

Bernd Roschitzki

List of Publications by Year in descending order

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56
papers

4,610
citations

172457

29
h-index

155660

55
g-index

58
all docs

58
docs citations

58
times ranked

8299
citing authors

#	ARTICLE	IF	CITATIONS
1	Community proteogenomics reveals insights into the physiology of phyllosphere bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16428-16433.	7.1	774
2	Who is who in litter decomposition? Metaproteomics reveals major microbial players and their biogeochemical functions. ISME Journal, 2012, 6, 1749-1762.	9.8	537
3	Altered Activation of Endothelial Anti- and Proapoptotic Pathways by High-Density Lipoprotein from Patients with Coronary Artery Disease. Circulation, 2013, 127, 891-904.	1.6	303
4	Phosphoproteomic Analysis Reveals Interconnected System-Wide Responses to Perturbations of Kinases and Phosphatases in Yeast. Science Signaling, 2010, 3, rs4.	3.6	277
5	PARP1 ADP-ribosylates lysine residues of the core histone tails. Nucleic Acids Research, 2010, 38, 6350-6362.	14.5	226
6	Identification of Proteins Associated with the <i>Pseudomonas aeruginosa</i> Biofilm Extracellular Matrix. Journal of Proteome Research, 2012, 11, 4906-4915.	3.7	198
7	Soil metaproteomics – Comparative evaluation of protein extraction protocols. Soil Biology and Biochemistry, 2012, 54, 14-24.	8.8	178
8	Deterministic protein inference for shotgun proteomics data provides new insights into Arabidopsis pollen development and function. Genome Research, 2009, 19, 1786-1800.	5.5	151
9	Identification and Functional Characterization of N-Terminally Acetylated Proteins in <i>Drosophila melanogaster</i> . PLoS Biology, 2009, 7, e1000236.	5.6	149
10	Implementation and evaluation of relative and absolute quantification in shotgun proteomics with label-free methods. Journal of Proteomics, 2010, 73, 1740-1746.	2.4	139
11	Isoform-specific localization of DNMT3A regulates DNA methylation fidelity at bivalent CpG islands. EMBO Journal, 2017, 36, 3421-3434.	7.8	99
12	High-throughput proteomics reveal alarmins as amplifiers of tissue pathology and inflammation after spinal cord injury. Scientific Reports, 2016, 6, 21607.	3.3	96
13	A Novel Th Cell Epitope of <i>Candida albicans</i> Mediates Protection from Fungal Infection. Journal of Immunology, 2012, 188, 5636-5643.	0.8	95
14	Phosphoproteome analysis of isoflurane-protected heart mitochondria: phosphorylation of adenine nucleotide translocator-1 on Tyr194 regulates mitochondrial function. Cardiovascular Research, 2008, 80, 20-29.	3.8	94
15	Directed shotgun proteomics guided by saturated RNA-seq identifies a complete expressed prokaryotic proteome. Genome Research, 2013, 23, 1916-1927.	5.5	91
16	Plastid Proteome Assembly without Toc159: Photosynthetic Protein Import and Accumulation of N-Acetylated Plastid Precursor Proteins. Plant Cell, 2011, 23, 3911-3928.	6.6	77
17	Mass Spectrometry: A Tool for Enhanced Detection of Hemoglobin Variants. Clinical Chemistry, 2008, 54, 69-76.	3.2	73
18	Characterization of the phosphoproteome of mature Arabidopsis pollen. Plant Journal, 2012, 72, 89-101.	5.7	73

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19	iTRAQ-Based and Label-Free Proteomics Approaches for Studies of Human Adenovirus Infections. <i>International Journal of Proteomics</i> , 2013, 2013, 1-16.	2.0	73
20	Diurnal changes in concerted plant protein phosphorylation and acetylation in Arabidopsis organs and seedlings. <i>Plant Journal</i> , 2019, 99, 176-194.	5.7	59
21	Redox Labile Site in a Zn ₄ Cluster of Cu ₄ Zn ₄ ~Metallothionein-3. <i>Biochemistry</i> , 2003, 42, 9822-9828.	2.5	58
22	Epitope mapping on bovine prion protein using chemical cross-linking and mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2008, 43, 185-195.	1.6	55
23	Tyrosine phosphorylation by Src within the cavity of the adenine nucleotide translocase 1 regulates ADP/ATP exchange in mitochondria. <i>American Journal of Physiology - Cell Physiology</i> , 2010, 298, C740-C748.	4.6	55
24	Zn ₇ Metallothionein-3 and the Synaptic Vesicle Cycle:~Interaction of Metallothionein-3 with the Small GTPase Rab3A. <i>Biochemistry</i> , 2005, 44, 3159-3165.	2.5	54
25	A distinct Cu ₄ -thiolate cluster of human metallothionein-3 is located in the N-terminal domain. <i>Journal of Biological Inorganic Chemistry</i> , 2002, 7, 611-616.	2.6	52
26	Discovery of serum proteomic biomarkers for prediction of response to infliximab (a monoclonal) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4 2012, 77, 372-382.	2.4	45
27	Engineered peptide barcodes for in-depth analyses of binding protein libraries. <i>Nature Methods</i> , 2019, 16, 421-428.	19.0	37
28	Extracellular Hemoglobin Polarizes the Macrophage Proteome toward Hb-Clearance, Enhanced Antioxidant Capacity and Suppressed HLA Class 2 Expression. <i>Journal of Proteome Research</i> , 2011, 10, 2397-2408.	3.7	36
29	Analysis of Ewing Sarcoma (EWS)-Binding Proteins: Interaction with hnRNP M, U, and RNA-Helicases p68/72 within Protein~RNA Complexes. <i>Journal of Proteome Research</i> , 2009, 8, 4455-4465.	3.7	34
30	Mycobacterium smegmatis PafBC is involved in regulation of DNA damage response. <i>Scientific Reports</i> , 2017, 7, 13987.	3.3	34
31	Secretome Analysis Defines the Major Role of SecDF in Staphylococcus aureus Virulence. <i>PLoS ONE</i> , 2013, 8, e63513.	2.5	31
32	An Integrated Systems Approach Unveils New Aspects of Microoxia-Mediated Regulation in Bradyrhizobium diazoefficiens. <i>Frontiers in Microbiology</i> , 2019, 10, 924.	3.5	31
33	Brain Citrullination Patterns and T Cell Reactivity of Cerebrospinal Fluid-Derived CD4+ T Cells in Multiple Sclerosis. <i>Frontiers in Immunology</i> , 2019, 10, 540.	4.8	31
34	Natural Genetic Variation Influences Protein Abundances in C. elegans Developmental Signalling Pathways. <i>PLoS ONE</i> , 2016, 11, e0149418.	2.5	28
35	Inconsistencies in the red blood cell membrane proteome analysis: generation of a database for research and diagnostic applications. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav056-bav056.	3.0	25
36	BAF complexes drive proliferation and block myogenic differentiation in fusion-positive rhabdomyosarcoma. <i>Nature Communications</i> , 2021, 12, 6924.	12.8	25

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37	Natural Genetic Variation Differentially Affects the Proteome and Transcriptome in <i>Caenorhabditis elegans</i> . <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1670-1680.	3.8	23
38	Independent Candidate Serum Protein Biomarkers of Response to Adalimumab and to Infliximab in Rheumatoid Arthritis: An Exploratory Study. <i>PLoS ONE</i> , 2016, 11, e0153140.	2.5	19
39	Identification and characterization of chloroplast casein kinase II from <i>Oryza sativa</i> (rice). <i>Journal of Experimental Botany</i> , 2015, 66, 175-187.	4.8	18
40	A proteomics approach to study synergistic and antagonistic interactions of the fungal-bacterial consortium <i>Fusarium oxysporum</i> wild-type MSA 35. <i>Proteomics</i> , 2010, 10, 3292-3320.	2.2	17
41	Identification of Distinct Amino Acids as ADP-Ribose Acceptor Sites by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2011, 780, 57-66.	0.9	17
42	Proteomic profiling of <i>Cronobacter turicensis</i> 3032, a foodborne opportunistic pathogen. <i>Proteomics</i> , 2009, 9, 3564-3579.	2.2	15
43	The Mass Distance Fingerprint: A statistical framework for de novo detection of predominant modifications using high-accuracy mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2007, 854, 173-182.	2.3	13
44	Antibody Phage Display Assisted Identification of Junction Plakoglobin as a Potential Biomarker for Atherosclerosis. <i>PLoS ONE</i> , 2012, 7, e47985.	2.5	13
45	Reduced thrombogenicity of surface-treated Nitinol implants steered by altered protein adsorption. <i>Acta Biomaterialia</i> , 2022, 137, 331-345.	8.3	13
46	Insights into the Gene Expression Profile of Uncultivable Hemotrophic <i>Mycoplasma suis</i> during Acute Infection, Obtained Using Proteome Analysis. <i>Journal of Bacteriology</i> , 2012, 194, 1505-1514.	2.2	12
47	Phosphorylated serine and threonine residues promote site-specific fragmentation of singly charged, arginine-containing peptide ions. <i>Rapid Communications in Mass Spectrometry</i> , 2009, 23, 1435-1445.	1.5	10
48	Infusion of anti-Nogo-A antibodies in adult rats increases growth and synapse related proteins in the absence of behavioral alterations. <i>Experimental Neurology</i> , 2013, 250, 52-68.	4.1	10
49	Recognition of Host Proteins by <i>Helicobacter</i> Cysteine-Rich Protein C. <i>Current Microbiology</i> , 2011, 63, 239-249.	2.2	9
50	Polystyrene beads as an alternative support material for epitope identification of a prion-antibody interaction using proteolytic excision-mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2009, 395, 1395-1401.	3.7	7
51	Proteomic Analysis of the Rat Canalicular Membrane Reveals Expression of a Complex System of P4-ATPases in Liver. <i>PLoS ONE</i> , 2016, 11, e0158033.	2.5	7
52	Differential regulation of germ line apoptosis and germ cell differentiation by CPEB family members in <i>C. elegans</i> . <i>PLoS ONE</i> , 2017, 12, e0182270.	2.5	5
53	In search of cerebrospinal fluid biomarkers of fatigue in multiple sclerosis: A proteomics study. <i>Journal of Sleep Research</i> , 2019, 28, e12721.	3.2	4
54	Characterization of recombinant human and bovine thyroid-stimulating hormone preparations by mass spectrometry and determination of their endotoxin content. <i>BMC Veterinary Research</i> , 2013, 9, 141.	1.9	2

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55	Grape ASR-Silencing Sways Nuclear Proteome, Histone Marks and Interplay of Intrinsically Disordered Proteins. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1537.	4.1	2
56	Identification of Fungal T Cell Epitopes by Mass Spectrometry-Based Proteomics. <i>Methods in Molecular Biology</i> , 2017, 1625, 65-74.	0.9	0