

CURRICULUM VITAE

Name: Rune Matthiesen
Nationality: Danish citizen
Languages: Danish, English, German, Portuguese (Simple communication)

Present position: Principal Investigator
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Education and Employment

2016-2018: Principal Investigator, CEDOC, Lisbon, Portugal
2013-2016: Principal Investigator, National Institute of Health Dr Ricardo Jorge, Lisbon, Portugal
2008-2013: Principal investigator of Proteolysis in Diseases, IPATIMUP, Porto, Portugal
2006-2008: Principal Investigator, CIC bioGUNE, Bilbao Spain
2004-2006: Assistant Professor, Protein research group, University of Southern Denmark
2004-2005: Assistant Professor, EBI, Hinxton and University of Southern Denmark
2000-2004: Ph.D. thesis: Mass spectrometry in Proteomics, University of Aalborg
1999-2000: Research Assistant, Developmental biology, EMBL, Heidelberg
1998-1999: Cand. Scient in Crystallography, Aarhus University

Mission statement

The computational and experimental biology group (CEB) aims at being forefront in clinical proteogenomics research. We have established experimental and computational quantitative technologies for MS-based profiling useful for clinical proteomics (e.g. label free quantitation, triple dimethyl labeling, SILAC and tandem tags). More specifically we have over the last eight years obtained considerably experience in global MS-based drug profiling used in combination with genomics technologies such as next generation sequencing methodologies (Proteogenomics). We have experience in using proteogenomics in clinical samples, human cell lines and in multi drug resistance bacteria. Our main interest is to apply our technologies on lung cancer, cardiovascular diseases and hematological diseases. Although the main focus is on chronic diseases, pathogens are also questioned to address the role of host-pathogen interactions in chronic diseases. In other words, we work in the interface between clinicians, biomedical and biochemistry researchers.

Oral Presentations

Selected recent oral communications:

2016 Nov	Organizer and session chair of the Proteostasis cost action meeting in Lisbon, Portugal
2016 Jun	Post translational modification in clinical samples , University of Aveiro, Portugal.
2015 Dec	Hospital São Francisco Xavier, Lisbon, “High throughput MS-based proteomics”
2015 Nov	Invited presentation, Proteogenomics for global drug profiling and biomarker discovery , CEDOC, Lisbon, Portugal
2015 Sep	Invited STMS presentation, N-terminomics for biomarker discovery in bronchoalveolar lavage, COST action Proteostasis and EMBO meeting, Croatia
2014 Oct	Invited presentation, Post translational modifications and drug resistance , Proteostasis meeting, Valencia, Spain
2014 Sep	Invited presentation, Global MS- and transcriptomics array drug profiling , ITQB, Portugal
2013 Oct	Invited presentation “Waters day, Lisbon”, Global MS- and transcriptomics array drug profiling provides novel insight into glucosamine-induced ER stress
2013 Feb	Invited presentation, Computational methods in high throughput MS-based proteomics , CRBM, Montpellier, France
2013 Jan	Invited presentation, Computational methods in high throughput MS-based proteomics , ITQB, Portugal
2012 Dec	Invited presentation, High-throughput clinical proteomics , ICBAS , Porto, Portugal
2012 Jun	Invited presentation, New strategies for protein inference , Aveiro, Portugal
2012 Mar	Invited presentation, Overview of MS-based proteomics technologies , Jornadas, Braga, Portugal
2012 Feb	Invited presentation, Overview of MS-based proteomics technologies , INL, Braga, Portugal
2011 Jul	Invited to present at ICAP II, Ourense, Spain
2011 Feb	Invited to present and open the computation proteomics session in the conference “New Trends in Proteomics”, SEPROT, Segovia, Spain
2009 April	Invited speaker, Functional enrichment on large scale , CNIO, Madrid, Spain
2009 Mar	Invited speaker, Functional enrichment on large scale , "From genomes to organisms: an evolutionary perspective", Portugalia Genetica, Porto, Portugal

Teaching activities (selected)

General:

1. Experience with both ungraduated and graduate teaching.
2. Attended obligatory course in “Basic course in theory of education” (see PhD certificate also PhD certificate for documentation).
3. Participated in establishing the BiotechHealth (PhD program “Cellular and Molecular Biotechnology Applied to Health Sciences”), University of Porto, Oporto, Portugal.

Graduate teaching (recent yearly events):

1. Lectures on clinical proteomics, iBiMED International Advanced Training School in Molecular Medicine, Department of Medical Sciences, University of Aveiro, Portugal.
2. Lectures on clinical proteomics, BIOSys - PhD Program in Biological Systems, Functional & Integrative Genomics, Faculty of Sciences of the University of Lisbon, Lisbon, Portugal
3. Medical doctors training in clinical proteomics, Chronic Diseases Research Center, CEDOC, Nova Medical School, Lisbon, Portugal

Past graduate teaching:

2009-2013: Advanced PhD course in Cancer cell biology (The GABBA Program is the Graduate Program in Areas of Basic and Applied Biology), University of Porto, Oporto, Portugal

2006-2008: Consulting startup companies in bioinformatics and machine learning (CIC bioGUNE, Derio, Spain)

2004-2006: MS-based proteomics course, University of *Southern* Denmark, Odense

Ungraduated teaching (selected):

1. Biochemistry course on 3rd semester.
2. Protein chemistry lab course 7th semester
3. Protein stability lab course 7th semester
4. Investigation of enzyme stability lab course 3rd semester
5. Enzyme stability lab course 2nd semester
6. “Design and construction of a Soybean Seed Coat Peroxidase/YfaI Autotransporter Fusion Vector for expression in *Escherichia coli*”, master project
7. “Construction of a phoA-Cutinase-Peroxidase Fusion Protein for Expression of Plant Peroxidases in the Periplasmic Space of *E.coli*”, master project

Awards

Ramon y Cajal (RYC-2006-001446)
FCT Investigator 2012

Completed additional courses

2010	Biological sequence and genome analysis, Cold Spring Harbor, Not graded
2011	Machine learning, by Andrew Ng, completed with distinction
2012	Computing for Data Analysis, Coursera, completed with distinction
2015	Algorithms for DNA sequencing, Coursera, completed with distinction

Organizational responsibilities

2016	Member of the organizing committee of Proteostasis MC/WG meeting in Lisbon, Portugal
2015	Member of the organizing committee of the Proteostasis webinars (EU COST action)
2015	Teaching of Medical PhD students from CEDOC, Lisbon, Portugal in clinical proteomics
2014-	Member of American Society for Biochemistry and Molecular Biology (ASBMB)
2014-	Nominated as management committee for Portugal in COST action “PROTEOSTASIS”
2014	Opponent on PhD thesis “Role of Ubiquitin and SUMO molecules in the regulation of essential cellular factors”, PhD Elisa Aida da Silva Ferrada, San Sebastian, Spain
2014-2015	External evaluator of assistance professor position in Institut for Biokemi og Molekylær Biologi, University of Southern Denmark
2014	Evaluator of first phase of PhD student Sara Inês de Ascensão Tavares Canato “The ER quality control: Dissecting protein networks to identify drug targets for Cystic Fibrosis”
2014	Evaluator of first phase of PhD student Solange Pacheco “Disclosing effects of tobacco smoke on occupationally exposed workers”
2014	Teaching in high throughput mass spectrometry in the BioSys - PhD Program in Biological Systems, Functional & Integrative Genomics BIOSys PhD course, Faculty of Sciences of the University of Lisbon, Lisbon, Portugal
2011-2013	Editor on second edition of “Mass Spectrometry Data Analysis in Proteomics”, Springer
2009 -2012	Involved in teaching PhD students, GABBA Graduated Program, University of Porto, Portugal

- 2012** Lara Silva, “ASPP2: regulating p63/p73 and Notch pathways in tumourigenesis”, University of Aveiro, Portugal (Supervisor Prof. Xin Lu, Director of Ludwig Institute for Cancer Research da Universidade de Oxford).
- 2010** Organiser of the international meeting “Portugalia genetica”, Porto, Portugal
- 2010 May** Opponent on MS thesis “Bioinformatics in mass spectrometry-based proteomics”, SDU, Odense, Denmark
- 2010 Mar** Opponent on PhD thesis “Development of tools for analyzing and sharing proteomics data” at Department of Informatics, University of Bergen, Norway
- 2007-2010** Editorial board member of the **Oxford journal Bioinformatics**
- 2007-2009** Editor on “Bioinformatics in clinical research”, Humana Press
- 2007 Oct** Opponent on PhD thesis “Computational methods in high-throughput proteomics research”
- 2004-2006** Editor on “Mass Spectrometry Data Analysis in Proteomics”, Humana Press

Grant evaluation

- 2016** "Bilateral Scientific Cooperation China" application to the Research Foundation Flanders – FWO
- 2011-2016** Evaluator and rapporteur of national projects submitted to the **research council of Romania** (bioinformatics, proteomics and clinical projects)
- 2014-** Czech-Norwegian Research Programme (CZ09)
- 2013** Evaluator of FCT investigators
- 2010** EU INDIGO projects in the area of biomarker discovery, bioinformatics and proteomics
- 2009 -** Evaluator of Spanish National projects (**MEC projects**)

External evaluations of Rune Matthiesen

- 2010** Evaluated qualified as group leader by external advisory board of IPATIMUP, Porto, Portugal
- 2016** Evaluated qualified as Professor in bioinformatics by assessment committee appointed by DTU, Denmark

Supervision (* co-supervisor)

(Selected supervision after obtaining first independent group leader position in 2006)

- 2013-2016:** Post docs: Ana Sofia Carvalho, INSA, Portugal
- 2011-2013:** Researcher: Susana Seixas, IPATIMUP, Portugal
- 2013-2016:** PhD students: Patricia Marques, IPATIMUP, Portugal – external advisor
- 2013-2016:** PhD students: João D. Santos, University of Lisbon, Portugal – external advisor
- 2013-2016:** PhD students: Sara Canato, University of Lisbon, Portugal – external advisor
- 2013-2016:** PhD student: Ana Luisa Silva, iNOVA4Health – external advisor
- 2009-2013:** Post Doc: Ana Sofia Carvalho, IPATIMUP, Portugal
- 2014-2017:** Post Doc: Silvia Pereira, IPATIMUP, Portugal
- 2011-2014:** Post Doc: Silvia Pereira, IPATIMUP, Portugal
- 2006-2008:** Post Doc: Mikael Hackenberg, CIC bioGUNE, Spain
- 2007-2008:** Post Doc: Gorka Lasso, CIC bioGUNE, Spain
- 2006-2007:** Researcher PhD Ewa Gubb, CIC bioGUNE, Spain
- 2007-2010:** PhD students: Itziar Frades, CIC bioGUNE, Spain
- 2011-2015:** PhD students: Amélia Feliciano, Medical Faculty, Lisbon – co-supervisor
- 2012-2013:** MSc Helena Soares, IPATIMUP, Portugal
- 2012-2013:** MSc Elisa Barroso, IPATIMUP, Portugal
- 2012-2013:** MSc Vera Costa, IPATIMUP, Portugal
- 2010-2011:** MSc Catarina Fonseca, IPATIMUP, Portugal
- 2010-2012:** MSc João Mato, IPATIMUP, Portugal
- 2010-2012:** MSc Paula Voabil, IPATIMUP, Portugal
- In addition technical staff and researchers hired on research grants.

Editorial activities

- 2006** Editor on **Mass Spectrometry Data Analysis in Proteomics**, *Humana press*
- 2007-2010** Editorial board member of the **Oxford journal Bioinformatics**
- 2010** Editor on **Bioinformatics methods in clinical research**, *Springer*

- 2013** Editor on second edition of **Mass Spectrometry Data Analysis in Proteomics**, *Springer*
2016 Editor on **PROTEOSTASIS**, 31 chapters in press, *Springer*
2016 Editor on **PROTEOSTASIS in plants**, 22 chapters in press, *Springer*

Reviewing Duties

Reviewed manuscripts for Science, Nature Methods, Bioinformatics, Proteomics, Journal of Proteome Research, Journal of Mass Spectrometry. Reviewed book chapters on “Next Generation Sequencing” for the publisher Springer.

International peer reviewed publications 46

H-index 23, i10=35

*) **19 main author publications in international peer reviewed journals.**

1. *) Ana Sofia Carvalho, Henrik Molina and Rune Matthiesen, **New insights into functional regulation in MS-based drug profiling**, Scientific Reports from Nature Publishing Group, 2016, 6, 18826.
 2. *) Lydia Mata-Cantero, Mikel Azkargorta, Fabienne Aillet, Wendy Xolalpa, Maria, J. LaFuente1, Felix Elortza, Ana Sofia Carvalho, J. Julio Martin-Plaza, Rune Matthiesen (shared corresponds)*, Manuel S. Rodriguez*, **New insights into host-parasite TUBEs interactome dynamics in *P. falciparum* and infected red blood cells**. *Journal of Proteomics*, S1874-3919(16)30059-8.
 3. *) Ana Sofia Carvalho, Deborah Penque and Rune Matthiesen, **Bottom up proteomics data analysis strategies to explore protein modifications and genomic variants**, *Proteomics*, 2015, 15, 1789-92.
 4. *) Itziar Frades, Erik Andreasson, Jose Maria Mato, Erik Alexandersson, Rune Matthiesen and M^a Luz Martínez-Chantar, (shared last authorship) **Integrative genomic signatures of Hepatocellular carcinoma derived from Nonalcoholic fatty liver disease**, *PLOS ONE*, 2015, 10, e0124544
 5. Hongwei Cui, Yongping Mu, Lei Yu, Ya-guang Xi, Rune Matthiesen, Xiulan Su, Wenjie Sun, **Methylation of the miR-126 gene associated with glioma progression**, *Familial Cancer*, 1-8
 6. Amélia Feliciano, Vukosava Milic Torres, Fátima Vaz, Ana Sofia Carvalho, Rune Matthiesen, Paula Pinto, Atul Malhotra, Cristina Bárbara, Deborah Penque, **Overview of proteomics studies in obstructive sleep apnea**, *Sleep Medicine*, 2015, 16, 437-45
 7. *) Ana S. Carvalho, Helena Ribeiro, Paula Voabil, Deborah Penque, Ole N. Jensen, Henrik Molina & **Rune Matthiesen**, **Global MS- and transcriptomics array drug profiling provides novel insight into glucosamine-induced ER stress**, *Molecular and Cellular Proteomics*, 2014, 13, 3294-307
 8. Gomes S, Marques PI, Matthiesen R, Seixas S., **Adaptive evolution and divergence of SERPINB3: a young duplicate in Great Apes**, *PLoS One*. 2014, 9, e104935
 9. Juan Casado-Vela, **Rune Matthiesen**, Susana Sellés, José Ramón Naranjo, **Protein-protein interactions: gene acronym redundancies and current limitations precluding automated data integration**, *Proteomes*, 2013, 1, 3-24
 10. *) **Rune Matthiesen**, Gorka Prieto, Antonio Amorim, Kerman Aloria, Asier Fullaondo and Jesus M. Arizmendi, **SIR: Deterministic protein inference from peptides assigned to MS data**, *Journal of Proteomics*, 2012, 75, 4176--83
 11. *) Elisa Da Silva-Ferrada, Fernando Lopitz-Otsoa, Valérie Lang, Manuel S. Rodriguez, **Rune Matthiesen**, **Strategies to identify recognition signals and targets of SUMOylation**, *Biochemistry Research International*, 2012, 2012:875148
 12. Alexandra Lopes; Kenneth Aston; Filipa Carvalho; João Gonçalves; **Rune Matthiesen**; Ni Huang; Avinash Ramu; Jonathan Downie; Susana Fernandes; Antonio Amorim; Alberto Barros; Matthew Hurlles; Sergey Moskovtsev; Carole Ober; Joshua Schiffman; Peter Schlegel; Mario Sousa; Douglas Carrell; Donald Franklin Conrad, **Human spermatogenic failure purges deleterious mutation load from the autosomes and both sex chromosomes, including the gene DMRT1**, *PLoS Genetics*, 2013, 9, e1003349
 13. *) Gorka Prieto, Kerman Aloria, Nerea Osinalde, Asier Fullaondo, Jesus M Arizmendi and **Rune Matthiesen**, **PAnalyzer: A software tool for protein inference in shotgun proteomics**, *BMC Bioinformatics*, 2012, 13:288
 14. Otsoa FL, Rodriguez ES, Aillet F, Casado JV, Lang V, Matthiesen R, Elortza F, Rodriguez M. **Integrative analysis of the Ubiquitin Proteome Isolated using Tandem Ubiquitin Binding Entities (TUBEs)**, *Journal of Proteomics*, 2011, 75, 2998-3014
 15. Moleirinho A, Carneiro J, Matthiesen R, Silva RM, Amorim A, Azevedo L. **Gains, losses and changes of function after gene duplication: study of the metallothionein family**, *PLoS ONE*, 2011, 6, 6e18487
 16. *) Matthiesen R, Azevedo L, Amorim A, Carvalho AS. **Discussion on common data analysis strategies used in MS-based proteomics**. *Proteomics*, 2011, 11, 604-619
 17. López E, Matthiesen R, López I, Ashman K, Mendieta J, Wesselink JJ, Gómez-Puertas P, Ferreira A. **Functional phosphoproteomics tools for current immunological disorders research**. *JOURNAL OF INTEGRATED –OMICS*, 2011, 1, 1-16
 18. Vellon L, Royo F, Matthiesen R, Torres-Fuenzalida J, Lorenti A, Parada LA. **Functional blockade of alpha5beta1 integrin induces scattering and genomic landscape remodeling of hepatic progenitor cells**. *BMC Cell Biology* 2010, 11:81.
 19. Pereira F, Carneiro J, Matthiesen R, van Asch B, Pinto N, Gusmão L, Amorim A. **Identification of species by multiplex analysis of variable-length sequences**. *Nucleic Acids Res.* 2010, 38, e203
 20. Waraporn T, Mohammed S, Matthiesen R, Yamabhai M, Manassila M, Jensen ON, Boonkerd N, Teamroong N. **Identification of Salt-Tolerant *Sinorhizobium* sp Strain BL3 Membrane Proteins Based on Proteomics**. *Microbes and Environments*, 2010, 25, 275-280
 21. Qental R, Azevedo L, Matthiesen R, Amorim A. **Comparative analyses of the Conserved Oligomeric Golgi (COG) complex in vertebrates**. *BMC Evol Biol.* 2010, 10:212
 22. *) Rodríguez-Suárez E, Gubb E, Alzueta IF, Falcón-Pérez JM, Amorim A, Elortza F, Matthiesen R. **Virtual Expert Mass Spectrometry: iTRAQ tool for database-dependent search, quantitation and result storage**. *Proteomics*. 2010, 10, 1545-56
 23. Carvalho AS, Harduin-Lepers A, Magalhães A, Machado E, Mendes N, Costa LT, Matthiesen R, Almeida R, Costa J, Reis CA. **Differential expression of alpha-2,3-sialyltransferases and alpha-1,3/4-fucosyltransferases regulates the levels of sialyl Lewis x and sialyl Lewis x in gastrointestinal carcinoma cells**. *Int J Biochem Cell Biol.* 2010, 42, 80-9
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24. *) Matthiesen R, Kirpekar F. **Identification of RNA molecules by specific enzyme digestion and mass spectrometry – RNA mass mapping.** Nucleic acid research, 2009, 37, e48
25. *) Hackenberg M, Lasso G, Matthiesen R. **ContDist: a tool for the analysis of quantitative gene and promoter properties.** BMC Bioinformatics. 2009, 7,10-7
26. Molina H, Matthiesen R, Kandasamy K, Pandey A. **Comprehensive Comparison of Collision Induced Dissociation and Electron Transfer Dissociation.** Anal Chem. 2008, 80, 4825-35
27. Conde-Vancells J, Rodriguez-Suarez E, Embade N, Gil D, Matthiesen R, Valle M, Elortza F, Lu SC, Mato JM, Falcon-Perez JM. **Characterization and Comprehensive Proteome Profiling of Exosomes Secreted by Hepatocytes.** J Proteome Res., 2008, 7, 5157-66
28. *) Hackenberg M, Matthiesen R. **Annotation-Modules: A tool for finding significant combinations of multisource annotations in gene lists.** Bioinformatics, 2008, 24, 1386-93
29. Chantar MM, Ariz UVM, Martínez-Lopez N, Varela M, Luka Z, Capdevila A, Rodríguez, J, Matthiesen R, Yang H, Calvisi D, Esteller M, Fraga M, Lu S, Wagner C, Mato J. **Loss of the GNMT gene leads to steatosis and hepatocellular carcinoma in mice.** Hepatology, 2008, 47, 1191-9
30. Hägglund P, Matthiesen R, Elortza F, Højrup P, Roepstorff P, Jensen ON, Bunkenborg J. **An enzymatic deglycosylation scheme enabling identification of core fucosylated N-glycans and O-glycosylation site mapping of human plasma proteins.** J Proteome Res. 2007, 6, 3021-31
31. *) Omaetxebarria MJ, Elortza F, Rodríguez-Suárez E, Aloria K, Arizmendi JM, Jensen ON and Matthiesen R. **Computational approach for identification and characterization of GPI-anchored peptides in proteomics experiments.** Proteomics. 2007, 7, 2815-32
32. *) Matthiesen R. **Methods, algorithms and tools in computational MS-based proteomics: a practical point of view.** Proteomics. 2007, 7, 2815-32
33. Erba EB, Matthiesen R, Bunkenborg J, Schulze WX, Stefano PD, Cabodi S, Tarone G, Defilippi P, Jensen ON. **Quantitation of Multisite EGF Receptor Phosphorylation Using Mass Spectrometry and a Novel Normalization Approach.** J Proteome Res. 2007, 6, 2768-85
34. Mutenda KE, Matthiesen R and Roepstorff P. **Differential fragmentation patterns of pectin oligogalacturonides observed by nano-electrospray quadrupole ion-trap mass spectrometry using automated spectra interpretation.** J Mass Spectrom, 2007, 42, 428-39
35. Laukens K, Matthiesen R, Lemiere F, Esmans E, Onckelen HV, Jensen ON, Witters E. **Integration of gel-based proteome data with pProRep.** Bioinformatics, 2006, 22, 2838-40
36. Alloza I, Baxter A, Chen Q, Matthiesen R, Vandenbroeck K. **Celecoxib inhibits interleukin-12 alpha and beta2 folding and secretion by a novel COX2-independent mechanism involving chaperones of the endoplasmic reticulum.** Mol Pharmacol, 2006, 69, 1579-87
37. Hjerno K, Alm R, Canbäck B, Matthiesen R, Trajkovski K, Björk L, Roepstorff P, Emanuelsson C. **Down-regulation of the strawberry Bet v 1-homologous allergen in concert with the flavonoid biosynthesis pathway in colourless strawberry mutant.** Proteomics, 2006, 6, 1574-87
38. Fierro-Monti I, Mohammed S, Matthiesen R, Santoro R, Burns JS, Williams DJ, Proud CG, Kassem M, Jensen ON and Roepstorff P. **Quantitative proteomics identifies Gemin5, a scaffolding protein involved in ribonucleoprotein assembly as a novel partner for eukaryotic initiation factor 4E.** J. Proteome Res, 2006, 5, 1367-78
39. Beck HC, Jensen EC, Matthiesen R, Jensen LH, Finn P, Grauslund M, Hansen AM, and Jensen ON. **Quantitative proteomic analysis of post-translational modifications of human histones.** Mol. Cell. Proteomics 2006, 5, 1314-1325
40. *) Matthiesen R, Sørensen M, Bunkenborg J, Højrup P, and Jensen ON. **VEMS 3.0: Algorithms and computational tools for tandem mass spectrometry based identification of post-translational modifications in proteins.** J. Proteome Res 2005, 4, 2338–47
41. Gruhler A, Schulze W, Matthiesen R, Mann M, Jensen ON. **Stable isotope labeling of Arabidopsis thaliana suspension cells and analysis of differential protein expression by mass spectrometry.** Mol. Cell. Proteomics 2005, 4, 1697–709
42. *) Matthiesen R, Bauw G, Welinder KG. **Use of performic acid oxidation to expand the mass distribution of tryptic peptides.** Anal. Chem. 2004, 76, 6848-6852
43. *) Matthiesen R, Bunkenborg J, Stensballe A, Jensen ON, Welinder KG, Bauw G. **Database-independent, database-dependent, and extended interpretation of peptide mass spectra in VEMS v2.0.** Proteomics 2004, 9, 2583-93
44. *) Matthiesen R, Lundsgaard M, Welinder KG and Bauw G. **Interpreting peptide mass spectra by VEMS.** Bioinformatics 2003, 19, 792-93
45. Pedersen NR, Wimmer R, Matthiesen R, Pedersen LH, Gessesse A. **Synthesis of sucrose laurate using a new alkaline protease.** Tetrahedron: Asymmetry 2003, 14, 667-73
46. Pedersen NR, Halling PJ, Pedersen LH, Wimmer R, Matthiesen R, Veltman OR. **Efficient transesterification of sucrose catalysed by the metalloprotease thermolysin in dimethylsulfoxide.** FEBS Lett., 2002, 519, 181-184

Book chapters 29

*) 26 main author book chapters

1. *) **Identification and localisation of post translational modifications by High-Resolution Mass Spectrometry,** Rune Matthiesen and Ana Sofia Carvalho, Editor Conrad Bessant, Royal Society of Chemistry, Cambridge, UK, in press
 2. *) **Review and literature mining on proteostasis and cancer,** Rune Matthiesen and Ana Sofia Carvalho, Proteostasis, *Methods Mol Biol.*, 2016, in press
 3. *) **MS-based global proteomics drug profiling,** Ana Sofia Carvalho and Rune Matthiesen, Proteostasis, *Methods Mol Biol.*, 2016, in press
 4. **Identification and localisation of post translational modifications by High-Resolution Mass Spectrometry,** Proteome Informatics, Edited by Conrad Bessant, Royal Society of Chemistry, Thomas Graham House, Science Park, Milton Road, Cambridge CB4 0WF, UK, in press
 5. **TUBEs-Mass spectrometry for identification and analysis of the ubiquitin-proteome,** Mikel Azkargorta, Iraide Escobes, Felix Elortza, Rune Matthiesen and Manuel S. Rodríguez, *Methods Mol Biol.*, 2016, in press
 6. *) **Introduction to mass spectrometry-based proteomics.** (Update from first edition), PhD Rune Matthiesen and Jakob Bunkenborg, *Methods Mol Biol.*, 2013, 1007, 1-45
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7. *) **LC-MS spectra processing**, (Update from first edition), PhD Rune Matthiesen, *Methods Mol Biol.*, 2013, 1007, 47-63
8. *) **Algorithms for database-dependent search of MS/MS data**, PhD Rune Matthiesen, *Methods Mol Biol.*, 2013, 1007, 119-38
9. *) **Interpretation of tandem mass spectra of posttranslationally modified peptides**. (Update from first edition) PhD Jakob Bunkenborg and PhD Rune Matthiesen, *Methods Mol Biol.*, 2013, 1007, 139-71
10. *) **Methods and algorithms for quantitative proteomics by mass spectrometry**, (Update chapter), PhD Ana Sofia Carvalho and PhD Rune Matthiesen, *Methods Mol Biol.*, 2013, 1007, 183-217
11. *) **Tools for Protein Posttranslational Modifications Analysis: FAK, a Case Study** Paula Voabil, Catarina Fonseca, PhD Ana Sofia Carvalho and PhD Rune Matthiesen, *Methods Mol Biol.*, 2013, 1007, 335-58
12. *) **Introduction to omics**, Gubb E, Matthiesen R, *Methods Mol Biol.*, 2010, 593, 1-23.
13. **SNP-PHAGE – High throughput SNP discovery pipeline**, Aransay AM, Matthiesen R, Regueiro MM, *Methods Mol Biol.*, 2010, 593, 49-65.
14. *) **Overview on techniques in cluster analysis**, Frades I, Matthiesen R, *Methods Mol Biol.*, 2010, 593, 81-107
15. *) **Proteomics facing the combinatorial problem**, Matthiesen R, *Methods Mol Biol.*, 2010, 593, 175-86.
16. *) **Methods and algorithms for relative quantitative proteomics by mass spectrometry**, Matthiesen R, Carvalho AS, *Methods Mol Biol.*, 2010, 593, 187-204
17. *) **Computational Methods For Analyze of Two-Dimensional Gels**, Lasso G, Matthiesen R, *Methods Mol Biol.*, 2010, 593, 231-62
18. *) **Algorithms and methods for correlating experimental results with annotation databases**, Hackenberg M, Matthiesen R, *Methods Mol Biol.*, 2010, 593, 315-40
19. *) **Analysis of mass spectrometry data in proteomics**. Matthiesen R, Jensen ON, *Methods Mol Biol.* 2008, 453, 105-22.
20. *) **Introduction to proteomics**. Matthiesen R, Mutenda KE, *Methods Mol Biol.* 2006, 367, 1-36.
21. *) **Extracting monoisotopic single-charge peaks from liquid chromatography-electrospray ionization-mass spectrometry**. Matthiesen R, Jensen ON. *Methods Mol Biol.* 2006, 367, 37-48.
22. *) **Virtual Expert Mass Spectrometrist v3.0: An Integrated Tool for Proteome Analysis** . *Methods Mol Biol.* 2006, 367, 121-38. Matthiesen R
23. *) **Quantitation with virtual expert mass spectrometrist**. Gruhler A, Matthiesen R. *Methods Mol Biol.* 2006, 367, 139-52.
24. *) **Sequence Handling by Sequence Analysis Toolbox v1.0**. Ingrell CR, Matthiesen R, Jensen ON. *Methods Mol Biol.* 2006, 367, 153-68
25. *) **Interpretation of collision-induced fragmentation tandem mass spectra of posttranslationally modified peptides**. Bunkenborg J, Matthiesen R. *Methods Mol Biol.* 2006, 367, 169-94
26. **Organisation of Proteomics Data with YassDB**. Thomsen AL, Laukens K, Matthiesen R, Jensen ON. *Methods Mol Biol.* 2006, 367, 271-88
27. *) **Analysis of carbohydrates by mass spectrometry**. Mutenda K, Matthiesen R. *Methods Mol Biol.* 2006, 367, 289-302
28. *) **Useful mass spectrometry programs freely available on the internet**. Matthiesen R. *Methods Mol Biol.* 2006, 367, 303-6
29. *) **Annotation of class I peroxidase genes in Arabidopsis thaliana VI INTERNATIONAL PLANT PEROXIDASES SYMPOSIUM Proceedings 2002**, Murcia, Spain, 163-166. Matthiesen R, Duroux L, Welinder KG. available on publishers' homepage

Research Grants

Current:

ECT investigator program 2012 (Principal Investigator) – **five year group leader salary**.

2014-2019: National representative for the COST action PROTEOSTASIS

2014-2019: COST action Proteostasis. We have so far been selected for two post doctoral exchange grants (Principal Investigator).

2016-2019: **PTDC/BBB-BEP/2463/2014** ProbeCOPD. Protease activity-based probes for Chronic Obstructive Pulmonary Disease diagnostics ~**200,000.00 Euro**.

2014-2017: Remote ischemic per-conditioning in acute stroke – clinical trial for improving outcome and disclosing novel circulating biomarkers, iNOVA for health, (Research member) - **100,000.00 Euro**.

2016-2021: Invited participant for the recent approved COST action network Transautophagy.

Previous:

2013-2015: PTDC-BEX-GMG-0242-2012 “Evaluating the role of proteolysis in the male reproductive system through the study of KLK (19q13.4) and WFDC (20q13) gene clusters.” (Research member)- ~**200,000.00 Euro**.

2014-2015: **EXPL/DTP-PIC/0616/2013** “Global MS-based profiling of bronchial aspirate: targeting lung cancer specific modifications” (Principal Investigator) - **49,800.00 Euro**.

2010-2013: **PTDC/QUI-BIQ/099457/2008** “Dissection of the molecular role of O-GlcNAc in the multinucleation phenotype of the neoplastic cells in Hodgkin’s lymphoma.” (Principal Investigator) ~**200,000.00 Euro**.

2010-2013: **PTDC/EIA-EIA/099458/2008** “Computational disease prediction system based on molecular markers” (Principal Investigator) ~**50,000.00 Euro**.

2010-2013: **PTDC/SAU-FCF/100930/2008** “Molecular and nanotechnology-based approaches to improve the antitumor activity of small molecules” (Research member) ~**200,000.00 Euro**.

2010-2013: **PTDC/SAU-GMG/101229/2008** “Search for genomic structural variants in azoospermia: a study in Portuguese population” **Contract with Novo Nordisk (2010) - 10,000.00 Euro**.

Ramon Cajal (Principal Investigator) – **five year group leader salary**.

Carlsberg foundation (Principal Investigator) – **two year post doc salary**.

Etorrek Research Programs 2005 / 2006 (CIC bioGUNE) (Principal Investigator).

Profit (Gaiker), (research member).

La Caixa (research member).

EU Temblor (research member).