



Hyphenated Elemental Mass Spectrometry for the Biosciences

by Sarah Meyer

Thesis submitted in fulfilment of the requirements for the degree of

Doctor of Philosophy: Science

under the supervision of Dist. Prof. Philip Doble, Dr. David Bishop, Dr. David Clases, and Dr. Raquel Gonzalez de Vega

University of Technology Sydney
Faculty of Science

July 2022

Certificate of Authorship

I, Sarah Meyer, declare that this thesis is submitted in fulfilment of the requirements for the award of Doctor of Philosophy: Science, in the Faculty of Science at the University of Technology Sydney.

This thesis is wholly my own work unless otherwise referenced or acknowledged. In addition, I certify that all information sources and literature used are indicated in the thesis.

This document has not been submitted for qualifications at any other academic institution.

This research is supported by the Australian Government Research Training Program.

Signature: Production Note:
Signature removed prior to publication.

Date: 19th of July 2022

Acknowledgements

I would like to thank all the people who supported, motivated, and inspired me along my path and who contributed to this work in multiple ways.

First, I would like to thank my supervisor Dist. Prof. Philip Doble for the opportunity to do my PhD in Australia in his group. Thank you for being a great mentor and supervisor, for your support, advice, and encouragements, for teaching me everything about CE, the challenging projects, and your funny and charismatic nature. I am very grateful for the last 3.5 years and have developed myself so much, both scientifically and personally.

Moreover, I would like to acknowledge my supervisors David Bishop, David Clases and Raquel Gonzalez de Vega. Dave – thank you for supporting me with all imaging and ICP-MS questions, and especially for being a great supervisor during my first visit that inspired me to come back to UTS for my PhD. David – for motivations and encouragements, for scientific and personal discussions, for teaching me everything you know, especially about single particle ICP-MS and ICP-MS operation modes, and last but not least for being a great friend. My experience at UTS would not have been the same without you. Raquel – for all the meetings, support, and advice, for always being available for me, for being a competent advisor for everything that has to do with immunohistochemistry, and for your friendship. I miss and wish you all the best for your future.

I would like to make a special mention to Ariane Roseblade, Matt Padula and technical staff members Anthea Harris, Dayanne Bordin and Tom Lockwood. Ariane – for being a great, fun, and smart person to be around, for bouncing ideas off each other, and for having a similar obsession with pretty Origin figures and

Acknowledgements

Excel spreadsheets. Matt – for your support in the protein project and for providing me with protein standards and surfactants. Anthea, Dayanne and Tom – for keeping the instruments running in the teaching and research labs, for somehow always finding spare parts or rare chemical equipment that is useful for my research, and for your willingness to help in many situations.

Furthermore, I gratefully acknowledge the philanthropic support from George Miklos and the Miklos Family.

Thank you to the members of the research group: David G., Dylan, Jacob, Jake, Karen, Monique, Prashina, Siobhan, and Tash for all the good times and making me feel welcome. I would like to mention Mika and Tom especially for the scientific discussions, regular check-ins, for your help, and all the restaurant and bar recommendations.

A special thank you to my fellow PhDs at UTS: Alisha, Amber, Ana, Blake, Brooke, Caleb, Camilla, Ciara, Dan, Eda, Edward, Freddy, Helen, Minh, Oksana, Sandi, Sharni, Simon, and Tom G. for the lunch breaks, birthday cakes, wine dates, picnics, good chats, weekend get-aways, being there in challenging times, and for making me feel so welcome even though I am such a busy bee running around.

I would further like to acknowledge Prof. Dr. Uwe Karst for inspiring me to get into analytical chemistry and for supporting me along my way, as well as my fellow students from Münster: Arne, Carina, Jordi, Patrick B., Patrick H., Niklas, Sabsi and Sommel for making the time in Münster so valuable and being the best friends I could wish for.

Thank you to all my friends outside from uni, specifically Aileen, Jessica M, Maike and Naomi - I know I can count on you and call at any time, in any situation.

A huge thank you goes to Diane and Van Wallace for your acceptance, interest, support, and being my Australian family. I don't take this for granted and really appreciate you both.

Mein größter Dank gehört meiner Familie: meinem Bruder Nicolas, meinen Eltern Martina und Norbert Meyer sowie meine Großeltern Elfriede und Ewald Meyer, und Gerta und Josef Becker. Ich weiß, es nicht einfach für euch ist, dass ich nach Australien gegangen und daher ich bin euch dankbar, dass ihr mich meinen Weg gehen lasst. Ohne euch und eure Unterstützung wäre diese Arbeit nicht möglich gewesen. Danke für das Vertrauen, den bedingungslosen Rückhalt und eure Fürsorge. Euch ist diese Arbeit gewidmet.

Finally, I would like to thank my partner Cheyne Wallace, who has been an unwavering support since the day I have met you. You have such amazing listening and problem-solving skills, and often a great answer for all kinds of questions. Thanks for your encouragements, understanding, for showing me the fun side of life, and accepting me as the person I am. As they say in Bondi: "You are my rock, babe."

List of Publications

Sarah Meyer, David Clases, and Philip A. Doble, *A Simple, Low-Cost and Robust CE-ICP-MS Interface for the Analysis of Gadolinium-based Contrast Agents in Biological Samples*, in preparation.

Sarah Meyer, David Clases, Raquel Gonzalez de Vega, Matthew P. Padula and Philip A. Doble, *Separation of Intact Proteins by Capillary Electrophoresis*, *Analyst* (**2022**), 147, 13, 2988-2996.

Sarah Meyer, Raquel Gonzalez de Vega, Xiaoxue Xu, Ziqing Du, Philip A. Doble, and David Clases, *Characterisation of Upconversion Nanoparticles by Single-Particle ICP-MS Employing a Quadrupole Mass Filter with Increased Bandpass*, *Anal. Chem.* (**2020**), 92, 22, 15007–15016.

Sarah Meyer, Callum Clarke, Robson Oliveira dos Santos, David Bishop, Marco A. Krieger and Lucas Blanes, *Developing self-generated calibration curves using a capillary-driven wax-polyester lab on a chip device and thermal gates*, *Microchemical Journal* 146 (**2019**) 709-712.

“Studies derived from manganese-based atomic research have resulted in a profound new understanding of cancer radiotherapy. The data obtained are totally unexpected. They are of fundamental importance and will certainly have deep implications for patient treatment.”

Edmond H. Fisher

Nobel prize in Physiology and Medicine,
1992

Table of Contents

<u>Acknowledgements</u>	I
<u>List of Publications</u>	V
<u>Table of Contents</u>	IX
<u>List of Figures</u>	XV
<u>List of Tables</u>	XXIII
<u>Abbreviations</u>	XXV
<u>Abstract</u>	XXXI
<u>Chapter 1</u>	
<u>Introduction and Scope of the Thesis</u>	1
1.1 Manganese and tumour radioresistance	2
1.1.1 <i>Cancer and cancer treatment</i>	2
1.1.2 <i>Manganese and radioresistance</i>	3
1.1.3 <i>Manganese transporters</i>	5
<i>Cellular manganese influx mechanisms</i>	5
<i>Cellular manganese efflux mechanisms</i>	7
<i>Dysregulation of manganese transporters</i>	8
1.2 Spatial analysis of biological tissues via LA-ICP-MS	9
1.2.1 <i>Elemental bioimaging</i>	9

Table of Contents

1.2.2	<i>Immuno-mass spectrometry imaging</i>	11
1.3	Analysis of proteins via CE and CE-ICP-MS	13
1.3.1	<i>Fundamentals of CE</i>	13
1.3.2	<i>Introduction to CE-ICP-MS</i>	16
1.3.3	<i>Strategies for protein analysis via CE</i>	18
1.4	Advanced ICP-MS operation modes	20
1.4.1	<i>Triple quadrupole ICP-MS operation modes</i>	20
1.4.2	<i>Single-particle ICP-MS</i>	22
1.5	Aims and scope	24

Chapter 2

Separation of Intact Proteins by Capillary Electrophoresis **27**

2.1	Introduction	28
2.2	Experimental section	31
2.2.1	<i>Chemicals and consumables</i>	31
2.2.2	<i>Capillary dimensions and coatings</i>	32
2.2.3	<i>BGE, standards and sample preparation</i>	32
	<i>BGE preparation</i>	32
	<i>Standard preparation</i>	34
	<i>Milk sample preparation</i>	34
2.2.4	<i>CE experimental parameters</i>	34
2.2.5	<i>Data analysis</i>	35
2.3	Results and discussion	35
2.3.1	<i>Suitability of PDMS capillaries</i>	35
2.3.2	<i>Dynamic coating of PDMS capillaries</i>	37
2.3.3	<i>Systematic evaluation of BGEs and capillaries for protein analyses</i>	40
2.3.4	<i>Proof-of-principle: Analysis of proteins in milk</i>	49
2.4	Conclusion	53

Chapter 3**Development of a CE-ICP-MS Interface 55**

3.1	Introduction	56
3.2	Experimental section	59
3.2.1	<i>Chemicals and consumables</i>	59
3.2.2	<i>Instrumentation</i>	60
3.2.3	<i>Method information</i>	61
3.2.4	<i>Standard and sample preparation</i>	61
3.2.5	<i>Data analysis</i>	62
3.3	Results and discussion	63
3.3.1	<i>Interface design</i>	63
3.3.2	<i>Method optimization</i>	65
3.3.3	<i>GBCA quantification in urine samples</i>	67
3.4	Conclusion	70

Chapter 4**Characterisation of Metal Labelled Antibodies by CE-ICP-MS 73**

4.1	Introduction	74
4.2	Experimental section	77
4.2.1	<i>Chemicals and consumables</i>	77
4.2.2	<i>Instrumentation and experimental parameters</i>	78
4.2.3	<i>Standard and sample preparation</i>	79
4.2.4	<i>Data analysis</i>	80
4.3	Results and discussion	80
4.3.1	<i>Isotopic abundance in natural and isotopic enriched gadolinium</i>	80
4.3.2	<i>CE analysis of gadolinium-polymer labelled antibodies</i>	81
4.3.3	<i>CE analysis of nanoparticle conjugated antibodies</i>	85
4.4	Conclusion	87

Chapter 5

Characterisation of Nanoparticles by CE-ICP-MS **89**

5.1	Introduction	90
5.2	Experimental section	93
5.2.1	<i>Chemicals and consumables</i>	93
5.2.2	<i>UCNP synthesis and characterisation</i>	94
	<i>Synthesis of NaYF₄ host UCNPs</i>	94
	<i>Synthesis of NaGdF₄ host UCNPs</i>	94
	<i>UCNPs characterisation</i>	95
5.2.3	<i>SP ICP-MS analysis and experimental parameters</i>	96
5.2.4	<i>Data analysis</i>	98
5.3	Results and discussion	99
5.3.1	<i>Maximizing ion transmission</i>	99
5.3.2	<i>Analysis of AuNPs</i>	105
5.3.3	<i>Characterisation of UCNPs</i>	108
5.3.4	<i>Poisson model for UCNP interactions</i>	113
5.4	Conclusion	115

Chapter 6

Elemental and Molecular Imaging of Manganese Transporters **117**

6.1	Introduction	118
6.2	Experimental Section	120
6.2.1	<i>Chemicals and consumables</i>	120
6.2.2	<i>Pathological material: tissue microarrays</i>	121
6.2.3	<i>Calibration standard preparation and quantification</i>	122
	<i>Gelatine standard preparation</i>	122
	<i>Cross quantification via solution nebulization ICP-MS</i>	122
6.2.4	<i>iMSI workflow</i>	124
	<i>Antibody labelling and labelling characterisation</i>	124
	<i>Immunohistochemical staining</i>	124

6.2.5	<i>LA-ICP-MS parameters</i>	125
6.2.6	<i>Data processing</i>	125
6.3	Results and Discussion	126
6.3.1	<i>Comparison of protein visualization approaches</i>	126
6.3.2	<i>Elemental and molecular imaging of human melanomas</i>	128
6.4	Conclusions	133
6.5	Acknowledgements	134
<u>Chapter 7</u>		
<u>Summary and Future Perspectives</u>		135
<u>References</u>		141

List of Figures

- Figure 1-1:** The typical CE set up is simple and consists of a BFS capillary immersed into two BGE vials, two electrodes that are connected to a high voltage power supply, and a ultraviolet (UV) detector on cathode side (A). The application of a high voltage results in the formation of the EOF, which is the movement of the bulk solutions towards the cathode (B). Compared to a hydrodynamic flow profile, the flow profile of the EOF is flat, resulting in narrow peak shapes (C). **14**
- Figure 1-2:** Electrophoretic mobility of the EOF and differently charged analyte ions in BFS capillaries (A). Resulting electropherogram with typical migration order (B). **16**
- Figure 1-3:** Schematic set-up of a quadrupole (A) and Mathieu stability diagrams (B). A quadrupole consists of four metallic rods and is operated with a set of DC and RF voltages. The Mathieu stability diagram gives an overview of DC/RF combinations that stipulate stable trajectories for a target ion through the quadrupole. **22**
- Figure 1-4:** The SP ICP-MS analysis of dilute NP suspensions leads to the detection of discrete signals (A). After collecting a sufficient number of NPs, the signal distribution (B) and size distribution (C) can be calculated using basic statistical tools. **23**
- Figure 2-1:** Analysis of a standard comprising of acetone, His and Tf on uncoated and a CTAB coated PDMS capillary at pH 3.2 (A), and effect of the CTAB coating time on the migration time of the three compounds (B). **38**

- Figure 2-2:** Longevity of the surfactant layer (A) and effect on the migration times (t_M) and peak width (FWHM) (B). Successive analysis of the three analytes acetone, Tf and His after removal of CTAB from the BGE. **39**
- Figure 2-3:** Analysis of a standard comprising of acetone, His and Tf on uncoated and a SDS coated PDMS capillary at pH 8.4 (A), and effect of the SDS coating time on the migration time of the compounds (B). **40**
- Figure 2-4:** MWs and pls of selected model proteins. The amino acid His was added as a marker due to its charge over a wide pH range. The analytes were selected to cover a wide range of MWs and pls. **41**
- Figure 2-5:** Systematic evaluation of the CTAB-PDMS, SDS-PDMS and BFS capillary employing BGEs with pH values ranging from 3.0 to 9.6. The electropherograms (A1) were obtained at -30 kV for the CTAB-PDMS capillary and at +30 kV for the SDS-PDMS and BFS capillary. The arrows indicate the EOF (E) and system peaks are marked with a S. The tuneable manipulation of the selectivity may be monitored when plotting the analytes effective mobility against the pH value of the BGE (A2). A high consistency was observed across all three capillaries and a line of best fit crosses the x-axis at approximately the pl of the protein. **44**
- Figure 2-6:** Electropherograms (B1) and mobility vs. pH value plots (B2) for Tf obtained with the CTAB-PDMS, SDS-PDMS and BFS capillary employing BGEs with pH values ranging from 3.0 to 9.6. The arrows in the electropherograms indicate the EOF (E) and system peaks are marked with an S. **45**
- Figure 2-7:** Electropherograms (C1) and mobility vs. pH value plots (C2) for β -Lg obtained with the CTAB-PDMS, SDS-PDMS and BFS capillary employing BGEs with pH values ranging from 3.0 to 9.6. The arrows in the electropherograms indicate the EOF (E) and system peaks are marked with an S. **46**

- Figure 2-8:** Electropherograms (D1) and mobility vs. pH value plots (D2) for Mb obtained with the CTAB-PDMS, SDS-PDMS and BFS capillary employing BGEs with pH values ranging from 3.0 to 9.6. The arrows in the electropherograms indicate the EOF (E) and system peaks are marked with an S. **46**
- Figure 2-9:** Electropherograms (E1) and mobility vs. pH value plots (E2) for RNase obtained with the CTAB-PDMS, SDS-PDMS and BFS capillary employing BGEs with pH values ranging from 3.0 to 9.6. The arrows in the electropherograms indicate the EOF (E) and system peaks are marked with an S. **47**
- Figure 2-10:** Electropherograms (F1) and mobility vs. pH value plots (F2) for HSA obtained with the CTAB-PDMS, SDS-PDMS and BFS capillary employing BGEs with pH values ranging from 3.0 to 9.6. The arrows in the electropherograms indicate the EOF (E) and system peaks are marked with an S. **47**
- Figure 2-11:** Electropherograms (G1) and mobility vs. pH value plots (G2) for CK obtained with the CTAB-PDMS, SDS-PDMS and BFS capillary employing BGEs with pH values ranging from 3.0 to 9.6. The arrows in the electropherograms indicate the EOF (E) and system peaks are marked with an S. **48**
- Figure 2-12:** Electropherograms (H1) and mobility vs. pH value plots (H2) for IgG Antibody obtained with the CTAB-PDMS, SDS-PDMS and BFS capillary employing BGEs with pH values ranging from 3.0 to 9.6. The arrows in the electropherograms indicate the EOF (E) and system peaks are marked with an S. **48**
- Figure 2-13:** CE analysis of eight model analytes with various MWs and pls at low (A, CTAB-PDMS capillary) and high pH (B, SDS-PDMS capillary; C, BFS capillary). A fast EOF and symmetrical peaks for all analytes were produced with the CTAB-PDMS capillary (A). The peaks HSA, Tf and CK were symmetrical and adsorption free with the SDS capillary (B). The BFS capillary was superior for all other

analytes with a sufficient separation efficiency for the isoforms β -Lg A and β -Lg A (C). **49**

Figure 2-14: Simultaneous analysis of caseins and whey proteins in fresh cow's milk employing a CTAB-PDMS capillary (total length = 110 cm, effective length = 102 cm) and two BGEs. BGE M-I (pH 3.2) is suitable for the separation of total two isoforms A1 β -CN and A2 β -CN, BSA, α -CN and α -Lac (A). The analysis of the two isoforms β -Lg A and β -Lg B requires BGE M-II (pH 3.8) with a slightly higher pH value due the higher pI of the two analytes (B). **51**

Figure 2-15: Protein identification in fresh cow's milk. The milk samples were spiked with the individual protein standards in their appropriate concentrations (A-H). **52**

Figure 3-1: Molecular structures of the GBCAs used in this study. Gadopentetic acid, gadodiamide, and gadoxetic acid are linear complexes (top). Gadoteric acid and gadobutrol and are macrocyclic chelates (bottom). **57**

Figure 3-2: CE-ICP-MS schematic. **60**

Figure 3-3: CE-ICP-MS interface kept in place with a 3D printed mounting. **64**

Figure 3-4: Optimization of the make-up flow rate using a 1000 mg·L⁻¹ mix containing gadodiamide (1, blue), gadobutrol (2, purple), and gadopentetic acid (3, teal). **66**

Figure 3-5: Optimization of the injection conditions using a 1000 mg·L⁻¹ mix containing gadodiamide (1, blue), gadobutrol (2, purple), and gadopentetic acid (3, teal). **67**

Figure 3-6: Separation of a 600 mg·L⁻¹ mix of the GBCAs gadodiamide (1), gadobutrol (2), gadoteric acid (3) and gadopentetic acid (5) spiked to the gadoxetic acid (4) containing urine sample. The sample was injected hydrodynamically (97 mbar for 10 s). The analysis was performed at 30 kV with a 5 mM sodium tetraborate BGE and a make-up flow rate of 4.6 μ g·min⁻¹ (500 mbar). **68**

Figure 3-7: Excretion profile of gadoxetic acid in urine over a time of 12 hours, with sample collection perform every 2 hours. The gadoxetic acid

content was quantified via external calibration using gadodiamide (blue), gadobutrol (purple), gadoteric acid (magenta) and gadopentetic acid (teal). The determined gadolinium gadopentetic acid concentration showed a good compliance using the four different GBCAs. **70**

Figure 4-1: Schematic representation of a lanthanide labelled antibody. The DTPA polymer is conjugated with the antibody over a maleimide linker in the Fc region. **75**

Figure 4-2: Comparison of the natural abundance and the abundance in the enriched gadolinium used in the MAXPAR™ reagents. **81**

Figure 4-3: Electropherograms obtained in MS/MS mode. Adding oxygen gas induced a mass shift for S^+ to SO^+ , the ratio of Gd^+ to GdO^+ was approximately 60:40 under these tune conditions. The sulfur signal did not overlap with the gadolinium signal and was caused by sulfur compounds present in the antibody stabilizer that was added to the standards. **82**

Figure 4-4: CE analysis of seven gadolinium labelled antibodies. **83**

Figure 4-5: Overview of the determined number of gadolinium atoms per antibody. **84**

Figure 4-6: Electropherograms for a free 15 nm AuNP dispersion (blue) and a secondary antibody conjugated 15 nm AuNP dispersion (teal). Compared is the non-processed signal (top) with the signal obtained after smoothing with a 40-point FFT filter (bottom). **86**

Figure 5-1: TEM (A) and XRD (B) characterisation of the synthesised UCNP. Type I consisted of a 90 nm NaYF₄ host structure which was doped with 20%Yb and 2% Er. Type II consists of a 20 nm NaYF₄ host structure which was doped with 20%Yb and 1% Er. Type III consists of a 15 nm NaGdF₄ host structure which was doped with 20%Yb and 2% Er. All UCNPs crystallised hexagonally. **96**

Figure 5-2: (A) Schematic stability diagram for m/z 197. The scan lines for standard operation (unit mass resolution) and for the bandpass mode are marked. (B) Mass spectrum of Au using a standard scan

line and the bandpass mode. (C) Stability diagrams for all relevant Yb isotopes. Operating the bandpass mode results in a signal convolution. (D) Yb mass spectrum recorded in the bandpass mode. (E, F) Simulated convolution of Yb isotope signals. **101**

Figure 5-3: Gd, Er, Yb, and Au were analysed in the standard mode (SM) and bandpass mode (BPM) to compare mass resolution and sensitivity. Ion transmission in the bandpass mode was increased by two mechanisms: First, the quadrupole transmission of individual isotopes was enhanced, exemplified by the monoisotopic Au. Second, the transmission was further increased by the simultaneous acquisition of several isotopes as shown for Gd, Er, and Yb. **103**

Figure 5-4: Analysis of a 10.9 nm AuNP dispersion. The standard method for SP ICP-MS (A1-2) is compared to a method with modified ion extraction and transport (B1-2). Operating the quadrupole additionally in the bandpass mode allows background-free NP detection (C1-2). **106**

Figure 5-5: Yb signal distribution following single-particle analysis of dispersed 20 nm UCNPs (NaYF₄: 20% Yb, 1% Er, type II) using the standard method for SP ICP-MS (A). Particle registration was improved after optimising ion extraction and transport (B). The bandpass mode (C) allowed background-free detection of individual UCNPs and resolved several maxima corresponding to aggregated UCNPs. **109**

Figure 5-6: SP ICP-MS analyses of three types of UCNPs. Type I (top, (A)–(C)) consisted of a NaYF₄ host structure doped with 20% Yb and 2% Er. Type II (bottom left, (D)–(F)) consisted of a NaYF₄ host structure doped with 20% Yb and 1% Er. Type III (bottom right, (G)–(I)) consisted of a NaGdF₄ host structure doped with 20% Yb and 2% Er. The signal distributions for each type of UCNP and targeted elements are shown in (A), (D), and (G). Calibration allowed determination of the corresponding particle sizes as shown in (B),

(E), and (H). The experimental molar ratios of targeted elements in detected UCNPs are shown in (C), (F), and (I). *For types II and III, Er was not detected and was not further considered. **111**

Figure 5-7: Mass spectrum covering the mass range for Gd and Yb isotopes in bandpass mode. For UCNP type III, GdO can interfere with the analysis of Yb. The oxide rate was determined to be 1.8% and its influence on the Yb determination was corrected mathematically. **113**

Figure 5-8: Comparison of the Poisson model and experimental results. **114**

Figure 6-1: Microscope image (left) and iMSI images using two protein visualization approaches. The ZIP8 expression was visualised with a directly labelled ^{153}Eu -ZIP8 antibody (middle). The ZIP14 expression was visualised indirectly with an unlabelled ZIP14 antibody and a secondary antibody-15 nm AuNP conjugate (right). **127**

Figure 6-2: Comparison of the H&E image, ZIP8 and ZIP14 spatial distributions and transition metals in eight samples of human melanoma. **129**

Figure 6-3: Light microscope image of ROI A and ROI B in sample 6 (left) and comparison of the average ZIP8 and ZIP14 expression levels as well as metal concentrations in the corresponding ROIs (right). **131**

Figure 6-4: Light microscope image of ROI A and ROI B in sample 7 (left) and comparison of the average ZIP8 and ZIP14 expression levels as well as metal concentrations in the corresponding ROIs (right). **132**

Figure 6-5: Co-localisation of manganese, ZIP8 and ZIP14 in melanotic tissues. **133**

List of Tables

- Table 1-1:** Clinically inferred radiation responsiveness and patient survival after radiation treatment in different tumour categories [10]. **5**
- Table 2-1:** BGE composition and experimental pH values. All BGEs have the same basic composition. For the CTAB and SDS capillary, 0.1 mM CTAB and 0.01 mM SDS were added to the BGE, respectively. (- not used for systematic evaluation.) **33**
- Table 2-2:** Average current and RSD recorded using BGE I to BGE VI and a PDMS capillary. The acquisition time was 10 minutes, and a voltage of +30 kV was applied. **36**
- Table 2-3:** MWs and pls for analytes used in the systematic evaluation. **42**
- Table 2-4:** MWs and pls for proteins identified in milk. **50**
- Table 3-1:** Figures of merit for each GBCA standard. **68**
- Table 3-2:** Calculated recoveries using species-unspecified (black) and species-specific (bold, red) quantification. **69**
- Table 5-1:** Experimental Parameters. The standard method featured soft extraction parameters. Based on this method, ion extraction and transport were optimised for Yb, Au, and lanthanides (optimised ion lenses). Finally, a bandpass mode employing the quadrupole with increased mass bandpass was developed and applied to the analysis of Gd, Er, Y, and Au. **97**
- Table 5-2:** Relative Sensitivities Obtained for Y, Gd, Er, Yb, and Au. For the standard method and optimised ion optics method, the most abundant lanthanide isotopes (^{158}Gd , ^{166}Er , and ^{174}Yb) were monitored. For the bandpass mode, higher sensitivities were achieved monitoring Gd at 155 amu, Er at 163 amu, and Yb at 172

	amu. All methods monitored ^{197}Au and ^{89}Y . Values are relative to the standard method for SP ICP-MS.	104
Table 5-3:	sDLs for Y, Gd, Er, Yb, and Au for all types of NPs analyzed. Y was analyzed employing the optimised ion optics (OIO) method. Lanthanides were analyzed employing the bandpass mode (BPM). For comparisons, the sDL for Au was also determined with the standard SP ICP-MS method (SM).	107
Table 6-1:	Specifications of the selected melanoma samples.	121
Table 6-2:	Mn, Zn, Fe, Cu concentration levels [ppm] in the gelatine standards used for quantification of the tissue samples.	123
Table 6-3:	Signal intensities and concentrations in the selected ROIs. The maximum and minimum values are highlighted in red and blue.	130

Abbreviations

A1 β-CN	A1 β -casein
A2 β-CN	A2 β -casein
α-CN	α -casein
α-Lac A	α -lactalbumin a
BFS	bare fused silica capillaries
BGE	background electrolyte
BPM	bandpass mode
BSA	bovine serum albumin
β-Lg	β -lactoglobulin
β-Lg A	β -lactoglobulin a
β-Lg B	β -lactoglobulin b
CA	citric acid
CE	capillary electrophoresis
CEI	capillary electrophoresis interface
CIC	compound-independent calibration

CK	creatine kinase
CMC	critical micellar concentration
CTAB	cetyltrimethylammonium bromide
DC	direct current
DIHEN	direct injection high efficiency nebulizer
DMT1	divalent metal transporter 1
DNA	deoxyribonucleic acid
DOTA	1,4,7,10-tetraazacyclododecane-1,4,7,10-tetraacetic acid
DTPA	diethylenetriaminepentaacetic acid
DTTA	diethylenetriaminetetra-acetic acid
EBI	elemental bioimaging
EOF	electroosmotic flow
Fab	fragment antigen binding
Fc	fragments crystallizable
FFT	fast fourier transform
Fpn	ferroportin
FWHM	Full width at half maximum
GBCA	gadolinium-based contrast agent
Gd-BT-DO3A	gadobutrol (Gadovist®)
Gd-DOTA	gadoteric acid (Dotarem®)

Gd-DTPA	gadopentetic acid (Magnevist®)
Gd-DTPA-BMA	gadodiamide (Omniscan®)
Gd-EOB-DTPA	gadoxetic acid (Primovist®)
GC	gas chromatography
His	histidine
HPLC	high performance liquid chromatography
HPMC	hydroxypropylmethylcellulose
HSA	human serum albumin
ICP-MS	inductively coupled plasma-mass spectrometry
IgG	sheep igg antibody
IHC	immunohistochemistry
iMSI	immuno-mass spectrometry imaging
IR	ionising radiation
LA	laser ablation
LOD	limit of detection
LOQ	limit of quantification
m/z	mass-to-charge ratio
Mb	myoglobin
MeCAT	metal coded affinity tags
MRI	magnetic resonance imaging

MW	molecular weight
NCX	sodium-calcium exchanger
NP	nanoparticle
NRAMP	natural resistance-associated macrophage protein
NSF	nephrogenic systemic fibrosis
OIO	optimised ion optics
PBS	phosphate buffered saline
PDMS	dimethyl polysiloxane
pI	isoelectric point
PM	plasma membrane
RF	radio frequency
RNase	ribonuclease a
ROI	regions of interest
ROS	reactive oxygen species
rpm	revolutions per minute
RSD	relative standard deviation
sDL	size detection limit
SDS	sodium dodecyl sulfate
SEC	size exclusion chromatography
SLG	scan line gain

SLS	scan line slope
SM	standard mode
SMIL	successive multiple ionic polymer layers
SP	single-particle
SQ or Q	single quadrupole
TEM	transmission electron microscopy
Tf	transferrin
TfR	transferrin receptor
TQ or QQQ	triple quadrupole
TRIS	tris(hydroxymethyl)aminomethan
UCNPs	upconversion nanoparticles
UV	ultraviolet
ZIP	zrt- and irt-like proteins
ZnT10	zinc transporter 10

Abstract

The underlying biological mechanisms of widespread radioresistance of many human tumours remain elusive despite decades of investigations. Research efforts have largely focussed on the genomics/proteomics-based enzymology of DNA repair and free radical scavenging enzymes such as the superoxide dismutases. A recent novel hypothesis is that radiation resistance is predominantly underpinned by non-enzymatic complexes of manganese and small molecular metabolites. These complexes are thought to act as free radical scavengers which provide metabolic radioprotection that render cells variably resistant to the products of ionising radiation.

Multiple influx and efflux metal transporters are involved in manganese homeostasis and are potentially differentially expressed on the surface of cancer cells, leading to variable concentrations of manganese within tumours. Uncovering the mechanisms of tumour radioresistance requires complementary, reliable, and well characterised methods to spatially quantify manganese and its transporter proteins. Laser ablation-inductively coupled plasma-mass spectrometry (LA-ICP-MS) provides a single technological platform to construct quantified images of elements and may be extended to measure biomolecules via incorporation of immunoassays. However, high quality and reproducible analyses require quality assurance across all steps of the workflow including the characterisation of antibodies, nanoparticles and antibody tagging protocols. Accordingly, this thesis introduces a portfolio of methods of hyphenated ICP-MS for quality assurance of elemental and biomolecule analyses.

Chapter 2 introduces novel and universal workflows for the analysis of intact proteins via capillary electrophoresis (CE) and presents guidelines for the targeted selection of appropriate background electrolytes via consideration of the target proteins' isoelectric point. Neutral dimethyl polysiloxane capillaries with dynamic coatings of cationic cetyltrimethylammonium bromide or anionic sodium dodecyl sulfate, and bare fused silica capillaries were systematically evaluated for the analysis of seven model proteins over a wide pH range. Multiple capillary and background electrolyte combinations were suitable for the analysis of each protein. The concept was demonstrated by the analysis of caseins and whey proteins in milk which separated the most abundant proteins, including the isoforms of A1 and A2 β -casein and β -lactoglobulin A and B.

Chapter 3 presents the development of a simple, robust, and cost-effective interface to hyphenate CE and ICP-MS to enhance the sensitivity and specificity for the analysis of limited volume and complex biological samples. The interface components were thoroughly investigated to highlight crucial aspects that need to be considered when developing and assembling a CE-ICP-MS interface. The interface's functionality, linearity and robustness were evaluated by separation and quantification of gadolinium-based contrast agents in urine samples collected after magnetic resonance imaging (MRI) examination.

Chapter 4 combined these advancements to determine labelling efficiencies of metal conjugated antibodies by CE-ICP-MS, which are widely used in cytometry and imaging for the identification and examination of protein expression. The number of lanthanide ions per protein was measured in seven MAXPAR™ polymer conjugated antibodies. Variable numbers of lanthanides were observed between different antibodies, as well as antibodies of the same kind, highlighting the importance of quality control workflows. The CE-ICP-MS method was also applied to 15 nm gold nanoparticles to demonstrate feasibility to distinguish un-conjugated and antibody conjugated nanoparticles.

Chapter 5 details novel methods of single-particle ICP-MS to characterise the composition, size distribution and particle-particle interactions of (upconversion)

nanoparticles. The optimization of ion extraction, ion transport, and the operation of the quadrupole with increased mass bandwidth improved the signal-to-noise ratios significantly and decreased the size detection limits for all nanoparticle dispersions investigated. Gold nanoparticles were analysed as a model system to demonstrate the effects of increasing ion transmission, subsequently the methods were applied to determine stoichiometries and size distributions of three types of lanthanide-doped upconversion nanoparticles. A Poisson model was further applied to assess particle–particle interactions in the nanoparticle dispersions.

Chapter 6 deployed these advanced techniques to demonstrate immuno-mass spectrometry imaging and elemental bioimaging of manganese transporters and transition metals in human melanomas. The transporter protein ZIP8 was visualised with an ^{153}Eu polymer labelled anti-ZIP8 antibody, and the expression levels of the ZIP14 transporter protein were localised with an immunoassay of an unlabelled primary antibody with a secondary antibody-nanoparticle conjugate. Manganese, copper, zinc, and iron distributions were imaged on consecutive sections of the microarray and co-localised with the ZIP8 and ZIP14 expressions. The results show a variable correlation of transition elements and proteins, demonstrating the complex interplay between metals and their respective transporters.

