

# Katrin Marcus

## List of Publications by Year in descending order

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Version: 2024-02-01

66  
papers

1,492  
citations

361045

20  
h-index

360668

35  
g-index

71  
all docs

71  
docs citations

71  
times ranked

2599  
citing authors

#	ARTICLE	IF	CITATIONS
1	N471D WASH complex subunit strumpellin knockâ€”in mice display mild motor and cardiac abnormalities and BPTF and KLHL11 dysregulation in brain tissue. <i>Neuropathology and Applied Neurobiology</i> , 2022, 48, .	1.8	4
2	The impact of the COVID-19 pandemic on non-COVID induced sepsis survival. <i>BMC Anesthesiology</i> , 2022, 22, 12.	0.7	11
3	Proteomic Analysis of Retinal Tissue in an S100B Autoimmune Glaucoma Model. <i>Biology</i> , 2022, 11, 16.	1.3	3
4	Transcriptome and Proteome Analysis in LUHMES Cells Overexpressing Alpha-Synuclein. <i>Frontiers in Neurology</i> , 2022, 13, 787059.	1.1	9
5	A Current Encyclopedia of Bioinformatics Tools, Data Formats and Resources for Mass Spectrometry Lipidomics. <i>Metabolites</i> , 2022, 12, 584.	1.3	10
6	Chronic Hyperglycaemia Inhibits Tricarboxylic Acid Cycle in Rat Cardiomyoblasts Overexpressing Glucose Transporter Type 4. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7255.	1.8	2
7	Quantitative Mass Spectrometry-Based Proteomics: An Overview. <i>Methods in Molecular Biology</i> , 2021, 2228, 85-116.	0.4	84
8	Proteome Analysis with Classical 2D-PAGE. <i>Methods in Molecular Biology</i> , 2021, 2228, 53-62.	0.4	1
9	Establishing a Custom-Fit Data-Independent Acquisition Method for Label-Free Proteomics. <i>Methods in Molecular Biology</i> , 2021, 2228, 307-325.	0.4	5
10	BIONDA: a free database for a fast information on published biomarkers. <i>Bioinformatics Advances</i> , 2021, 1, .	0.9	5
11	Protein Quantification Using the â€”Rapid Western Blotâ€”Approach. <i>Methods in Molecular Biology</i> , 2021, 2228, 29-39.	0.4	4
12	MaCPepDB: A Database to Quickly Access All Tryptic Peptides of the UniProtKB. <i>Journal of Proteome Research</i> , 2021, 20, 2145-2150.	1.8	6
13	MicroRNAs from extracellular vesicles as a signature for Parkinson's disease. <i>Clinical and Translational Medicine</i> , 2021, 11, e357.	1.7	14
14	Lysine 53 Acetylation of Cytochrome c in Prostate Cancer: Warburg Metabolism and Evasion of Apoptosis. <i>Cells</i> , 2021, 10, 802.	1.8	17
15	FLNC-Associated Myofibrillar Myopathy. <i>Neurology: Genetics</i> , 2021, 7, e590.	0.9	15
16	Advanced Fiber Type-Specific Protein Profiles Derived from Adult Murine Skeletal Muscle. <i>Proteomes</i> , 2021, 9, 28.	1.7	16
17	The Î²2-Subunit of Voltage-Gated Calcium Channels Regulates Cardiomyocyte Hypertrophy. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 704657.	1.1	3
18	Rat retinae data for use as spectral library, for pathway remodeling as well as protein mapping. <i>Data in Brief</i> , 2021, 37, 107212.	0.5	1

#	ARTICLE	IF	CITATIONS
19	CSF Diagnostics: A Potentially Valuable Tool in Neurodegenerative and Inflammatory Disorders Involving Motor Neurons: A Review. <i>Diagnostics</i> , 2021, 11, 1522.	1.3	6
20	Good Old-Fashioned Protein Concentration Determination by Amino Acid Analysis. <i>Methods in Molecular Biology</i> , 2021, 2228, 21-28.	0.4	7
21	Differential Proteome Analysis Using 2D-DIGE. <i>Methods in Molecular Biology</i> , 2021, 2228, 77-84.	0.4	1
22	Nanoenvironments of the $\beta_2$ -Subunit of L-Type Voltage-Gated Calcium Channels in Adult Cardiomyocytes. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 724778.	1.8	0
23	Laser Microdissection-Based Protocol for the LC-MS/MS Analysis of the Proteomic Profile of Neuromelanin Granules. <i>Journal of Visualized Experiments</i> , 2021, , .	0.2	3
24	Reproducibility, Specificity and Accuracy of Relative Quantification Using Spectral Library-based Data-independent Acquisition. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 181-197.	2.5	106
25	Human cerebrospinal fluid data for use as spectral library, for biomarker research. <i>Data in Brief</i> , 2020, 32, 106048.	0.5	0
26	Proteomic Characterization of Synaptosomes from Human Substantia Nigra Indicates Altered Mitochondrial Translation in Parkinson's Disease. <i>Cells</i> , 2020, 9, 2580.	1.8	16
27	What Room for Two-Dimensional Gel-Based Proteomics in a Shotgun Proteomics World?. <i>Proteomes</i> , 2020, 8, 17.	1.7	42
28	The first versatile human iPSC-based model of ectopic virus induction allows new insights in RNA-virus disease. <i>Scientific Reports</i> , 2020, 10, 16804.	1.6	9
29	How Do the Different Proteomic Strategies Cope with the Complexity of Biological Regulations in a Multi-Omic World? Critical Appraisal and Suggestions for Improvements. <i>Proteomes</i> , 2020, 8, 23.	1.7	8
30	Homozygous expression of the myofibrillar myopathy-associated p.W2710X filamin C variant reveals major pathomechanisms of sarcomeric lesion formation. <i>Acta Neuropathologica Communications</i> , 2020, 8, 154.	2.4	16
31	A patient-based model of RNA mis-splicing uncovers treatment targets in Parkinson's disease. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	24
32	miR-129-5p and miR-130a-3p Regulate VEGFR-2 Expression in Sensory and Motor Neurons during Development. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3839.	1.8	16
33	Glucocorticoid receptor complexes form cooperatively with the Hsp90 co-chaperones Pp5 and FKBP. <i>Scientific Reports</i> , 2020, 10, 10733.	1.6	19
34	Blood Contamination in CSF and Its Impact on Quantitative Analysis of Alpha-Synuclein. <i>Cells</i> , 2020, 9, 370.	1.8	30
35	CalibraCurve: A Tool for Calibration of Targeted MS-Based Measurements. <i>Proteomics</i> , 2020, 20, e1900143.	1.3	5
36	CRN2 binds to TIMP4 and MMP14 and promotes perivascular invasion of glioblastoma cells. <i>European Journal of Cell Biology</i> , 2019, 98, 151046.	1.6	9

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37	CSF Sample Preparation for Data-Independent Acquisition. <i>Methods in Molecular Biology</i> , 2019, 2044, 61-67.	0.4	2
38	Let me infuse this for you – A way to solve the first YPIC challenge. <i>EuPA Open Proteomics</i> , 2019, 22-23, 19-21.	2.5	0
39	Effects of 12 Weeks of Hypertrophy Resistance Exercise Training Combined with Collagen Peptide Supplementation on the Skeletal Muscle Proteome in Recreationally Active Men. <i>Nutrients</i> , 2019, 11, 1072.	1.7	49
40	Noninvasive diagnosis of urothelial cancer in urine using DNA hypermethylation signatures – Gender matters. <i>International Journal of Cancer</i> , 2019, 145, 2861-2872.	2.3	9
41	Spiked human substantia nigra proteome data set for use as a spectral library for protein modelling and protein mapping. <i>Data in Brief</i> , 2019, 23, 103711.	0.5	4
42	Protein Inference Using PIA Workflows and PSI Standard File Formats. <i>Journal of Proteome Research</i> , 2019, 18, 741-747.	1.8	33
43	Co-extraction for Metabolomics and Proteomics from a Single CSF Sample. <i>Methods in Molecular Biology</i> , 2019, 2044, 337-342.	0.4	2
44	The microRNA miR-375-3p and the Tumor Suppressor NDRG2 are Involved in Sporadic Amyotrophic Lateral Sclerosis. <i>Cellular Physiology and Biochemistry</i> , 2019, 52, 1412-1426.	1.1	24
45	Sample Fractionation Techniques for CSF Peptide Spectral Library Generation. <i>Methods in Molecular Biology</i> , 2019, 2044, 69-77.	0.4	1
46	Label-free identification of myopathological features with coherent anti-Stokes Raman scattering. <i>Muscle and Nerve</i> , 2018, 58, 456-459.	1.0	6
47	Autophagy inhibition promotes SNCA/alpha-synuclein release and transfer via extracellular vesicles with a hybrid autophagosome-exosome-like phenotype. <i>Autophagy</i> , 2018, 14, 98-119.	4.3	193
48	Protein variability in cerebrospinal fluid and its possible implications for neurological protein biomarker research. <i>PLoS ONE</i> , 2018, 13, e0206478.	1.1	31
49	Characterization of Cerebrospinal Fluid via Data-Independent Acquisition Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 3418-3430.	1.8	27
50	Intricate Crosstalk Between Lipopolysaccharide, Phospholipid and Fatty Acid Metabolism in <i>Escherichia coli</i> Modulates Proteolysis of LpxC. <i>Frontiers in Microbiology</i> , 2018, 9, 3285.	1.5	35
51	BioInfra.Prot: A comprehensive proteomics workflow including data standardization, protein inference, expression analysis and data publication. <i>Journal of Biotechnology</i> , 2017, 261, 116-125.	1.9	21
52	Morphological Plasticity of Emerging Purkinje Cells in Response to Exogenous VEGF. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 2.	1.4	13
53	Mutant desmin substantially perturbs mitochondrial morphology, function and maintenance in skeletal muscle tissue. <i>Acta Neuropathologica</i> , 2016, 132, 453-473.	3.9	57
54	Statically Adsorbed Coatings for High Separation Efficiency and Resolution in CE-MS Peptide Analysis: Strategies and Implementation. <i>Methods in Molecular Biology</i> , 2016, 1483, 53-75.	0.4	2

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55	Membrane tethering of APP c-terminal fragments is a prerequisite for T668 phosphorylation preventing nuclear sphere generation. <i>Cellular Signalling</i> , 2016, 28, 1725-1734.	1.7	11
56	Proteomic characterization of neuromelanin granules isolated from human substantia nigra by laser-microdissection. <i>Scientific Reports</i> , 2016, 6, 37139.	1.6	35
57	Nuclear spheres modulate the expression of BEST1 and GADD45G. <i>Cellular Signalling</i> , 2016, 28, 100-109.	1.7	5
58	Primary Central Nervous System (CNS) Lymphoma B Cell Receptors Recognize CNS Proteins. <i>Journal of Immunology</i> , 2015, 195, 1312-1319.	0.4	37
59	PIA: An Intuitive Protein Inference Engine with a Web-Based User Interface. <i>Journal of Proteome Research</i> , 2015, 14, 2988-2997.	1.8	69
60	Proteomics in neurodegenerative diseases: Methods for obtaining a closer look at the neuronal proteome. <i>Proteomics - Clinical Applications</i> , 2015, 9, 848-871.	0.8	11
61	Effects of Zinc on Particulate Methane Monooxygenase Activity and Structure. <i>Journal of Biological Chemistry</i> , 2014, 289, 21782-21794.	1.6	66
62	Identification of a Novel Human LAP1 Isoform That Is Regulated by Protein Phosphorylation. <i>PLoS ONE</i> , 2014, 9, e113732.	1.1	39
63	A Combined Laser Microdissection and Mass Spectrometry Approach Reveals New Disease Relevant Proteins Accumulating in Aggregates of Filaminopathy Patients. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 215-227.	2.5	74
64	Differential Proteome Analysis Using 2D-DIGE. <i>Methods in Molecular Biology</i> , 2012, 893, 75-82.	0.4	14
65	Two-Dimensional Polyacrylamide Gel Electrophoresis for Platelet Proteomics. , 2004, 273, 421-434.		11
66	Differential analysis of phosphorylated proteins in resting and thrombin-stimulated human platelets. <i>Analytical and Bioanalytical Chemistry</i> , 2003, 376, 973-993.	1.9	84