

CURRICULUM VITAE

Name: Rune Matthiesen
Nationality: Danish citizen
Languages: Danish, English, German, Portuguese
Date of birth: 12-01-1974

Present position: Principal Investigator
NOVA Medical School | Faculdade de Ciências Médicas
Universidade Nova de Lisboa
Campo dos Mártires da Pátria, 130 | 1169-056 Lisboa
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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

CV synopsis

R Matthiesen graduated in molecular biochemistry, with a master thesis in X-ray crystallography, from the University of Aarhus, Denmark in 1999 and completed a PhD degree in computational proteomics in 2003. R Matthiesen published 52 international peer reviewed papers of which 49 are without PhD supervisor and 21 are main author publications (first or last author). Eight of the papers include analysis of large scale molecular data on patient cohorts of typically 100 patients. The papers have been cited more than 2500 times. The publications are mainly in top proteomics, genomics and bioinformatics journals. Additionally, R Matthiesen published five books and 30 book chapters. The books are highly accessed e.g. the book on mass spectrometry data analysis from 2013 has more than 50000 downloads according to Springer Nature web site. R Matthiesen established his first independent group in CIC bioGUNE, Spain in 2006 in the same year that he was awarded a Ramon y Cajal (RYC-2006-001446) grant. He has been awarded five times during his career and evaluated qualified as full Professor by three international panels in the fields clinical proteomics, bioinformatics and protein Science in 2016 and 2017. He has supervised five post docs and seven PhDs. R Matthiesen has been opponent on six international PhD defences and a number of national defences. E.g. of former and current lab members active in science:

Ex. of former lab members:

<https://scholar.google.com/citations?user=qtXYrNUAAAAJ>

<https://www.scopus.com/authid/detail.uri?authorId=6602992150>

<https://scholar.google.com/citations?user=bo3lbUcAAAAJ&hl=en>

Ex. of current lab members:

<https://scholar.google.com/citations?user=TeJWqwwAAAAJ&hl=pt-PT>

His group is currently funded by four grants. He is national representative for the COST action Proteostasis and partner in the EU consortium UBICODE. R Matthiesen currently collaborates with four national hospitals in Portugal in a project on lung cancer diagnosis and with IPO Lisbon on a prognostic project on diffuse large B cell lymphoma.

He has past and on-going collaboration with companies such as Novo Nordisk (UBICODE consortium and project on antibody sequencing), Mission Therapeutics (global drug profiling experiments) and GlaxoSmithKline [* Journal of Proteomics, 2016, S1874-3919(16)30059-8]. R Matthiesen was registered as main organizer of the EU COST action meeting in CEDOC, Lisbon in 2016 and also participated in organizing the conferences Portugalia Genetica. He has evaluated projects for six funding agencies and served as editor six times. R Matthiesen has experience with under graduated and graduated teaching. Lately giving lectures to master students in clinical proteomics and genomics, exosome diagnostics and protein conformational stability in diseases. He also has experience in giving lectures in machine learning and clustering.

Mission statement

The computational molecular medicine group (CMM) 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 and SILAC). More specifically we have more than 10 years' experience in global MS-based drug profiling used in combination with genomics technologies such as next/third 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 chronic diseases to contribute to precision medicine

approaches. We currently have three biomarker projects funded on immune profiling in lung cancer and diffuse large B cell lymphoma. These projects will be running from 2018-2022. 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.

H-index and ORCID

ORCID id: 0000-0002-6353-2616

<https://scholar.google.com/citations?user=tsjn1BcAAAAJ&hl=en>

H-index: 27

I10-index: 41

Oral Presentations

Selected recent oral communications:

- | | |
|-------------------|---|
| 2018 April | Invited presentation from BIOSAM “Diagnostic potential of exosome proteome” at University of Lisbon. |
| 2018 Mar | Invited presentation “From lung cancer exosome diagnostics to DLBCL prognostics” at IPO, Lisbon. |
| 2018 Feb | Bioconductor R package for Proteostasis factors. UBICODE ETN Kick off meeting, Toulouse, France |
| 2017 Dec | Invited to present and discuss collaborations with Scientists from IPO, Lisbon, Portugal |
| 2017 Nov | Invited presentation “Functional regulation in lung cancer from clinical proteomics point of view “, UT Austin Portugal Workshop on Modeling and Simulations of Cardiovascular Diseases and Cancer |
| 2017 Sep | Invited presentation “Clinical proteogenomics from drug profiling to biomarker discovery” at University of Bilbao, Spain |
| 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 |
| 2016 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:

2017-2018: master courses in proteomics, OMICs, exosome diagnostics, conformational protein stability and diseases

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

Under graduated 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/Yfal 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/Fellowships

SPP/ Pfizer Vaccines 2016 – 10.000,- Euro

FCT Investigator 2012 – Five year group leader salary

Ciencia 2008 – Five year group leader salary

Ramon y Cajal (RYC-2006-001446) – Five year group leader salary

Carlsberg foundation 2004 – two year post doc salary

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
2017	Precision medicine, not graded

Organizational responsibilities

2018	Opponent on PhD thesis “The Endoplasmic Reticulum Quality Control: Dissecting Protein Networks in Cystic Fibrosis”, BIO-SYS, University of Lisbon
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2017	Opponent on PhD thesis “Methods to compare the proteome of the parasite Trypanosome brucei isolated from two different tissues of its host”, IMM, Lisbon, Portugal
2017	Opponent on PhD thesis “Mass spectrometry-based proteomic strategies to define protein NEDDylation”, Sofia Celeste Lobato, Bilbao, Spain
2016	Main organiser of 3 rd Proteostasis cost action 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”
2014-2018	Teaching in high throughput clinical mass spectrometry in the BioSys (3 hours course)- 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” , Bergen, Norway
2004-2006	Editor on “Mass Spectrometry Data Analysis in Proteomics”, Humana Press

Grant evaluation

2018	Evaluator H2020 projects
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 -2018	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 clinical proteomics, by international assessment committee appointed by SDU, Denmark
2016	Evaluated qualified as Professor in bioinformatics by international assessment committee appointed by DTU, Denmark
2017	Evaluated qualified as Professor in protein science, by international assessment committee appointed by SDU, Denmark

2018 Evaluated qualified as professor in clinical bioinformatics, by international assessment committee appointed by SDU, Denmark

Supervision (* co-supervisor)

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

2016-2020: Post docs: Ana Sofia Carvalho, INSA, Portugal
2016-2020: PhD students: Márcia Carina da Silva Faria, University of Lisbon, Portugal – external advisor
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
2013-2016: Post docs: Ana Sofia Carvalho, INSA, Portugal
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, *Methods Mol Biol.* 2016;1449, *Nature Springer*
2016 Editor on **PROTEOSTASIS in plants**, 22 chapters, *Methods Mol Biol.* 2016;1449, *Nature Springer*
2017 Editor on **Mass Spectrometry Data Analysis in clinical Proteomics**, *Nature Springer*

Reviewing Duties

Reviewed manuscripts for Science, Nature Methods, Nature Communication, 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 53

H-index 27, i10=41

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

1. Interplay between SUMOylation and NEDDylation regulates RPL11 localization and function. El Motiam A, Vidal S, de la Cruz-Herrera CF, Da Silva-Alvarez S, Baz-Martínez M, Seoane R, Vidal A, Rodríguez MS, Xirodimas DP, Carvalho AS, Beck HC, Matthiesen R, Collado M, Rivas C. *FASEB J.*, 2018 Jul, 30024791

2. *) Ana Sofia Carvalho, C élia Marina Cuco, Carla Lavareda, Francisco Miguel, Mafalda Ventura, Sónia Almeida, Paula Pinto, Tiago Tavares de Abreu, Luís Vaz Rodrigues, Susana Seixas, Cristina Bárbara, Mikel Azkargorta, Felix Elortza, Júlio Semedo, John K Field, Leonor Mota, Rune Matthiesen, **Bronchoalveolar Lavage Proteomics in Patients with Suspected Lung Cancer**, Scientific Reports, 2017, Sci Rep. 2017 Feb 7;7:42190
3. *) Jones-Dias D, Carvalho AS, Moura IB, Manageiro V, Igrejas G, Caniça M, Matthiesen R. **Quantitative proteome analysis of an antibiotic resistant Escherichia coli exposed to tetracycline reveals multiple affected metabolic and peptidoglycan processes**, J Proteomics. 2016, S1874-3919(16)30545-0
4. Feliciano A, Vaz F, Valentim-Coelho C, Torres VM, Silva R, Prosinecki V, Alexandre BM, Almeida A, Almeida-Marques C, Carvalho AS, Matthiesen R, Malhotra A, Pinto P, Bárbara C, Penque D. **Evening and morning alterations in Obstructive Sleep Apnea red blood cell proteome**. Data Brief. 2017 Jan 16;11:103-110
5. Amélia Feliciano, MD; Fátima Vaz ; Vukosava M Torres, PhD; Cristina Valentim-Coelho; Rita Silva; Vesna Prosinecki , PhD; Bruno M Alexandre, PhD; Ana S Carvalho, PhD; Rune Matthiesen, PhD; Atul Malhotra, MD, PhD; Paula Pinto, MD, PhD; Cristina Bárbara, MD, PhD; Deborah Penque, Ph.D. **Evening-morning peroxiredoxin-2 redox/oligomeric state changes in Obstructive Sleep Apnea red blood cells: correlation with polysomnographic and metabolic parameters**, BBA - Molecular Basis of Disease, 2016, S0925-4439(16)30301-5.
6. Marques PI, Fonseca F, Carvalho AS, Puente DA, Damião I, Almeida V, Barros N, Barros A, Carvalho F, Azkargorta M, Elortza F, Osório H, Matthiesen R, Quesada V, Seixas S. **Sequence variation at KLK and WFDC clusters and its association to semen hyperviscosity and other male infertility phenotypes**. Hum Reprod. 2016, 2881-2891.
7. *) 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.
8. *) 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, 2016, S1874-3919(16)30059-8.
9. *) 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.
10. *) 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
11. 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
12. 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
13. *) 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
14. 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
15. 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
16. *) **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
17. *) 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
18. Alexandra Lopes; Kenneth Aston; Filipa Carvalho; João Gonçalves; **Rune Matthiesen**; Ni Huang; Avinash Ramu; Jonathan Downie; Susana Fernandes; Antonio Amorim; Alberto Barros; Matthew

- Hurles; Sergey Moskvovtsev; 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
19. *) 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
 20. Otsa 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
 21. 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
 22. *) Matthiesen R, Azevedo L, Amorim A, Carvalho AS. **Discussion on common data analysis strategies used in MS-based proteomics**. Proteomics, 2011, 11, 604-619
 23. 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
 24. 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.
 25. 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
 26. 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
 27. 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
 29. *) Rodríguez-Suárez E, Gubb E, Alzueta IF, Falcón-Pérez JM, Amorim A, Elortza F, Matthiesen R. **Virtual Expert Mass Spectrometrist: iTRAQ tool for database-dependent search, quantitation and result storage**. Proteomics. 2010, 10, 1545-56
 30. 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 a and sialyl Lewis x in gastrointestinal carcinoma cells**. Int J Biochem Cell Biol. 2010, 42, 80-9
 31. *) Matthiesen R, Kirpekar F. **Identification of RNA molecules by specific enzyme digestion and mass spectrometry – RNA mass mapping**. Nucleic acid research, 2009, 37, e48
 32. *) Hackenberg M, Lasso G, Matthiesen R. **ContDist: a tool for the analysis of quantitative gene and promoter properties**. BMC Bioinformatics. 2009, 7,10-7
 33. Molina H, Matthiesen R, Kandasamy K, Pandey A. **Comprehensive Comparison of Collision Induced Dissociation and Electron Transfer Dissociation**. Anal Chem. 2008, 80, 4825-35
 34. 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
 35. *) Hackenberg M, Matthiesen R. **Annotation-Modules: A tool for finding significant combinations of multisource annotations in gene lists**. Bioinformatics, 2008, 24, 1386-93
 36. 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
 37. 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
 38. *) 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
 39. *) Matthiesen R. **Methods, algorithms and tools in computational MS-based proteomics: a practical point of view**. Proteomics. 2007, 7, 2815-32
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40. 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
41. Mutenda KE, Matthiesen R and Roepstorff P. **Differential fragmentation patterns of pectin oligogalacturonides observed by nanoelectrospray quadrupole ion-trap mass spectrometry using automated spectra interpretation.** *J Mass Spectrom,* 2007, 42, 428-39
42. 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
43. Alloza I, Baxter A, Chen Q, Matthiesen R, Vandebroek 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
44. 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
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Book chapters 30

*) 28 main author book chapters

1. *) Ana Sofia Carvalho and Rune Matthiesen, **Bronchoalveolar Lavage Quantitative Mass Spectrometry based Proteomics Analysis in Lung Diseases**, Serum/Plasma Proteomics: Methods and Protocols, Second Edition, Editors David Greening, PhD, and Richard Simpson, PhD, *Methods Mol Biol.* 2017;1619:487-494
 2. *) Ana Sofia Carvalho, Manuel S Rodriguez and Rune Matthiesen, **Red Blood Cells in Clinical Proteomics**, Serum/Plasma Proteomics: Methods and Protocols, Second Edition, Editors David Greening, PhD, and Richard Simpson, PhD, *Methods Mol Biol.* 2017, 1619:173-181
 3. *) **Identification and localisation of post translational modifications by High-Resolution Mass Spectrometry**, Rune Matthiesen and Ana Sofia Carvalho, *Proteome Informatics*, Editor Conrad Bessant, Royal Society of Chemistry, Cambridge, UK, DOI:10.1039/9781782626732
 4. *) **Review and literature mining on proteostasis and cancer**, Rune Matthiesen, Manuel S Rodriguez and Ana Sofia Carvalho, *Proteostasis*, *Mol Biol.*, 2016;1449:71-84
 5. *) **MS-based global proteomics drug profiling**, Ana Sofia Carvalho and Rune Matthiesen,
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 7. *) **Introduction to mass spectrometry-based proteomics**. (Update from first edition), PhD Rune Matthiesen and Jakob Bunkenborg, *Methods Mol Biol.*, 2013, 1007, 1-45
 8. *) **LC-MS spectra processing**, (Update from first edition), PhD Rune Matthiesen, *Methods Mol Biol.*, 2013, 1007, 47-63
 9. *) **Algorithms for database-dependent search of MS/MS data**, PhD Rune Matthiesen, *Methods Mol Biol.*, 2013, 1007, 119-38
 10. *) **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
 11. *) **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
 12. *) **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
 13. *) **Introduction to omics**, Gubb E, Matthiesen R, *Methods Mol Biol.*, 2010, 593, 1-23.
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 15. *) **Overview on techniques in cluster analysis**, Frades I, Matthiesen R, *Methods Mol Biol.*, 2010, 593, 81-107
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 17. *) **Methods and algorithms for relative quantitative proteomics by mass spectrometry**, Matthiesen R, Carvalho AS, *Methods Mol Biol.*, 2010, 593, 187-204
 18. *) **Computational Methods For Analyze of Two-Dimensional Gels**, Lasso G, Matthiesen R, *Methods Mol Biol.*, 2010, 593, 231-62
 19. *) **Algorithms and methods for correlating experimental results with annotation databases**, Hackenberg M, Matthiesen R, *Methods Mol Biol.*, 2010, 593, 315-40
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 23. *) **Virtual Expert Mass Spectrometrist v3.0: An Integrated Tool for Proteome Analysis** . *Methods Mol Biol.* 2006, 367, 121-38. Matthiesen R
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 27. **Organisation of Proteomics Data with YassDB**. Thomsen AL, Laukens K, Matthiesen R, Jensen ON. *Methods Mol Biol.* 2006, 367, 271-88
 28. *) **Analysis of carbohydrates by mass spectrometry**. Mutenda K, Matthiesen R. *Methods Mol Biol.* 2006, 367, 289-302
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Research Grants

Current:

2018-2021: Portugal 2020, 02/SAICT/2017, 30088, Immune- and microenvironment- proteogenomics profiling for classifying lung cancer patients, budget 239769,36 Euro (Principal Investigator)
2018-2021: Portugal 2020, 02/SAICT/2017, 30087, Impact of B-cell deregulated pathways on tumor immune evasion - relevance for Diffuse Large B-Cell Lymphoma therapy response-LED, budget 239769,36 Euro (Co-Principal Investigator)
2018-2020 Diffuse Large B-cell lymphoma blood based proteome signatures, iNOVA4Health, 48,125 Euro, Principal Investigator
2018-2022 ITN UBICODE, (Research member/associated partner) **3407194,- Euro** (http://cordis.europa.eu/project/rcn/211533_en.html)
2018-2021: Recovering neurofunction and promoting neuroprotection in diabetic retinopathy, (research member), FCT ACC 02/SAICT/2017, 239769,36 Euro
2018-2021 Lysosome dysfunction in age-related diseases, (research member), FCT ACC 02/SAICT/2017, 250000,- Euro
2018-2021 Molecular mechanisms in melanin-containing compartments, 29765, (research member), FCT ACC 02/SAICT/2017, 239769,36 Euro
2018-2021 Remote ischemic post-conditioning in acute phase of ischemic stroke – disclosing novel circulating biomarkers and clinical trial for improving outcome, (research member), FCT ACC 02/SAICT/2017, 239769,36,- Euro
2018-2021 Targeting RAC1-signaling to enhance iodide-related cancer therapy, (research member), FCT ACC 02/SAICT/2017, 239769,36 Euro
2016-2019: **PTDC/BBB-BEP/2463/2014** ProbeCOPD. Protease activity-based probes for Chronic Obstructive Pulmonary Disease diagnostics **~200,000.00 Euro**.
2014-2018: 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**.
FCT investigator programme 2012 (Principal Investigator) – **five year group leader salary**.
2014-2019: National representative for the COST action PROTEOSTASIS, Principal Investigator

Previous:

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**.
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**.
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**.
2014-2019: COST action Proteostasis. We have so far been selected for two post doctoral exchange grants (Principal Investigator).
Etortek Research Programs 2005 / 2006 (CIC bioGUNE) (Principal Investigator).
Profit (Gaiker), (research member).
La Caixa (research member).
EU Temblor (research member).