

# Rune Matthiesen

## List of Publications by Year in descending order

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Version: 2024-02-01

110  
papers

3,692  
citations

172457

29  
h-index

144013

57  
g-index

115  
all docs

115  
docs citations

115  
times ranked

6087  
citing authors

#	ARTICLE	IF	CITATIONS
1	Recent Developments in Clinical Plasma Proteomics Applied to Cardiovascular Research. <i>Biomedicines</i> , 2022, 10, 162.	3.2	17
2	Constitutive Activation of p62/Sequestosome-1-Mediated Proteophagy Regulates Proteolysis and Impairs Cell Death in Bortezomib-Resistant Mantle Cell Lymphoma. <i>Cancers</i> , 2022, 14, 923.	3.7	5
3	Messages from the Small Intestine Carried by Extracellular Vesicles in Prediabetes: A Proteomic Portrait. <i>Journal of Proteome Research</i> , 2022, 21, 910-920.	3.7	4
4	LAMP2A regulates the loading of proteins into exosomes. <i>Science Advances</i> , 2022, 8, eabm1140.	10.3	69
5	Pilot study in human healthy volunteers on the mechanisms underlying remote ischemic conditioning (RIC) Targeting circulating immune cells and immune-related proteins. <i>Journal of Neuroimmunology</i> , 2022, 367, 577847.	2.3	3
6	Classification of Amyloidosis by Model-Assisted Mass Spectrometry-Based Proteomics. <i>International Journal of Molecular Sciences</i> , 2022, 23, 319.	4.1	10
7	Glycation modulates glutamatergic signaling and exacerbates Parkinson's disease-like phenotypes. <i>Npj Parkinson's Disease</i> , 2022, 8, 51.	5.3	15
8	Comparative analysis of the bronchoalveolar microbiome in Portuguese patients with different chronic lung disorders. <i>Scientific Reports</i> , 2021, 11, 15042.	3.3	5
9	Shotgun mass spectrometry-based lipid profiling identifies and distinguishes between chronic inflammatory diseases. <i>EBioMedicine</i> , 2021, 70, 103504.	6.1	16
10	Proteomic Landscape of Extracellular Vesicles for Diffuse Large B-Cell Lymphoma Subtyping. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11004.	4.1	9
11	Extracellular Vesicle Proteome in Prostate Cancer: A Comparative Analysis of Mass Spectrometry Studies. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13605.	4.1	3
12	MS-Based Biomarker Discovery in Bronchoalveolar Lavage Fluid for Lung Cancer. <i>Proteomics - Clinical Applications</i> , 2020, 14, 1900077.	1.6	10
13	WNK1 phosphorylation sites in TBC1D1 and TBC1D4 modulate cell surface expression of GLUT1. <i>Archives of Biochemistry and Biophysics</i> , 2020, 679, 108223.	3.0	12
14	Is the Proteome of Bronchoalveolar Lavage Extracellular Vesicles a Marker of Advanced Lung Cancer?. <i>Cancers</i> , 2020, 12, 3450.	3.7	14
15	Transcriptome Reprogramming of CD11b+ Bone Marrow Cells by Pancreatic Cancer Extracellular Vesicles. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 592518.	3.7	10
16	Deep Sequencing Analysis Reveals Distinctive Non-Coding RNAs When Comparing Tumor Multidrug-Resistant Cells and Extracellular Vesicles with Drug-Sensitive Counterparts. <i>Cancers</i> , 2020, 12, 200.	3.7	13
17	Introduction to Mass Spectrometry-Based Proteomics. <i>Methods in Molecular Biology</i> , 2020, 2051, 1-58.	0.9	9
18	Data Imputation in Merged Isobaric Labeling-Based Relative Quantification Datasets. <i>Methods in Molecular Biology</i> , 2020, 2051, 297-308.	0.9	8

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19	Comparing Peptide Spectra Matches Across Search Engines. <i>Methods in Molecular Biology</i> , 2020, 2051, 133-143.	0.9	3
20	Extra-cellular vesicles carry proteome of cancer hallmarks. <i>Frontiers in Bioscience - Landmark</i> , 2020, 25, 398-436.	3.0	14
21	Interpretation of Tandem Mass Spectra of Posttranslationally Modified Peptides. <i>Methods in Molecular Biology</i> , 2020, 2051, 199-230.	0.9	0
22	Solution to Dark Matter Identified by Mass-Tolerant Database Search. <i>Methods in Molecular Biology</i> , 2020, 2051, 231-240.	0.9	1
23	LC-MS Spectra Processing. <i>Methods in Molecular Biology</i> , 2020, 2051, 59-77.	0.9	1
24	Methods and Algorithms for Quantitative Proteomics by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2020, 2051, 161-197.	0.9	10
25	Interplay between SUMOylation and NEDDylation regulates RPL11 localization and function. <i>FASEB Journal</i> , 2019, 33, 643-651.	0.5	20
26	Profiling of lung microbiota discloses differences in adenocarcinoma and squamous cell carcinoma. <i>Scientific Reports</i> , 2019, 9, 12838.	3.3	64
27	Folding Status Is Determinant over Traffic-Competence in Defining CFTR Interactors in the Endoplasmic Reticulum. <i>Cells</i> , 2019, 8, 353.	4.1	21
28	The Antitumor Activity of a Lead Thioxanthone is Associated with Alterations in Cholesterol Localization. <i>Molecules</i> , 2018, 23, 3301.	3.8	14
29	Proteomic interaction profiling reveals KIFC1 as a factor involved in early targeting of F508del-CFTR to degradation. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 4495-4509.	5.4	22
30	Bronchoalveolar Lavage Proteomics in Patients with Suspected Lung Cancer. <i>Scientific Reports</i> , 2017, 7, 42190.	3.3	46
31	Quantitative proteome analysis of an antibiotic resistant <i>Escherichia coli</i> exposed to tetracycline reveals multiple affected metabolic and peptidoglycan processes. <i>Journal of Proteomics</i> , 2017, 156, 20-28.	2.4	20
32	Red Blood Cells in Clinical Proteomics. <i>Methods in Molecular Biology</i> , 2017, 1619, 173-181.	0.9	5
33	Bronchoalveolar Lavage: Quantitative Mass Spectrometry-Based Proteomics Analysis in Lung Diseases. <i>Methods in Molecular Biology</i> , 2017, 1619, 487-494.	0.9	6
34	Evening and morning peroxiredoxin-2 redox/oligomeric state changes in obstructive sleep apnea red blood cells: Correlation with polysomnographic and metabolic parameters. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2017, 1863, 621-629.	3.8	10
35	Evening and morning alterations in Obstructive Sleep Apnea red blood cell proteome. <i>Data in Brief</i> , 2017, 11, 103-110.	1.0	7
36	New insights into functional regulation in MS-based drug profiling. <i>Scientific Reports</i> , 2016, 6, 18826.	3.3	13

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37	Review and Literature Mining on Proteostasis Factors and Cancer. <i>Methods in Molecular Biology</i> , 2016, 1449, 71-84.	0.9	15
38	Global MS-Based Proteomics Drug Profiling. <i>Methods in Molecular Biology</i> , 2016, 1449, 469-479.	0.9	2
39	TUBEs-Mass Spectrometry for Identification and Analysis of the Ubiquitin-Proteome. <i>Methods in Molecular Biology</i> , 2016, 1449, 177-192.	0.9	11
40	Sequence variation at <i>KLK</i> and <i>WFDC</i> clusters and its association to semen hyperviscosity and other male infertility phenotypes. <i>Human Reproduction</i> , 2016, 31, 2881-2891.	0.9	11
41	New insights into host-parasite ubiquitin proteome dynamics in <i>P. falciparum</i> infected red blood cells using a TUBEs-MS approach. <i>Journal of Proteomics</i> , 2016, 139, 45-59.	2.4	20
42	Methylation of the miR-126 gene associated with glioma progression. <i>Familial Cancer</i> , 2016, 15, 317-324.	1.9	19
43	Bottom up proteomics data analysis strategies to explore protein modifications and genomic variants. <i>Proteomics</i> , 2015, 15, 1789-1792.	2.2	4
44	Overview of proteomics studies in obstructive sleep apnea. <i>Sleep Medicine</i> , 2015, 16, 437-445.	1.6	17
45	Integrative Genomic Signatures Of Hepatocellular Carcinoma Derived from Nonalcoholic Fatty Liver Disease. <i>PLoS ONE</i> , 2015, 10, e0124544.	2.5	70
46	Global Mass Spectrometry and Transcriptomics Array Based Drug Profiling Provides Novel Insight into Glucosamine Induced Endoplasmic Reticulum Stress. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3294-3307.	3.8	42
47	Adaptive Evolution and Divergence of SERPINB3: A Young Duplicate in Great Apes. <i>PLoS ONE</i> , 2014, 9, e104935.	2.5	10
48	Introduction to Mass Spectrometry-Based Proteomics. <i>Methods in Molecular Biology</i> , 2013, 1007, 1-45.	0.9	26
49	LC-MS Spectra Processing. <i>Methods in Molecular Biology</i> , 2013, 1007, 47-63.	0.9	11
50	Algorithms for Database-Dependent Search of MS/MS Data. <i>Methods in Molecular Biology</i> , 2013, 1007, 119-138.	0.9	13
51	Methods and Algorithms for Quantitative Proteomics by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2013, 1007, 183-217.	0.9	15
52	Tools for Protein Posttranslational Modifications Analysis: FAK, a Case Study. <i>Methods in Molecular Biology</i> , 2013, 1007, 335-358.	0.9	1
53	Mass Spectrometry Data Analysis in Proteomics. <i>Methods in Molecular Biology</i> , 2013, , .	0.9	11
54	Human Spermatogenic Failure Purges Deleterious Mutation Load from the Autosomes and Both Sex Chromosomes, including the Gene DMRT1. <i>PLoS Genetics</i> , 2013, 9, e1003349.	3.5	118

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55	Protein-Protein Interactions: Gene Acronym Redundancies and Current Limitations Precluding Automated Data Integration. <i>Proteomes</i> , 2013, 1, 3-24.	3.5	1
56	Interpretation of Tandem Mass Spectra of Posttranslationally Modified Peptides. <i>Methods in Molecular Biology</i> , 2013, 1007, 139-171.	0.9	3
57	Strategies to Identify Recognition Signals and Targets of SUMOylation. <i>Biochemistry Research International</i> , 2012, 2012, 1-16.	3.3	34
58	SIR: Deterministic protein inference from peptides assigned to MS data. <i>Journal of Proteomics</i> , 2012, 75, 4176-4183.	2.4	30
59	PAnalyzer: A software tool for protein inference in shotgun proteomics. <i>BMC Bioinformatics</i> , 2012, 13, 288.	2.6	28
60	Integrative analysis of the ubiquitin proteome isolated using Tandem Ubiquitin Binding Entities (TUBEs). <i>Journal of Proteomics</i> , 2012, 75, 2998-3014.	2.4	90
61	Gains, Losses and Changes of Function after Gene Duplication: Study of the Metallothionein Family. <i>PLoS ONE</i> , 2011, 6, e18487.	2.5	67
62	Functional phosphoproteomics for current immunology research. <i>Journal of Integrated OMICS</i> , 2011, 1, .	0.5	3
63	Discussion on common data analysis strategies used in MS-based proteomics. <i>Proteomics</i> , 2011, 11, 604-619.	2.2	31
64	Identification of Salt-Tolerant <i>Sinorhizobium</i> sp. Strain BL3 Membrane Proteins Based on Proteomics. <i>Microbes and Environments</i> , 2010, 25, 275-280.	1.6	2
65	Comparative analyses of the Conserved Oligomeric Golgi (COG) complex in vertebrates. <i>BMC Evolutionary Biology</i> , 2010, 10, 212.	3.2	8
66	Functional blockade of $\alpha 5 \beta 1$ integrin induces scattering and genomic landscape remodeling of hepatic progenitor cells. <i>BMC Cell Biology</i> , 2010, 11, 81.	3.0	11
67	Virtual Expert Mass Spectrometrists: iTRAQ tool for database-dependent search, quantitation and result storage. <i>Proteomics</i> , 2010, 10, 1545-1556.	2.2	22
68	Identification of species by multiplex analysis of variable-length sequences. <i>Nucleic Acids Research</i> , 2010, 38, e203-e203.	14.5	53
69	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. <i>International Journal of Biochemistry and Cell Biology</i> , 2010, 42, 80-89.	2.8	109
70	Introduction to Omics. <i>Methods in Molecular Biology</i> , 2010, 593, 1-23.	0.9	8
71	Methods and Algorithms for Relative Quantitative Proteomics by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2010, 593, 187-204.	0.9	15
72	Algorithms and Methods for Correlating Experimental Results with Annotation Databases. <i>Methods in Molecular Biology</i> , 2010, 593, 315-340.	0.9	2

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73	Overview on Techniques in Cluster Analysis. <i>Methods in Molecular Biology</i> , 2010, 593, 81-107.	0.9	93
74	Proteomics Facing the Combinatorial Problem. <i>Methods in Molecular Biology</i> , 2010, 593, 175-186.	0.9	2
75	SNP-PHAGE: High-Throughput SNP Discovery Pipeline. <i>Methods in Molecular Biology</i> , 2010, 593, 49-65.	0.9	2
76	Computational Methods for Analysis of Two-Dimensional Gels. <i>Methods in Molecular Biology</i> , 2010, 593, 231-262.	0.9	0
77	Identification of RNA molecules by specific enzyme digestion and mass spectrometry: software for and implementation of RNA mass mapping. <i>Nucleic Acids Research</i> , 2009, 37, e48-e48.	14.5	41
78	ContDist: a tool for the analysis of quantitative gene and promoter properties. <i>BMC Bioinformatics</i> , 2009, 10, 7.	2.6	8
79	Loss of the glycine N-methyltransferase gene leads to steatosis and hepatocellular carcinoma in mice. <i>Hepatology</i> , 2008, 47, 1191-1199.	7.3	262
80	Analysis of Mass Spectrometry Data in Proteomics. <i>Methods in Molecular Biology</i> , 2008, 453, 105-122.	0.9	14
81	Characterization and Comprehensive Proteome Profiling of Exosomes Secreted by Hepatocytes. <i>Journal of Proteome Research</i> , 2008, 7, 5157-5166.	3.7	530
82	Comprehensive Comparison of Collision Induced Dissociation and Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2008, 80, 4825-4835.	6.5	97
83	Annotation-Modules: a tool for finding significant combinations of multisource annotations for gene lists. <i>Bioinformatics</i> , 2008, 24, 1386-1393.	4.1	32
84	Analysis of Carbohydrates by Mass Spectrometry. , 2007, 367, 289-302.		10
85	Introduction to Proteomics. , 2007, 367, 1-36.		7
86	Useful Mass Spectrometry Programs Freely Available on the Internet. , 2007, 367, 303-306.		5
87	Virtual Expert Mass Spectrometrist v3.0: An Integrated Tool for Proteome Analysis. , 2007, 367, 121-138.		8
88	Extracting Monoisotopic Single-Charge Peaks From Liquid Chromatography-Electrospray Ionization-Mass Spectrometry. , 2007, 367, 37-48.		2
89	Sequence Handling by Sequence Analysis Toolbox v1.0. , 2007, 367, 153-168.		1
90	Quantitation With Virtual Expert Mass Spectrometrist. , 2007, 367, 139-152.		2

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91	Organization of Proteomics Data With YassDB. , 2007, 367, 271-288.		1
92	Interpretation of Collision-Induced Fragmentation Tandem Mass Spectra of Posttranslationally Modified Peptides. , 2007, 367, 169-194.		0
93	Quantitation of Multisite EGF Receptor Phosphorylation Using Mass Spectrometry and a Novel Normalization Approach. Journal of Proteome Research, 2007, 6, 2768-2785.	3.7	27
94	An Enzymatic Deglycosylation Scheme Enabling Identification of Core Fucosylated <i>N</i> -Glycans and O-Glycosylation Site Mapping of Human Plasma Proteins. Journal of Proteome Research, 2007, 6, 3021-3031.	3.7	117
95	Differential fragmentation patterns of pectin oligogalacturonides observed by nanoelectrospray quadrupole ion-trap mass spectrometry using automated spectra interpretation. Journal of Mass Spectrometry, 2007, 42, 428-439.	1.6	7
96	Computational approach for identification and characterization of GPI-anchored peptides in proteomics experiments. Proteomics, 2007, 7, 1951-1960.	2.2	6
97	Methods, algorithms and tools in computational proteomics: A practical point of view. Proteomics, 2007, 7, 2815-2832.	2.2	91
98	Quantitative Proteomics Identifies Gemin5, A Scaffolding Protein Involved in Ribonucleoprotein Assembly, as a Novel Partner for Eukaryotic Initiation Factor 4E. Journal of Proteome Research, 2006, 5, 1367-1378.	3.7	44
99	Down-regulation of the strawberry Bet v 1-homologous allergen in concert with the flavonoid biosynthesis pathway in colorless strawberry mutant. Proteomics, 2006, 6, 1574-1587.	2.2	107
100	Celecoxib Inhibits Interleukin-12 p70 and p40 Folding and Secretion by a Novel COX2-Independent Mechanism Involving Chaperones of the Endoplasmic Reticulum. Molecular Pharmacology, 2006, 69, 1579-1587.	2.3	40
101	Integration of gel-based proteome data with pProRep. Bioinformatics, 2006, 22, 2838-2840.	4.1	5
102	Quantitative Proteomic Analysis of Post-translational Modifications of Human Histones. Molecular and Cellular Proteomics, 2006, 5, 1314-1325.	3.8	168
103	Stable Isotope Labeling of Arabidopsis thaliana Cells and Quantitative Proteomics by Mass Spectrometry. Molecular and Cellular Proteomics, 2005, 4, 1697-1709.	3.8	189
104	VEMS 3.0: Algorithms and Computational Tools for Tandem Mass Spectrometry Based Identification of Post-translational Modifications in Proteins. Journal of Proteome Research, 2005, 4, 2338-2347.	3.7	126
105	Database-independent, database-dependent, and extended interpretation of peptide mass spectra in VEMS V2.0. Proteomics, 2004, 4, 2583-2593.	2.2	60
106	Use of Performic Acid Oxidation To Expand the Mass Distribution of Tryptic Peptides. Analytical Chemistry, 2004, 76, 6848-6852.	6.5	24
107	Synthesis of sucrose laurate using a new alkaline protease. Tetrahedron: Asymmetry, 2003, 14, 667-673.	1.8	53
108	Interpreting peptide mass spectra by VEMS. Bioinformatics, 2003, 19, 792-793.	4.1	25

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109	Efficient transesterification of sucrose catalysed by the metalloprotease thermolysin in dimethylsulfoxide. FEBS Letters, 2002, 519, 181-184.	2.8	38
110	Multiple Myeloma-Derived Extracellular Vesicles Modulate the Bone Marrow Immune Microenvironment. Frontiers in Immunology, 0, 13, .	4.8	6