Quantitative immuno-mass spectrometry imaging by laser ablation-inductively coupled plasma-mass spectrometry

A thesis submitted for the degree of Doctor of Philosophy at

University of Technology Sydney

Faculty of Science

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2019

Abstract

Laser ablation inductively coupled plasma mass spectrometry (LA-ICP-MS) is an elemental bio-imaging technique that combines high sensitivity and spatial resolution of elements with quantification in two or three dimensions. LA-ICP-MS has recently been applied to detection and quantification of non-elemental analytes (eg. proteins) in tissue sections using immunohistochemical methods. This approach uses molecular probes such as antibodies, tagged with reporter elements such as the lanthanides which are not found naturally in biological samples. Analyses based on these methods is known as immuno-mass spectrometry imaging (iMSI) and has the potential for application to currently refractive research questions in cell and organ biology and new diagnostic platforms.

The drawbacks of commonly used matrix-matched tissue standards were addressed by development of novel facile methods for the preparation of moulded gelatin standards. Surface roughness and robustness were compared against cryo-sectioned gelatin and homogenised brain tissue standards. The moulded standards had significantly higher accuracy, precision and reproducibility and were easier to prepare. Additionally, background metals in gelatin were removed using chelating resins to increase the dynamic calibration range and to improve limits of analysis.

The resolution of LA-ICP-MS elemental bio-imaging is usually constrained by the diameter of the laser spot size and is often not adequate to explore in situ sub-cellular distributions of elements and proteins in biological tissue sections. Super-resolution reconstruction is a method used for many imaging modalities, combining multiple lower resolution images to create a higher resolution image. This thesis describes a super-resolution reconstruction method for LA-ICP-MS imaging by ablating consecutive layers of a biological specimen with offset orthogonal scans. Layer-by-layer image reconstruction was extended to the third dimension without the requirement of image registration across multiple sections. Quantitative super-resolution reconstruction provided superior image clarity and fidelity in two- and three-dimensions.

These methods were applied to the development of iMSI for both antibody and aptamer probes to quantify and localise dystrophin in muscle, and myelin basic protein in brain. Quantification of dystrophin is challenging by conventional methods and is central to development of Duchenne muscular dystrophy treatments. Samples were stained with a gadolinium labelled anti-dystrophin antibody and analysed by LA-ICP-MS. Normal mouse and normal human samples were found to have ~700 and ~300 parts per billion gadolinium respectively with under 20% relative standard deviation. The results improved on current methods and met FDA guidelines. The feasibility of using aptamers for iMSI was confirmed, which may enable analysis of challenging targets.

Certificate of Original Authorship

I certify that the work in this thesis has not previously been submitted for a degree nor

has it been submitted as part of requirements for a degree except as fully acknowledged

within the text.

I also certify that the thesis has been written by me. Any help that I have received in my

research work and the preparation of the thesis itself has been acknowledged. In

addition, I certify that all information sources and literature used are indicated in the

thesis.

This research is supported by an Australian Government Research Training Program

Signature of Student:

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Date: 31/07/19

iv

Dedicated to difficulty

Acknowledgements

I would like to acknowledge my three supervisors in order of chronological encounter. Firstly, Associate Professor Andrew McDonagh for introducing me to research during my undergraduate research project on ruthenium phthalocyanine and putting a secretly analytical chemistry project among the physics honours projects so that a naïve young nanotechnology student could unwittingly give it a try.

Secondly Professor Philip Doble for initially putting Andrew up to the task of luring students over to analytical chemistry dark arts and eventually for putting up with my physics brained peculiarities over the course of my PhD studies. Finally, I would like to thank Dr Nerida Cole for teaching me everything that is required to be a researcher worth one's salt from experiments in the lab to brainstorming in the pub and supporting my endeavours from near and afar.

Next I would like to thank the three postdocs that helped me throughout my PhD but especially during the final months of thesis writing. Dr David Bishop, Dr Raquel Gonzalez de Vega, and Dr David Clases were all extremely helpful. I would particularly thank David Bishop for the ongoing collaboration and helping me translate my research to clear and logical presentation.

The champions of the lab Ronald Shimmon, Alex Angeloski and Dayanne Mozaner Bordin who have helped me for the whole of my PhD, despite breaking machines, finishing all the reagents and being an all-round nuisance in the lab.

The physics kids both finished and fallen soldiers who supported me from undergrad through to PhD: Kerem Bray, Matt Tai, Marc Gali Labarias, Alba Santín Garcia, Rodolfo Previdi and Vince Ha-Hau.

Much love and thanks to the PhD students of the group formerly known as Elemental Bio-Imaging Group now known as Atomic Medicine Initiative. Phuc Nguyen Prashina Singh, Karen Duong, Natasha Benson, Matthew Diplock, Thomas Lockwood, Joel Steele, Jake Violi, David Gertner, Sarah Meyer, and Vitor Cesar Taranto. Also, our newly

minted *Goodest Bois* Helen Zeng, Fiona Dang, Siobhan Peters and Jacob Marecic. Friday beers at Staves were an essential destress from weeks of machine mishaps.

Finally, I would like to thank my family for their continued support over my many years of study.

List of Publications

Refereed journal publications

- [1] Mika T. Westerhausen*, David P. Bishop*, Annette Dowd, Jonathan Wanagat, Nerida Cole & Philip A. Doble, "Super-Resolution Reconstruction for Two-and Three-Dimensional LA-ICP-MS Bioimaging", Analytical Chemistry, October 2019.
- [2] Mika T. Westerhausen*, Thomas E. Lockwood *, David P. Bishop, , Raquel Gonzalez de Vega, Anna Röhnelt, Nerida Cole, Philip A. Doble & David Clases, "Low background mould-prepared gelatine standards for reproducible quantification in elemental bioimaging", The Analyst, October 2019.
- [3] Mika Westerhausen*, David P. Bishop*, Nerida Cole, Elizabeth Gibbs, Rachelle Crosbie-Watson, Florian Barthelemy, Stan Nelson, Carrie Miceli, Philip A. Doble, and Jonathan Wanagat, "Quantitative immuno-mass spectrometry imaging of skeletal muscle dystrophin", Article in preparation, Jan 2020.

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Conference oral presentations

Mika T Westerhausen, David Bishop, Nerida Cole, Philip Doble, "Orthogonal Anisotropic Acquisition LA-ICP-MS for 2D and 3D Super Resolution Reconstruction Bio-Imaging", Asia-Pacific Winter Conference on Plasma Spectrochemistry (APWC), 2017, Matsue, Japan

Mika T. Westerhausen, David P. Bishop, Nerida Cole, Jon Wanagat & Philip Doble, "Super-resolution reconstruction for bio-imaging by LA-ICP-MS", Euorpean Winter Conference on Plasma Spectrochemistry (EWCPS), 2019, Pau, France

Mika T. Westerhausen, David P. Bishop, Nerida Cole, Jon Wanagat & Philip Doble, "3D Super-resolution reconstruction for bio-imaging by LA-ICP-MS", Conference on Laser Ablation, 2019, Maui-Hawaii, USA

Table of Contents

Abstract	ii
Certificate of Original Authorship	iv
Acknowledgements	vi
List of Publications	viii
Refereed journal publications	viii
Conference oral presentations	viii
Table of Contents	ix
List of Figures	xiv
List of Tables	xix
Acronyms & Abbreviations	xx
1. Literature Review	1
1.1 Metals in biology	1
1.1.1 Sources of metals	1
1.1.2 Analysis of elements	2
1.1.3 Mass Spectrometry in bioanalysis	3
1.1.3.1 Elemental Mass Spectrometry	4
1.1.3.2 Inductively coupled plasma mass spectrometry	4
1.1.4 Elemental bio-imaging techniques	6
1.1.4.1 LA-ICP-MS: fundamentals, principles and fields of application	n10
1.1.4.1.1 Laser Ablation limits	11
1.1.4.1.2 Quantification strategies by means of LA-ICP-MS	13
1.1.4.1.3 Applications of LA-ICP-MS	15
1.1.4.2 Immuno-Mass Spectrometry Imaging and beyond	15
115 Tagging agents	18

	1.1.6	Image processing	21
	1.2	Thesis aims	24
2	Mate	erials and Methods	26
	2.1 I	nstrumentation	26
	2.1.1	Solution nebulization inductively coupled plasma mass spectrome	try 26
	2.1.2	Laser ablation inductively coupled plasma mass spectrometry	28
	2.1.3	Microscopy	30
	2.1.4	Profilometry	30
	2.1.5	Protein quantification via Spectrophotometry	31
	2.2 I	Data acquisition and processing	31
	2.2.1	Data acquisition	31
	2.2	2.1.1 Conversion from raw data to 2D representation	32
	2.2.2	Data visualization and manipulation	33
	2.3 I	Experimental Methods	33
	2.3.1	Chemicals and Reagents	33
	2.3.2	Matrix Matched Mouse Brain Standards	34
	2.3	3.2.1 Quantification of Metal Concentrations in Standards	34
	2.4	Calculations	35
	2.4.1	Linear regression analysis	35
	2.4.2	Limits of analysis and outliers	36
	2.5 A	Animals	36
	2.5.1	Immunohistochemistry	37
3	Stan	dard Preparation and Comparison	38
	3.1 A	Abstract	38
	3.2 I	ntroduction	38
	3.3 N	Method	41
	331	Gelatin Standards	41

	3.3.	2 Tissue Standards	44
	3.3.	3 SN-ICP-MS	44
	3.3.	4 Elemental extraction to decrease background levels	45
	3.3.	5 LA-ICP-MS	45
	3.3.	6 Data Analysis	46
	3.3.	7 Profilometry	46
	3.4	Results and Discussion	47
	3.4.	1 Qualitative comparison of mould methods	47
	3.4.	2 Topography and height characterisation	49
	3.4.	3 Post-analysis characterisation	52
	3.4.	4 Analytical figures of merit and background equivalent concentrations.	53
	3.5	Conclusion	56
	3.6	Acknowledgments	57
4	Sup	per resolution reconstruction for LA-ICP-MS imaging	58
	4.1	Abstract	58
		Introduction	58
		Method	60
	4.3.	1 Instrumentation	60
	4.3.	2 Reagents	61
	4.3.	3 Standard Preparation	61
	4.3.	4 Sample Preparation	62
	4.3.	5 Optimisation of image acquisition parameters	63
	4.3.	6 Super Resolution Reconstruction	65
	4.3.	7 Processing Algorithms	66
	4.3.	8 Image processing software	67
	4.3.	9 Statistical Analysis	67

	4.4	Res	ults and Discussion	67
	4.4	1.1	Optimisation of image acquisition parameters	67
	4.4	1.2	Calibration	71
	4.4	1.3	Quantification	76
	4.4	1.4	Three-Dimensional Reconstruction	78
	4.5	Cor	nclusions	80
5	Mı	uscul	lar Dystrophy	82
	5.1	Abs	stract	82
	5.2	Intr	oduction	82
	5.3	Met	thods	86
	5.3	3.1	Materials	86
	5.3	3.2	Mouse models	86
	5.3	3.3	Human tissue	87
	5.3	3.4	Histological preparation	87
	5.3	3.5	3-dimensional sample preparation	87
	5.3	3.6	Preparation of iMSI standards	88
	5.3	3.7	iMSI	89
	5.3	3.8	Image processing	89
	5.3	3.9	Statistical analysis	89
	5.4	Res	ults and Discussion	90
	5.4	1.1	iMSI in wild-type and mdx mouse skeletal muscle	90
	5.4	1.2	iMSI in normal human and DMD skeletal muscle	95
	5.4	1.3	3D iMSI of thick sections	99
	5.5	Cor	nclusion	103
6	To	war	ds aptamer imaging	105
	6.1	Abs	stract	105
	6.2	Intr	oduction	105

6	6.3 Me	thod	108
	6.3.1	Animal Handling	108
	6.3.2	Lanthanide Labelling of antibodies	108
	6.3.3	MBP Antibody labelling	108
	6.3.4	MBP Aptamer labelling	109
	6.3.5	Myelin Basic Protein Antibody and Aptamer specificity analysis	112
	6.3.6	Microscopy	112
	6.3.7	LA-ICP-MS.	113
	6.3.8	Preparation of iMSI standards	113
6	6.4 Res	sults and Discussion	114
	6.4.1	Antibody vs Aptamer	114
	6.4.2	Aptamer binding confirmation via dot blot	114
	6.4.3	Fluorescence microscopy comparison	116
	6.4.4	LA-ICP-MS comparison	119
6	6.5 Co	nclusion	121
7	Overal	l conclusions and future work	123
8	Refere	nces	126
9	Appendix		

List of Figures

Figure 1	1.1: Bioimaging of four transition metals (Cu, Fe, Zn and Mn) in mouse brain by
I	LA-ICP-QMS imaging, scale bar 2mm. [24]8
Figure	1.2: Laser ablation inductively coupled plasma mass spectrometry schematic
ι	using a helium and argon gas system [33]10
Figure	1.3: Comparison of ablation spot between a) nanosecond and b) femtosecond
I	pulse width LA-ICP-MS systems [44]12
Figure 1	1.4: Comparison of antibody and aptamer structures [85]
Figure 1	1.5: Schematic of indirect immunolabelling using fluorescent tagging [88] 18
Figure	1.6: Double immunolabeling of two cytokeratins, Ck14 (IgG3) and Ck8/18/19
((IgG1), in a duct wall of the human mammary gland (Twenty micrometers scale
ŀ	oar and colours are for Ck8/18/19 (a, FITC, green), Ck14 (b, Alexa-647, pink) and
f	for nuclei (DAPI, blue) [86]19
Figure 1	1.7: Scheme of selected bi-functional ligands used as labelling reagents and their
ŀ	pinding to amino acids of an antibody. The SCN-DOTA covalently binds to 3-
a	amino groups of lysine residues. The other opportunity shown here is the
1	abelling via a maleimide group which binds to the sulfhydryl residues after
I	partial reduction of the antibody's cysteine-based disulfide bridges. MeCAT and
9	SCN-DOTA contain a DOTA macro-cycle (pink circle) to complex lanthanide
i	ons whereas the MAXPAR polymer chain contains many DTPA residues as
(chelating compounds (yellow circle)21
Figure 1	1.8: Illustration of the basic principle of Super Resolution Reconstruction23
Figure 1	1.9: Scheme illustrating the super-resolution reconstruction from the acquisition
(of two orthogonal thick slices [122]24
Figure 2	2.1: Agilent 7500cx (left) and 7700x (right) Series Inductively Coupled Plasma
1	Mass Spectrometer fitted with Agilent Integrated Autosampler [124]26
Figure	2.2 NWR-193 Laser Ablation System [123] (left) and Agilent 7700 Series
I	Inductively Coupled Plasma Mass Spectrometer [124] (right)28
Figure 2	2.3: Leica FS CB microscope
Figure 2	2.4: DektakXT Profilometer30

Figure	2.5: Thermo Scientific™ NanoDrop 2000 Spectrophotometer
Figure	2.6: Representation of laser ablation raster and the resulting spectra32
Figure	2.7: Graphic user interface for ImaJar software
Figure	3.1: Moulding devices for gelatin standards: Cavity slide (A), Culturewell TM (B)
	and Hybriwell TM (C)
Figure	3.2: 6-well Hybriwell™ gasket schematic [152]43
Figure	3.3: Cavity slide gelatin standards. Plan view and single concavity aspect47
Figure	3.4: Culturewell TM silicon gasket gelatin standards. Plan view and aspect of 4
	wells
Figure	3.5 : Hybriwell $^{\mathrm{TM}}$ slide gelatin standards left in the freezer too long. Plan view and
	aspect of 2 wells
Figure	3.6 : Hybriwell $^{\mathrm{TM}}$ slide gelatin standards. Plan view and aspect of 2 wells48
Figure	$3.7\ Teflon\ tape\ manufactured\ schematic\ and\ as\ fabricated\ gelatine\ standards49$
Figure	3.8: Normalised heights as determined by profilometry showing deviations in
	height and heterogeneity in surface topography. The measured height of the
	tissues/standards was normalised to the expected height50
Figure	3.9: Visual comparison of an ablated homogenised animal tissue standard (A) and
	a gelatin standard (B). (C): Profilometry data standards ablated eleven times with
	increasing laser power. (D): Signal intensities for Mn, Cu, and Zn derived from
	repeated ablation of standard material53
Figure	4.1: Orthogonal acquisition, (A) first line scans, (B) second line scans offset by
	half the magnitude of the laser spot size, (C) combined pattern for SRR
	processing. Arrows denote direction of scan65
Figure	4.2: SRR processing of two ablated layers. (A) The two layers acquired with an
	AR of 2 in the horizontal and vertical directions. (B) and (C) Representation of
	the two layers brought to congruence using the Kronecker Product. (D) Up-
	sampling with null values into a checkerboard pattern. (E) Layers offset and
	stacked into a 3D array and null values and trilinearly interpolated. (F) Populated
	layers summed together to produce final 2D image66
Figure	4.3: Representative photomicrograph of dystrophin in murine quadriceps. The
-	expression of the protein is clearly seen as a honeycomb structure in the

membranes of the muscle fibres. The protein was stained with Gd-labelled
MANDYS8 primary antibody and detected using a goat anti-mouse secondary
antibody (Sigma) conjugated to alkaline phosphatase with NBT/BCIP substrate
(Sigma)68
Figure 4.4: Image panel of acquisition parameter optimisation. Seven acquisitions were
considered representing ARs ranging from 1 to 10. The SRR images are in column
1, except for (A), which was constructed in the conventional manner. Column 2
are the images after application of the Gaussian filter, whilst column 3 represents
images after RLTV70
Figure 4.5: Post ablation raster pattern after two passes in the horizontal and vertical
directions
Figure 4.6 Representative calibration curves and image panels. (A) Anisotropic single
layer calibration curve in horizontal direction. (B) Image of calibration standards
in horizontal direction. (C) Anisotropic single layer calibration curve in vertical
direction. (D) Image of calibration standards in vertical direction (E) Calibration
curve after SRR with AR = 2. (F) Image of calibration standards after SRR. (G)
Calibration curve after application of the Gaussian filter. (H) Image of calibration
standards after Gaussian filter. (I) Calibration curve after RLTV. (J) Image of
calibration standards after RLTV73
Figure 4.7: Effect of image processing on two-layer test. (A) Anisotropic acquisition of
single layer in horizontal direction. (B) Same layer as (A), transposed to vertical
direction. (C) SRR of (A) and (B). (D) Application of Gaussian filter. (E) RTLV
image
Figure 4.8: Three-dimensional reconstructions of continuously ablated 50 μm section.
(A) Planar view of single focus acquisition. (B) and (C) Oblique and isometric
views of refocused laser acquisition at 5 μm for each pass. (D), (E), and (F) Planar,
oblique and isometric views of single focus laser acquisition. The structural
integrity of the dystrophin is clearly seen throughout the 10 layers79
Figure 5.1: Dystrophin iMSI in wild type and mdx mouse quadriceps muscle. A, low-
resolution iMSI (15\mathbb{M}m) of whole mouse quadriceps cross section showing
expected sarcolemmal distribution of dystrophin. High-resolution (1.75 ⊠m)

images of dystrophir	by iMSI in wild-type (B) and mdx mouse quadriceps (C)
Quantification scale	in A denotes ppb of gadolinium for all panels90
Figure 5.2: Histograms with	the 3 tested thresholding methods (A). Intensity map of WT
quadricep (B) with th	ne correlating threshold methods: Raw (C), Median (D) and
Otsu's (E) using the	histogram colours to represent the areas of the image used
for quantification	92
Figure 5.3: Representative a	areas of ablation of murine quadriceps, A, B and C. Black
scale bar represents 1	000 μm93
Figure 5.4: IHC with hemato	oxylin counterstain (A) and iMSI (B) for dystrophin in serial
sections of human q	uadriceps muscle (80 year old). Scale bar in A denotes 100
microns and applie	s to both images. The same gadolinium-labeled anti-
dystrophin antibody	was used in both. Quantification scale in C denotes ppb of
gadolinium	95
Figure 5.5: Exemplar iMSI in	nage of section from 18-year-old male vastus lateralis biopsy
Scale bar is in ppb G	d96
Figure 5.6: IHC (A) and iMS	SI (B) of dystrophin in serial muscle sections from a patient
with Duchenne mus	cular dystrophy. Quantification scale in C denotes ppb of
gadolinium in panel	B. Black bar in A denotes 100 microns97
Figure 5.7: Consecutive sect	ions of human quadricep tissue (1-4) on the same intensity
scale	100
Figure 5.8: Two-dimensiona	l image in the X-Z plane of 12-layer 3D stack of 30 μ m thick
sections incubated fo	er 30 (A) ,60 (B) and 120 (C) minutes on the same intensity
scale. Red line signifi	es the final layer with signal above the LOQ101
Figure 5.9: Two-dimension	al image in the X-Z plane of 16-layer 3D stack of 30min
incubated tissue of	thickness 10 μm (A), 30 μm (B) 50 μm (C) on the same
intensity scale Red li	ne signifies the final layer with signal above the LOQ102
Figure 5.10: 3D image of 12	Omin incubation time 30um section, scale in ppb of Gd103
Figure 6.1: Dot blots of ME	P only control (A), MBP Aptamer only control(B), human
serum albumin contr	ol (C), unfolded MBP aptamer 5' biotin (D), and folded MBP
aptamer 5' biotin (E)	all visualized with streptavidin HRP and TMB substrate
	115

Figure 6.2: Elemental images of dot blots for folded Scrambled MBP aptamer 5' thiol
tagged with $^{153}\mathrm{Eu}$ control (A), folded MBP aptamer 5' thiol tagged with $^{153}\mathrm{Eu}$ (B)
unfolded MBP 5' biotin tagged with streptavidin Eu (C), folder MBP 5' biotin
tagged with streptavidin Eu (D), MBP only control with streptavidin Eu (E), MBP
aptamer 5' thiol tagged with 153Eu only control(F), and MBP aptamer 5' Biotin
only control (G).
Figure 6.3: Mouse hippocampal formation stained with Rabbit antiMBP AntiRabbit-
FITC (Green) and Hoechst 33342 (Blue) (A) and MBP aptamer 5' Biotin and
Streptavidin FITC (Green) and Hoechst 33342 (Blue) (B). The white arrow points
to an oligodendrocyte117
Figure 6.4: Mouse hippocampus stained with MBP aptamer 5' Biotin and Streptavidin
Qdot (Red) and Hoechst 33342 (Blue). The white arrow points to a possible
oligodendrocyte118
Figure 6.5: Mouse hippocampus (A) and hippocampal formation (B) stained with MBF
aptamer 5' Biotin and Streptavidin FITC (Green) and Hoechst 33342 (Blue)
courtesy of the Human Protein Atlas[240] The white arrows point to possible
oligodendrocytes119
Figure 6.6: Low resolution images of MBP aptamer biotin 5'-Streptavidin Eu (A), MBF
aptamer thiol 5'-153Eu (B) and antiMBP-153Eu (C). Calibration bar denotes ppb Eu
120
Figure 6.7: High resolution image of MBP aptamer 5'biotin-streptavidin Eu (A) and
correlating antiMBP-FITC micrograph courtesy of the Human Protein Atlas [240]
Calibration bar denotes ppb Eu121

List of Tables

Table 2.1: Typical ICP-MS parameters for SN-ICP-MS.	27
Table 2.2: Typical LA-ICP-MS parameters.	29
Table 2.3: Table of formulas used in the excel function LINEST.	35
Table 2.4: General equations used for statistical analysis.	36
Table 3.1: Metal salts used in Gel Standards	42
Table 3.2: Concentrations of external calibration standards.	45
Table 3.3: Comparison of accuracy derived from different preparation methods as	nd
materials	51
Table 3.4: Characterisation of standard materials. The concentrations and error of ea	ch
calibration level were cross-quantified by solution-based ICP-MS. LO	D,
Sensitivity and Linearity were determined from the calibration curve construct	ed
by LA-ICP-MS.	54
Table 3.5: Background concentration [pg/g] of gelatin materials prior and after	an
additional extraction step with different resins, respectively	55
Table 4.1: Concentrations of gelatin standards.	61
Table 4.2: Concentration of liquid standards.	62
Table 4.3: Super resolution reconstruction acquisition parameters	64
Table 4.4: Analytical Figures of Merit after application of the processing algorithms	74
Table 4.5: Average Response and %RSD for calibration standard near or above the LO	Q.
	76
Table 4.6: Average concentrations and %RSD for simulated two-layer sample	77
Table 5.1: Incubation and section parameters for 3D atlas incubation	88
Table 5.2: Concentrations of gelatin standards (ng/g± ng/g)	89
Table 5.3: Average values of gadolinium (ppb) and % RSDs from the regions of interesting the second	est
and thresholding methods for wildtype murine quadriceps	94
Table 5.4: Technical replicates of dystrophin iMSI from consecutive serial musc	cle
sections	98
Table 6.1: Sequences and Functionalisation of Oligonucleotides1	10
Table 6.2: Concentrations of gelatin standards (ng/g)	13

Acronyms & Abbreviations

2D Two Dimensional3D Three DimensionalLOQ Limit of Quantification

AP Alkaline Phosphatase lPIXE Ion Particle induced X-ray

AR Anisotropic Ratio emission

CRM Certified Reference Material

MALDI Matrix Assisted Laser

Desorption/Ionization

DAPI 4',6-diamidino-2-phenylindole

MeCAT Metal-coded affinity tags

DMD Duchenne's Muscular Dystrophy

MBP Myelin Basic Protein

EBI Elemental Bio-Imaging

MC Multicollector

EDTA Ethylenediaminetetraacetic acid

Mdx Mutation Dystrophin X-

FDA Food and Drug Administration Chromosome

FITC Fluorescein isothiocyanate

spectroscopy

FFPE Formalin-Fixed Paraffin- MRI Magnetic Resonance Imaging

Embedded PBS Phosphate Buffered Saline

PMMA Poly(methyl methacrylate)

FM Fluorescence Microscopy

ppb Parts per billion

HRP Horseradish Peroxidase

ppm Parts per million

ICP-MS Inductively coupled plasma
PTFE Polytetrafluoroethylene
mass spectrometry

IHC Immunohistochemistry

RLTV Richardson-Lucy Total Variance

LA-ICP-MS Laser Ablation Inductively

RNA Ribonucleic acid

Coupled Plasma Mass Spectrometry SCN-DOTA 2-(4-

LIBS Laser-induced breakdown isothiocyanatobenzyl)-1,4,7,10-

tetraazacyclododecane-1,4,7,10-tetraacetic acid

SIMS Secondary Ion Mass Spectrometry

SN-ICP-MS Solution Nebulisation Inductively Coupled Plasma Mass Spectrometry

SRR Super Resolution Reconstruction

ssDNA single stand Deoxyribonucleic acid

TBS Tris Buffered Saline

 $\begin{tabular}{ll} TCEP\ Tris (2-carboxyethyl) phosphine \end{tabular}$

TOF Time of flight

WT Wildtype

XFM X-Ray Fluorescence Microscopy

 $\pmb{XPS} \ X\text{-ray photoelectron spectroscopy}$