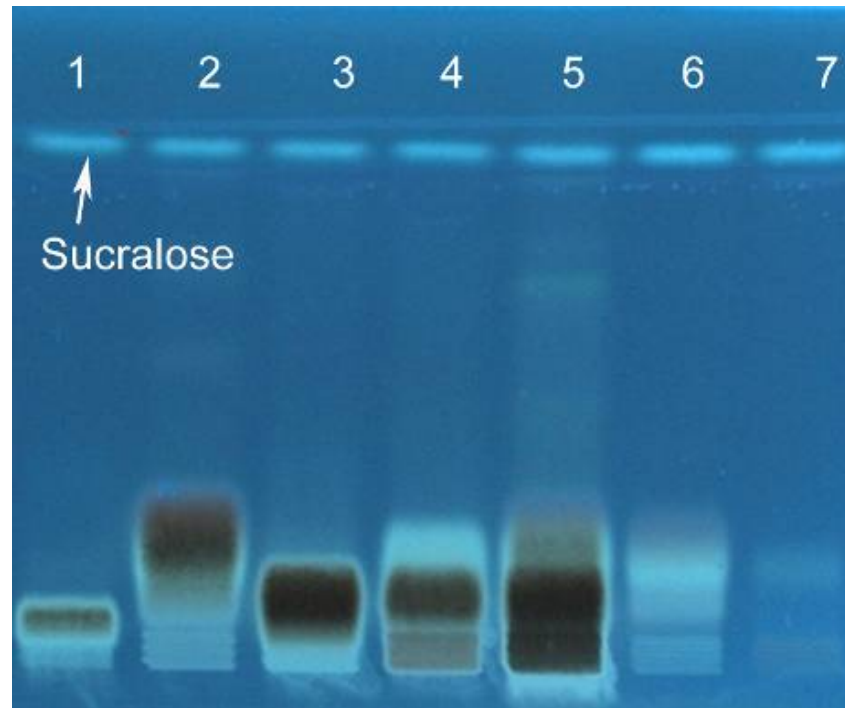
Sample	Manufacturer	Coumarin (mg/kg)	Repeatabilities (%RSD, n=2)	Reproducibility (%RSD, n=2)
Spice	Sonnentor - gemahlen	3732	0.4/1.2	1.0
	Lidl Kania - gemahlen	1615	0.4/0.3	2.4
Tea	YogiTea - Frauenpower	19	1.4/3.2	4.5
	TeeGeschwendner – Kaminfeuer	22	3.3/2.0	0.5
Cereals	Aldi Knusperone - Zimt Chips	1	3.8/5.9	0.4
Cinnamon bun	IKEA - Kanelbullar	16	1.4/4.5	6.6
Jam	Grafschafter Konfitüre – Winterzauber	4	1.6/1.6	1.6

L. Winheim, S. Krüger, G. Morlock, in preparation

Confirmation by HPTLC-ESI-MS



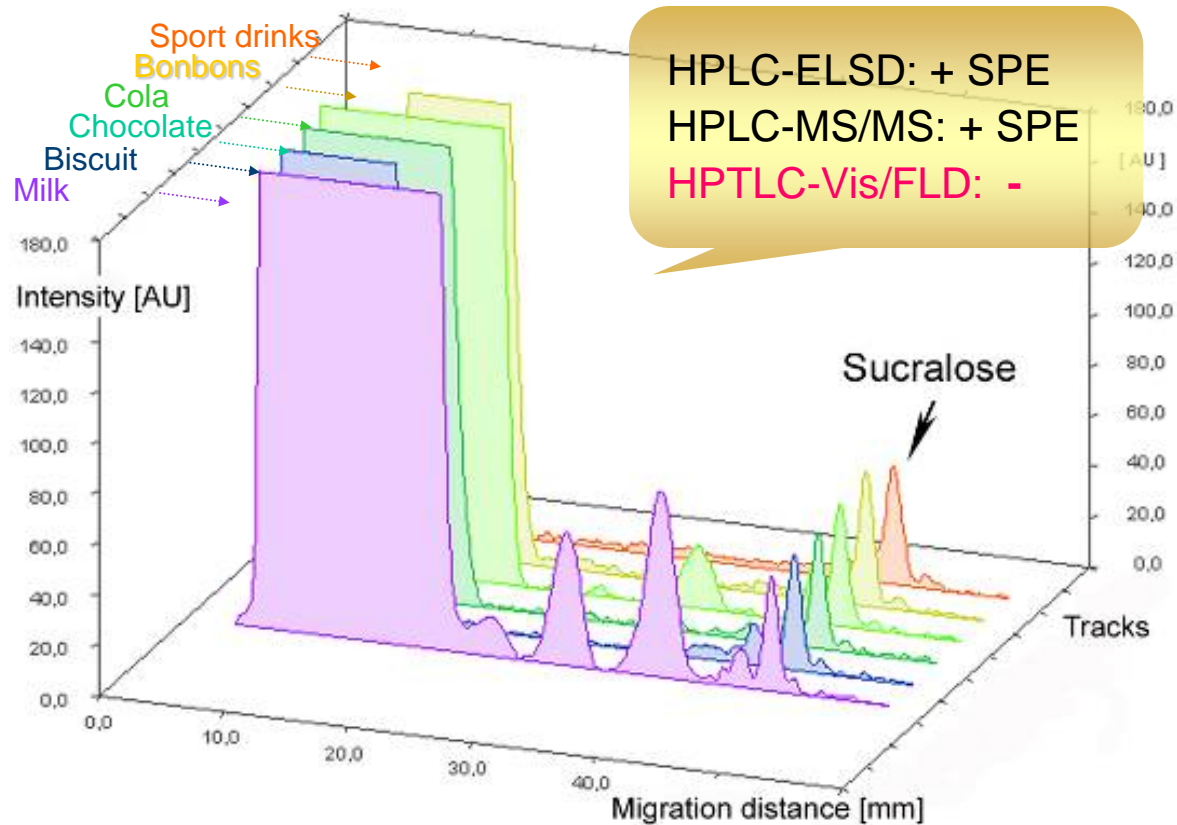
HPTLC is worth to keep in mind



Milk, biscuit, chocolate, cola, bonbons, energy/sport drinks

G. Morlock, M. Vega, J Planar Chromatogr 20 (2007) 411-417

Sample preparation and chromatography



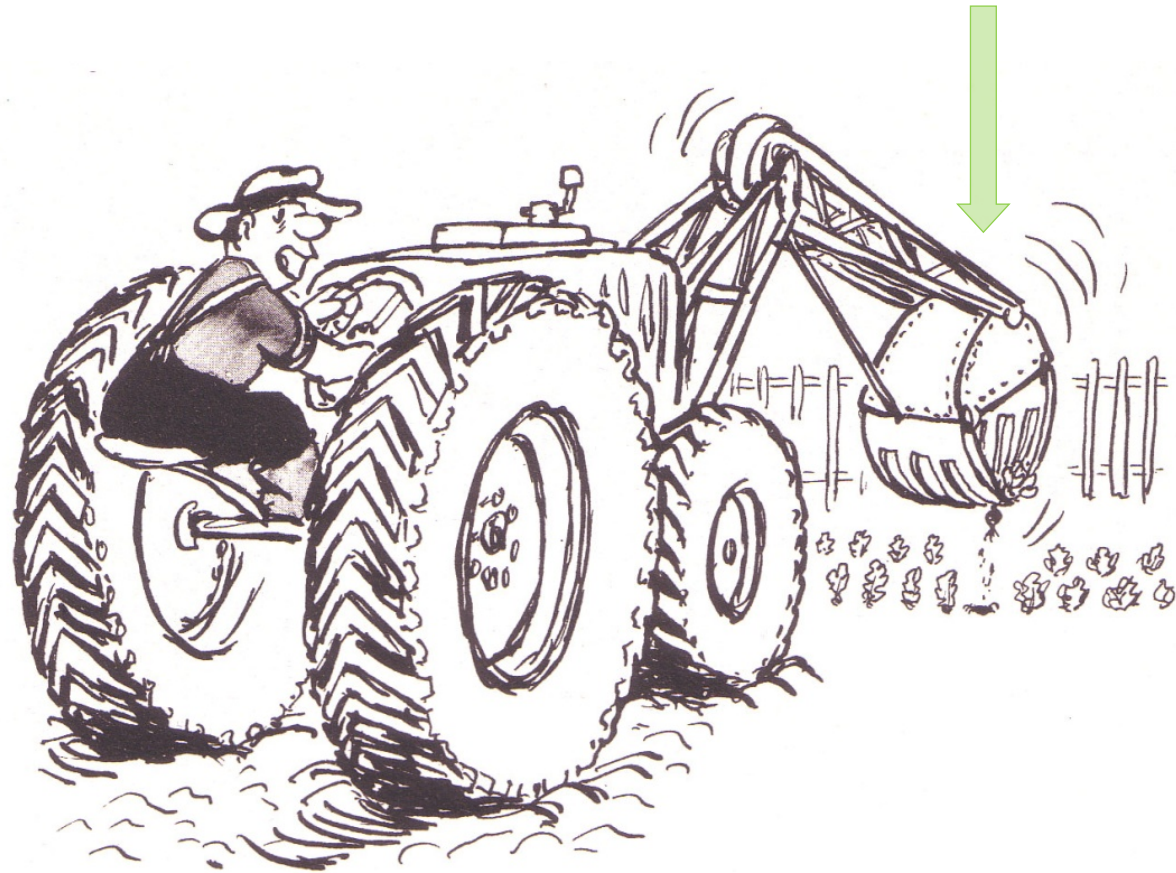
Facts for sucralose analysis

- High throughput (46 runs in 15 min by (anti-)parallel development, 15 min-staggered offline system) → 1000 runs/8h-day
- Resulting in 20-s runs with 330 µL solvent consumption
- Almost no disposal costs < 0.01 Cent/run
- Selective derivatization → compensates low separation power
- Reduced sample preparation: no SPE
- Analysis without acetonitrile!

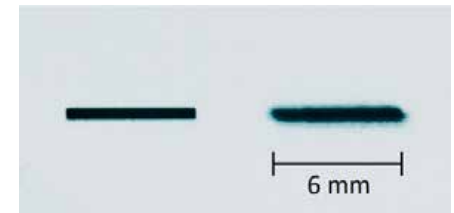
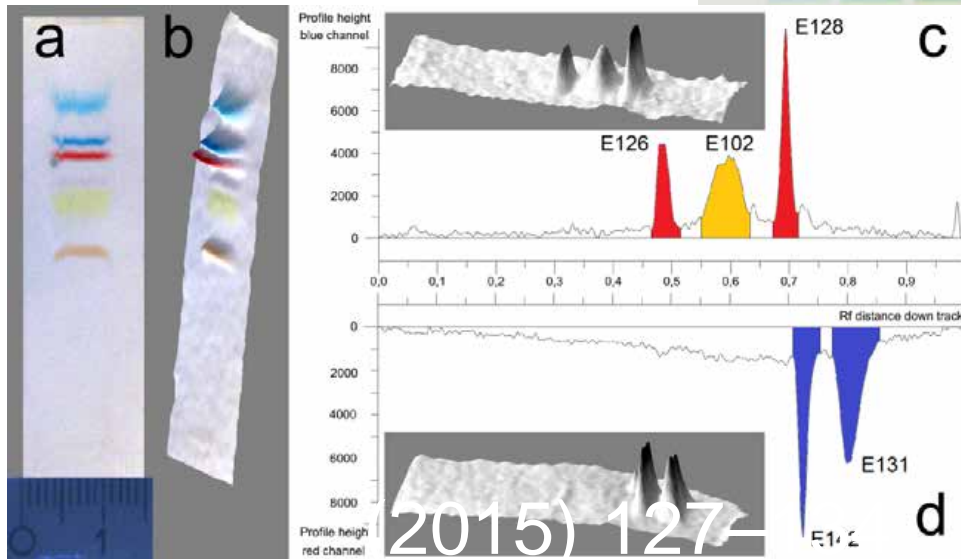
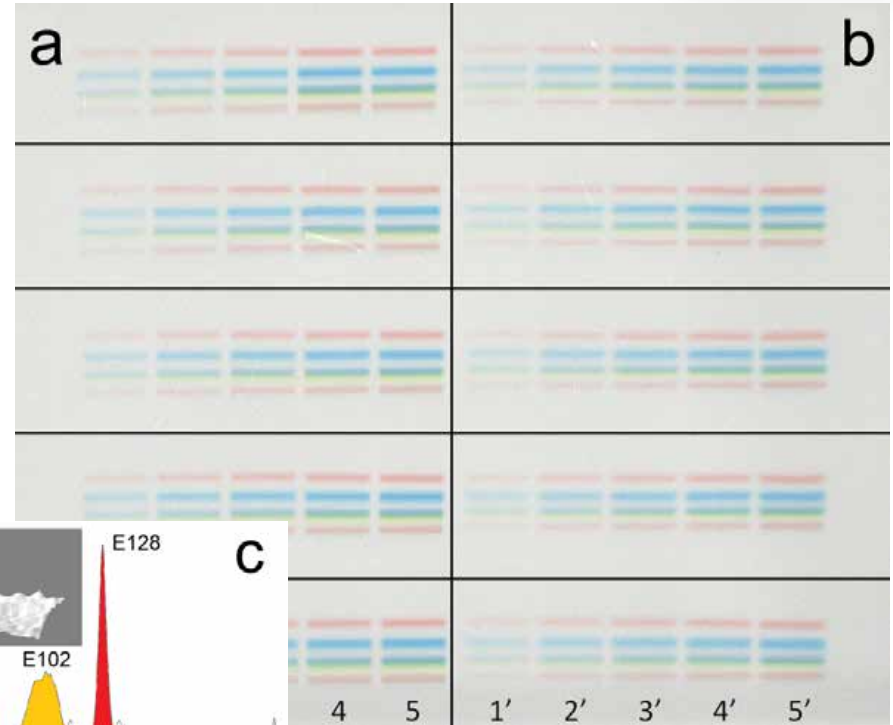
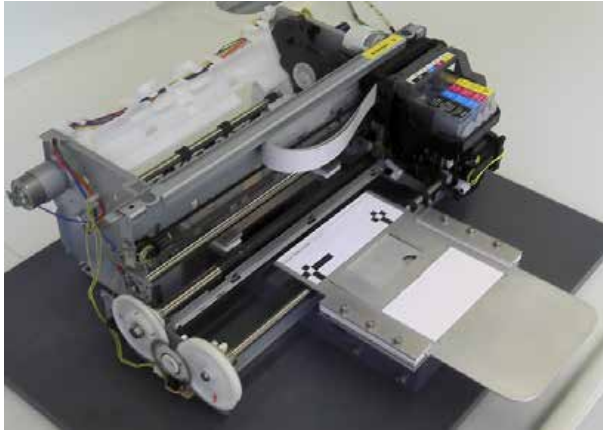


- Ultra-rapid HPLC with 2 min gradient: 720 runs/24-h day
- Sample preparation: Need of SPE for MS or ELSD as detector

...not to end like this



Office chromatography





Thank you!

JUSTUS-LIEBIG-
UNIVERSITÄT
GIESSEN
Food Science 

