Navigate flying molecular elephants safely to the ground: mass-selective soft landing up to the Mega-Dalton range by Electrospray Controlled Ion-Beam Deposition

SUPPORTING INFO

Andreas Walz, Karolina Stoiber, Annette Huettig, Hartmut Schlichting and Johannes V. Barth.

Physics Department E20, Technical University of Munich, 85748 Garching, Germany.

Table of Contents

1. Differentially pumped vacuum system 2
2. Components of the ES-CIBD 3
3. Mass deviation assessment for Insulin 4
4. Cylindrical Rayleigh limit and pUC19-DNA 6
5. Overall efficiency benchmarking 7
6. Typical CIBD-parameters for Rhodamine B 8
7. Recipes and spray conditions 8
8. Reagents 8
9. References 9
1. Differentially pumped vacuum system

The first vacuum chamber (d) is evacuated by a 500 m³/h Roots pump (Pfeiffer WKP 500) with a 35 m³/h scroll fore pump (Edwards XDS35i). The chamber achieves a pressure of approximately 2 mbar during operation.

The second vacuum chamber (f) is pumped by a 250 m³/h Roots pump (Pfeiffer WKP250) with a scroll fore pump (Edwards XDS35i). The typical operation pressure is 10⁻² mbar.

The pressure in the third chamber (h) is in the 10⁻⁷ mbar regime during operation, pumped by a 600 l/s turbomolecular pump (Leybold TURBOVAC MAG W 600 iP). The fore pump is shared with the Roots pump of chamber 2.

The fourth and fifth chamber (j) and (l) are evacuated by two 400 l/s turbomolecular pumps (Leybold TURBOVAC MAG W 400 iP) with a separate pre-vacuum system shared with the attached Scanning Tunneling Microscope (STM). The partial pressure in the fourth chamber is in the low 10⁻¹⁰ mbar regime with the inlet capillary open and the electrospray running. This differs only slightly from the base pressure of the chamber. This pressure would be far sufficient for depositions. Due to the design history of the system combined with a steady progress in the reduction of gas loads, the fifth chamber, where deposition takes place, reaches a calculated partial pressure in the 10⁻¹³ mbar regime, which is not detectable with the current setup. See Figure S 1 and Figure 1.

![Figure S 1: Schematic of the ES-CIBD system, its key components and their performance: (a) syringe with a pump. (b) electrospray emitter connected to a high voltage supply. (c) counter electrode and atmospheric pressure interface with funnel shaped inlet. (d, f, h, j, l) differentially pumped vacuum system (e) Twin. (g, i, k) high order multipoles, so-called small wire ion guides (SWIGs). (m) digital quadrupole mass spectrometer (dQMS). (n) conical multipole from metal plate electrodes, a so-called Blade ion guide. (o) target surface. (p, q) gate-valves. The ion currents in the table are measured at the output of the respective ion guide for the test molecule Rhodamine B with a concentration of 10⁻⁴ M. The transmission efficiency per ion guide is around 80% and the overall transmission efficiency from an ion ejected by the source (c) to be deposited on the sample (o) is 22 % when considering a dQMS resolution of about 110 (see Rhodamine B overview spectrum in the main text). Comparable transmission efficiencies have been found for other test molecules too.](image-url)
2. Components of the ES-CIBD

Standard ESI ion source
The ESI source consists of a syringe (typically 100-500 µL, operated by an infusion pump) that supplies the liquid to the emitter. The pumping speed ranges from 100 to 500 nL/min. The liquid is a solution of analyte molecules, dissolved in an electrolyte at final concentrations between 10⁶ and 10⁻³ M. The ESI emitter consists of a thin needle, with an inner diameter of 50-75 µm made from fused silica, the end is cut off straight. High voltage of the desired polarity is applied by an adjustable ± 5 kV DC power supply, monitoring the ion-current. The emitter is located in a box under ambient pressure, which can be flooded with a defined atmosphere, e.g. CO₂ to reduce sparking probability.

The capillary, transferring ions from the emitter to the first vacuum chamber, consists of a funnel shaped inlet followed by a 60 mm long tube with a clear diameter of 1.1 mm. It is connected to an adjustable ± 1kV DC power supply with a current sensor to record the received current. The capillary can be heated up to 200°C, crucial for good ion transmission and prevention of freezing in the ion cloud upon pressure drop.

TWIN
The TWIN consists of 272 ring electrodes made from laser cut stainless steel plates of 0.2 mm thickness. In the conical funnel-section the clear diameter ranges from 30 mm down to 12 mm, with a spacing of 0.4 mm. Downstream, the spacing is reduced to 0.2 mm, while the clear diameter decreases to 1.5 mm. Here gaskets between the electrodes seal the funnel radially. In the tunnel-section, the spacing is kept constant at 1.5 mm, the tunnel is radially sealed with gaskets to make it a “pseudo-tube” for the neutrals. Neighbouring plates with opposite phase have different shapes to further reduce capacity, mandatory to apply RF-voltages with continously changing frequency and low power consumption. The total length of the TWIN is about 100 mm.

The funnel section focuses the ions towards the tunnel section, while the neutrals can escape and are pumped off. In the funnel section near the tunnel inlet, gaskets stop this process and the ions enter a tubular pressure interface of 40 mm length and 1.5 mm clear diameter. Neutrals undergo a strong pressure drop inside this pseudo-tube, depending on its length. Compared to a thin aperture of equal diameter, such a tube reduces the residual gas load between adjacent vacuum chambers by a factor of about 20, calculated from the measured pressures and the known pumping speed. Typical RF parameters of the TWIN are some ten Volts in amplitude and a frequency up to a few MHz. An overlying DC gradient up to a few hundred Volts along the axis pulls the ions downstream. The DC potential is applied via a resistor cascade, connected to each electrode individually.

SWIG
The pressure interface of SWIG 1 consists of a solid tube with 80 mm length and 2.5 mm diameter around the electrodes. The clear diameter between the SWIG electrodes is 1.6 mm. Compared to an aperture with the same diameter, gas-load between adjacent vacuum chambers is reduced by a factor of about 10, calculated from the measured pressures and the known pumping speed. SWIG 2 and SWIG 3 have comparable but slightly larger dimensions, though pressure reduction is lower in this pressure regime. Basically the electrodes and the resulting RF field of a single SWIG might span all differentially pumped vacuum chambers without interruption.

Typical RF parameters of the SWIGs are some ten Volts in amplitude, up to 100 Vpp and a frequency up to 10 MHz.

dQMS
SWIG as well as dQMS are operated with a square-wave voltage in contrast to conventional sine-shaped driven ion guides and QMS. This allows for a continuous variation of the frequency in contrast to conventional supplies operated with an LC-resonator. The latter has the advantage of low power consumption on the expense of a fixed frequency, there is no tunable inductivity or capacity available with parameters needed for this purpose. However, the power consumption of the square wave generator is a multiple of the sinus value. This is due to the resistive losses while charging the QMS rods capacity, which are mainly dissipated in the output transistors of the power supply.

Our rod system made by Exteql has 19 mm diameter and 210 mm length, including pre- and post-filters. The differential capacity of the main rods is about 100 pF. There is a power ranging up to several kW needed to drive the rod system to frequencies in the MHz regime with square wave amplitudes in the kV regime. The software of our home-built power supply limits the maximum possible power dissipation to around 1 kW to reach a square RF amplitude of 2 kVpp at the maximum frequency of 2 MHz. Rise and fall times of the square wave signal are about 30 ns. Pre- and post-filters are coupled to the main rods via their capacities against these.
In the ES-CIBD, the dQMS fulfills two functions. First, it is used as a mass spectrometer to investigate the composition of the ion beam. Second, it is used as a filter to exclusively transmit a desired range of m/z ratios for deposition.

**BLADE**

The BLADE is the last ion guide before the ions are deposited on the sample. It consists of 16 metall wedges (here represented as plain sheets with 0.5 mm thickness) compressing the ion beam from 7 mm to 4 mm over a length of 65 mm, re-focussing the beam on the sample. The BLADE$^4$ does not contribute to pressure reduction between the stages, it is operated under UHV.

Typical RF parameters of the BLADE reach up to 80 V$_{pp}$ at 3 MHz.
3. **Mass deviation assessment for Insulin**

Insulin has a mass of 5807.65 Da. Assuming charging with protons, Insulin monomer attributed peaks in the overview spectrum have calculated mass-to-charge ratios of: 968.9 Th (6+), 1162.5 Th (5+), 1452.9 Th (4+), and 1936.9 Th (3+), and the 7+ dimer 1660.3 Th. The high-resolution mass spectrum of Insulin ($R = 490$ in insert of Figure 3 of main section) revealed at least three satellite signals in the right flank of the 5+ main peak.

We consider these as potential adduct ions as those are often observed in ESI-based MS and frequently described in literature. By calculation, these satellite peaks coincide with either monovalent metal cations as well as solvent components (water, acetic acid, acetonitrile) adducts. Although current resolution of the raw spectrum does not allow for clear distinction of those adducts, obvious discrimination is feasible by calculating mass deviation (Figure S2) from baseline as follows:

$$\text{Deviation} = (m_{\text{Add}}^\text{exp} - m_{\text{Ref}}^\text{exp}) - (m_{\text{Add}}^\text{theo} - m_{\text{Ref}}^\text{theo}), \text{ with } m_{\text{Add}}^\text{exp} = \text{experimental mass of the adduct ion derived from m/z value by Gaussian fit; } m_{\text{Add}}^\text{theo} = \text{theoretical mass of that ion based on molecular weight; } m_{\text{Ref}}^\text{exp} \text{ and } m_{\text{Ref}}^\text{theo} = \text{respective masses of reference ion (here [insulin+5H]^{5+})}.$$

We presume from the results a higher likelihood of generating insulin adducts with potassium or sodium cations and acetic acid, while water or acetonitrile adducts seem less likely. However, these assumptions are yet to be validated experimentally. We suggest as highly probable (in the order of peak numbering):

i) Ins + Na\(^+\) + 4H\(^+\) with 1166.9 Th
ii) Ins + K\(^+\) + 4H\(^+\) with 1170.1 Th.
iii) Ins + Acetic acid + 5H\(^+\) with 1174.5 Th,
    or Ins + Na\(^+\) + K\(^+\) + 3H\(^+\) with 1175.5 Th,
    and less probable:
   i) Ins + H\(_2\)O + 5H\(^+\) with 1166.1 Th
   ii) Ins + 2H\(_2\)O + 5H\(^+\) with 1169.7 Th or Ins + ACN + 5H\(^+\) with 1169.7 Th

![Figure S2: Mass deviation assessment of Insulin mass spectrum. Bars reflect grade of experimental vs. theoretical mass difference of presumed adduct ions from reference ion depicted as deviation from baseline. Base line (Zero line) is defined by the 5+ charged insulin ion as reference. This assessment reveals, that insulin adducts with potassium or sodium or acetic acid (solid bars) seem to be more likely than those with water or acetonitrile (hatched bars).](image-url)
4. Cylindrical Rayleigh limit and pUC19-DNA

The mass spectrum in Figure 5D of the main section appears as a broad curve with a wide charge state distribution, typical for extended molecules following the chain ejection ionization model (CEM). In this aspect DNA differs significantly from the “classical” Rayleigh assumptions applied for globular species, why we calculate a “cylindrical Rayleigh limit” instead.

Cylindrical Rayleigh limit defines charge states

Assuming a cylindrical shape of the dsDNA instead of a globular one, the corresponding adapted Rayleigh limit for pUC19 can be estimated by: $q_R = \pi l \sqrt{6 \gamma \varepsilon_0 r} \approx 1100 e$, with the surface tension of water $\gamma = 72.25 \text{ mN/m}$ at $T = 20 ^\circ\text{C}$ and the permittivity $\varepsilon_0$. The length of a dsDNA strand in aqueous solution can be estimated from the number of bases via $l = 2686 \times 0.34 \text{ nm} \approx 910 \text{ nm}$ and its radius is about $r \approx 1 \text{ nm}$.

Desolvation and Dimerisation

Furthermore, we postulate a potential second fraction of pUC19-DNA appearing as shoulder to the right in Figure 5D (main section). One interpretation refers to the different desolvation behavior of more dense (tighter packed, supercoiled) molecules versus open-relaxed molecules. The first might be harder = less charged and harder “drained” translating in higher $m/z$ signals.

This shoulder might also be attributed to a dimerization process discussed by Schultz et al. The $m/z$ position of the main peak was determined at 1500 Th, while the center of gravity of the shoulder peak is at ~1850 Th. This value seems reasonable to assign the shoulder to a dimer considering scheme in Figure S3. Every monomeric DNA molecule carries a certain number of charges, defined by its individual charge/length value and expressed as $\frac{m}{z} = x$. In our case is between 1150 and 2000 Th centering at 1500 Th, see Figure 5D, main section). In case of 100 % dimerization, total mass of the build dimer is doubled, however the maximum number of charges stays almost constant since the outer area accessible for charges has not changed (*Note: Dimerization also results in slight increase of the Rayleigh diameter, which of course has some effect on charge level. For the sake of simplification this is not discussed), resulting in a $m/z$ value of 2x. To the other extreme of only point to point contact, the contact area of two monomers is almost zero, why charge almost proportional increases with increasing mass, resulting in $m/z = 1 \cdot x$. Any partial overlap of the molecules at dimerization results in a $m/z$ value between 2x and 1x. This might be the case for our pUC19 spectrum too, as $m/z$ at peak-to-peak differs by a factor of ~1.2 translating in a 20 % overlap of the monomers in a dimer. Further investigation of this finding is being performed by STM analysis in a different project (to be published).
5. Overall efficiency benchmarking

The overall efficiency $T_{\text{Total}} = \frac{\text{Deposited molecules per s}}{\text{Sprayed molecules per s}}$ is defined as the probability of an analyte molecule that passes the ESI emitter to be landed on the deposition target (see main section).

The ionization process in the ESI source, the utilization efficiency $T_{\text{ESI}} = \frac{\text{Current leaving capillary}}{\text{Charge of sprayed molecules per s}}$, is the dominant loss process, see below.

The transmission through the vacuum, the total transmission efficiency $T_{\text{CIBD}} = \frac{\text{Current at sample}}{\text{Current leaving capillary}}$ with some 22% however is widely independant of ion mass, charge and type in our CIBD-system, thanks to the frequency adaption of the RF-voltages in all ion guides and the dQMS.

$T_{\text{Total}} = T_{\text{ESI}} \cdot T_{\text{CIBD}}$. $T_{\text{ESI}}$ is dominated by the details of the spray process $T_{\text{ESI}}$:
- the ionization probabilities of the molecule
- the molecule concentration in solution
- the flow rate
- the solvent composition – resolving power, viscosity, surface tension, conductivity, vapor pressure
- the drying conditions
- the extraction voltage
- the geometry of emitter and inlet-funnel into the first vacuum chamber

At least all these parameters affects droplet-size, charge of the droplet and its evaporation rate. In consequence the ESI process ($T_{\text{ESI}}$) is much more subtle than the guiding process through the vacuum chambers ($T_{\text{CIBD}}$). The overall efficiencies $T_{\text{Total}}$ listed in Figure S 4 are not dominated by the construction of the deposition system but by the molecule sprayed.

Nevertheless, one can see progress in overall efficiency over the years:

| Molecule                               | Molecular Weight (Da) | Concentration (mol/l) | Current (nA) | Overall Efficiency T | Resolution R | Reference |
|----------------------------------------|-----------------------|-----------------------|--------------|----------------------|--------------|-----------|
| Polydisperse polypropylene glycol      | 1.276                 | ?                     | ?            | 0.0001%              | ?            | 10        |
| Insulin bovine                         | 5.733                 | 2.2x10^{-6}           | 0.001        | 0.10%                | 11,12        |
| Ala-His                                | 227                   | 1.0x10^{-4}           | 0.04         | 0.016%               | 16           |
| Ala-Pro-Gly                            | 244                   | 1.0x10^{-4}           | 0.04         | 0.0087%              | 16           |
| Gly-Gly-His                            | 270                   | 1.0x10^{-4}           | 0.04         | 0.091%               | 16           |
| His-Phe                                | 303                   | 1.0x10^{-4}           | 0.04         | 0.020%               | 16           |
| Gly-Leu-Phe                            | 336                   | 1.0x10^{-4}           | 0.04         | 0.013%               | 16           |
| Rhodamine B                            | 443                   | 1.0x10^{-4}           | 0.60         | 0.120%               | 16           |
| Crystal violet                         | 372                   | 1.0x10^{-4}           | 0.30         | 0.055%               | 16           |
| Crystal violet                         | 372                   | 1.0x10^{-4}           | 0.50         | 0.20%                | 13           |
| Jacobsen’s catalyst                    | 635                   | 1.0x10^{-4}           | 0.25         | 0.20%                | 16           |
| Rhodamine B                            | 443                   | 1.0x10^{-5}           | 0.15         | 0.47%                | 16           |
| Tetrapeptide MLFA                     | 535                   | 1.0x10^{-4}           | 0.15         | 0.047%               | 16           |
| Sodium dodecyl benzene sulfonate       | 348                   | 1.0x10^{-4}           | 0.15         | 0.062%               | 16           |
| Jacobsen’s catalyst                    | 635                   | 1.8x10^{-5}           | 0.15         | 0.26%                | 16           |
| Polyoxometalate (POM)                 | 1.822                 | 1.5x10^{-4}           | 2.5          | 0.30%                | 17           |
| Rhodamine B                            | 443                   | 1.0x10^{-4}           | 2.2          | 2.70%                | 110          |
| Cu-TCPP                                | 854                   | 8.0x10^{-5}           | -0.4         | 0.30%                | 110          |
| Insulin                                | 5.808                 | 8.0x10^{-5}           | 0.4          | 0.71%                | 110          |
| pUC19                                  | 1.740.000             | 1.0x10^{-8}           | -0.4         | 4.40%                | this paper   |

Figure S 4: Overall efficiency of deposition systems reported compared to efficiencies listed in this paper.
6. Typical CIBD-parameters for Rhodamine B

The emitter is supplied with a high voltage of 2.8 kV to provide a spray voltage of 2.5 kV with respect to the counter electrode on 300 V. The counter electrode is heated to about 120 °C. The entrance electrode of the TWIN has the same DC offset as the counter electrode. Parameters of subsequent ion guides can be found in the table below. A typical soft-landing potential for the sample would be slightly below the SWIG 1 field axis potential. Ions do not scatter with residual gas downstream SWIG 1, which makes its field axis potential to a reference for the kinetic energy of the ions in z-direction in subsequent ion guides and the landing process.

| Ionguide | TWIN Funnel section | TWIN Tunnel section | SWIG 1 | SWIG 2 | SWIG 3 | dQMS | Blade |
|----------|---------------------|---------------------|--------|--------|--------|------|-------|
| Frequency [MHz] | 1 | 2 | 10 | 6 | 4 | 0.55 | 4 |
| Amplitude [V] | 30 | 30 | 20 | 20 | 20 | ~1kV | 30 |
| Field axis [V] with respect to ground | 300 at first electrode | 0 at last electrode | -10 | -25 | -25 | -15 | -15 |
| Kinetic energy in z-direction [eV] | 0.025 scattering with residual gas | 0.025 scattering with residual gas | 0.025 scattering with residual gas | -15 | -15 | ~5 | ~5 |

7. Recipes and spray conditions

| Sample prep. | Rhodamine B | Cu-TPCP | Insulin | pUC19 DNA |
|--------------|-------------|---------|---------|-----------|
| Solvent      | Methanol/water | Methanol/water | Water/ACN | Water/ACN  | |
| Proton donor / acceptor | Acetic acid | Ammonia | Acetic acid | n.a. |
| Final concentrations | 10^4M Rhodamine, 47.5% / 47.5% / 5% v/v methanol / water / acetic acid | 8.3x10^7M Cu-TPCP in methanol, 1.7x10^3M Ammonia in water | 8x10^7M Insulin in water 47.5% v/v ACN, 5% v/v acetic acid (final conc: 8x10^7M acetic acid) | 10^8 M pUC in water, 66% v/v ACN |
| Spray conditions | | | | |
| Emitter | Silica, 75 µm i.d., 360 µm o.d. | Silica, 75 µm i.d., 360 µm o.d. | Silica, 50 µm i.d., 360 µm o.d. | Silica, 75 µm i.d., 360 µm o.d. |
| Flow rate | 500 nL/min | 500 nL/min | 167 nL/min | 500 nL/min |
| Voltage | +2.5 kV | -1.95 kV | +2.6 kV | -2.3 kV |

8. Reagents

Methanol: Sigma Aldrich, CHROMASOLV ≥99.9%, for HPLC;
Water: Carl Roth, ROTISOLV Ultra LC-MS;
Acetonitrile: Sigma Aldrich, puriss., absolute
Ammonia: Carl Roth, Ammonia solution 25%, ROTIPURAN;
Acetic Acid: Fluka Analytical, ≥ 99.8 % puriss.
Rhodamine B: Sigma Aldrich, ≥ 95 % (HPLC)
Insulin: Sigma Aldrich, Human Recombinant, dry powder, for research or further manufacturing use
Plasmid DNA pUC19: Carl Roth
9. References

(1) Pauly, M.; Sroka, M.; Reiss, J.; Rinke, G.; Albarghash, A.; Vogelgesang, R.; Hahne, H.; Kuster, B.; Sesterhenn, J.; Kern, K.; Rauschenbach, S.: A Hydrodynamically Optimized Nano-Electrospray Ionization Source and Vacuum Interface, Analyst 2014, 139, 1856, doi:10.1039/c4an01836a.

(2) Schlichting, H.; Walz, A.; Kaposí, T.; Barth, J.: Partly Sealed Ion Guide and Ion Beam Deposition System, Patent 2019, WO 2019/193170 A1, US 2021/043436A1, EP 3776623A1, CN 111937116A.

(3) Schlichting, H.; Walz, A.; Kaposí, T.; Barth, J.: Ion Guide Comprising Electrode Wires and Ion Beam Deposition System, Patent 2019, WO 2019/193171 A1, US 2021/159064A1, EP 3776624A1, CN 111937115A.

(4) Schlichting, H.; Walz, A.; Barth, J.: Ion Guide Comprising Electrode Plates and Ion Beam Deposition System, Patent 2019, WO 2019/193170 A1, EP 3776625A1.

(5) Rayleigh, Lord.: On The Equilibrium Of Liquid Conducting Masses Charged With Electricity, Philos Mag 1882, 14, 184–186, doi:10.1080/14786448208628425.

(6) Lide, D. R.: CRC Handbook of Chemistry and Physics, Internet Version 2005; Lide, D. R., Ed.; CRC Press LLC, 2005; Vol. 2005, doi:http://www.hbcpnetbase.com.

(7) Lederer, H.; May, R. P.; Kjems, J. K.; Baer, G.; Heumann, H.: Solution Structure of a Short DNA Fragment Studied by Neutron Scattering, Eur J Biochem 1986, 161 (1), 191–196, doi:10.1111/j.1432-1033.1986.tb10141.x.

(8) Adrian, M.; Heggeler-Bordier, B. ten; Wahli, W.; Stasiak, A. Z.; Stasiak, A.; Dubochet, J.: Direct Visualization of Supercoiled DNA Molecules in Solution., EMBO J 1990, 9 (13), 4551–4554, doi:10.1002/j.1460-2075.1990.tb07907.x.

(9) Schultz, J. C.; Hack, C. A.; Benner, W. H.: Mass Determination of Megadalton-DNA Electrospray Ions Using Charge Detection Mass Spectrometry, J Am Soc Mass Spectrom 1998, 9 (4), 305–313, doi:10.1016/S1044-0305(97)00290-0.

(10) Siuzdak, G.; Hollenbeck, T.; Bothner, B.: Preparative Mass Spectrometry with Electrospray Ionization, J Mass Spectrom 1999, 34 (10), 1087–1088, doi:10.1002/(SICI)1096-9888(199910)34:10<1087::AID-JMS872>3.0.CO;2-A.

(11) Blake, T. A.; Ouyang, Z.; Wiseman, J. M.; Takats, Z.; Guymon, A. J.; Kothari, S.; Cooks, R. G.: Preparative Linear Ion Trap Mass Spectrometer for Separation and Collection of Purified Proteins and Peptides in Arrays Using Ion Soft Landing, Anal Chem 2004, 76 (21), 6293–6305, doi:10.1021/ac048981b.

(12) Ouyang, Z.; Takats, Z.; Blake, T. A.; Gologan, B.; Guymon, A. J.; Wiseman, J. M.; Oliver, J. C.; Davison, V. J.; Cooks, R. G.: Preparing Protein Microarrays by Soft-Landing of Mass-Selected Ions, Science 2003, 301, 1351–1354, doi:10.1126/science.1088776.

(13) Mayer, P. S.; Turecek, F.; Lee, H.-N.; Scheidemann, A. A.; Olney, T. N.; Schumacher, F.; Strop, P.; Smrcina, M.; Patek, M.; Schirlin, D.: Preparative Separation of Mixtures by Mass Spectrometry, Anal Chem 2005, 77 (14), 4378–4384, doi:10.1021/ac050444j.

(14) Yang, X.; Mayer, P. S.; Turecek, F.: Preparative Separation of a Multicomponent Peptide Mixture by Mass Spectrometry, J Mass Spectrom 2006, 41 (2), 256–262, doi:10.1002/jms.986.

(15) Feng, W.-P.; Goodwin, M. P.; Nie, Z.; Volny, M.; Ouyang, Z.; Cooks, R. G.: Ion Soft Landing Using a Rectilinear Ion Trap Mass Spectrometer, Anal Chem 2008, 80 (17), 6640–6649, doi:10.1021/ac800929w.

(16) Nie, Z.; Li, G.; Goodwin, M. P.; Gao, L.; Cyriac, J.; Cooks, R. G.: In Situ SIMS Analysis and Reactions of Surfaces Prepared by Soft Landing of Mass-Selected Cations and Anions Using an Ion Trap Mass Spectrometer, J Am Soc Mass Spectrom 2009, 20 (6), 949–956, doi:10.1016/j.jasms.2009.02.019.

(17) Gunaratne, K. D. D.; Prabhakaran, V.; Ibrahim, Y. M.; Norheim, R. V.; Johnson, G. E.; Laskin, J.: Design and Performance of a High-Flux Electrospray Ionization Source for Ion Soft Landing, Analyst 2015, 140 (9), 2957–2963, doi:10.1039/c5an00220f.