

Jakob Bunkenborg

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

7,089
citations

159585

30
h-index

161849

54
g-index

58
all docs

58
docs citations

58
times ranked

10615
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of a novel 70ÅDa modification in rhGM-CSF expressed in <i>E. coli</i> using chemical assays in combination with mass spectrometry. <i>Amino Acids</i> , 2021, , 1.	2.7	3
2	Magnitude of Ubiquitination Determines the Fate of Epidermal Growth Factor Receptor Upon Ligand Stimulation. <i>Journal of Molecular Biology</i> , 2021, 433, 167240.	4.2	3
3	Genomic adaptations of the green alga <i>Dunaliella salina</i> to life under high salinity. <i>Algal Research</i> , 2020, 50, 101990.	4.6	18
4	Introduction to Mass Spectrometry-Based Proteomics. <i>Methods in Molecular Biology</i> , 2020, 2051, 1-58.	0.9	9
5	Interpretation of Tandem Mass Spectra of Posttranslationally Modified Peptides. <i>Methods in Molecular Biology</i> , 2020, 2051, 199-230.	0.9	0
6	Enhanced trypsin on a budget: Stabilization, purification and high-temperature application of inexpensive commercial trypsin for proteomics applications. <i>PLoS ONE</i> , 2019, 14, e0218374.	2.5	28
7	Evaluation of spectral libraries and sample preparation for DIA-LC-MS analysis of host cell proteins: A case study of a bacterially expressed recombinant biopharmaceutical protein. <i>Protein Expression and Purification</i> , 2018, 147, 69-77.	1.3	15
8	DNA damage-induced dynamic changes in abundance and cytosol-nuclear translocation of proteins involved in translational processes, metabolism, and autophagy. <i>Cell Cycle</i> , 2018, 17, 2146-2163.	2.6	9
9	Discrimination of Isoleucine and Leucine by Dimethylation-Assisted MS3. <i>Analytical Chemistry</i> , 2018, 90, 9055-9059.	6.5	11
10	Covalent perturbation as a tool for validation of identifications and PTM mapping applied to bovine alpha-crystallin. <i>Proteomics</i> , 2016, 16, 545-553.	2.2	3
11	Regulated assembly of a supramolecular centrosome scaffold in vitro. <i>Science</i> , 2015, 348, 808-812.	12.6	170
12	A redox-dependent dimerization switch regulates activity and tolerance for reactive oxygen species of barley seed glutathione peroxidase. <i>Plant Physiology and Biochemistry</i> , 2015, 90, 58-63.	5.8	3
13	Inducing autophagy. <i>Autophagy</i> , 2014, 10, 339-355.	9.1	65
14	S100A11 is required for efficient plasma membrane repair and survival of invasive cancer cells. <i>Nature Communications</i> , 2014, 5, 3795.	12.8	175
15	Glycopeptide Enrichment Using a Combination of ZIC-HILIC and Cotton Wool for Exploring the Glycoproteome of Wheat Flour Albumins. <i>Journal of Proteome Research</i> , 2014, 13, 2696-2703.	3.7	36
16	The <i>Caenorhabditis elegans</i> pericentriolar material components SPD-2 and SPD-5 are monomeric in the cytoplasm before incorporation into the PCM matrix. <i>Molecular Biology of the Cell</i> , 2014, 25, 2984-2992.	2.1	31
17	Identification of Thioredoxin Target Disulfides Using Isotope-Coded Affinity Tags. <i>Methods in Molecular Biology</i> , 2014, 1072, 677-685.	0.9	3
18	The human cap-binding complex is functionally connected to the nuclear RNA exosome. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1367-1376.	8.2	199

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19	The barley grain thioredoxin system – an update. <i>Frontiers in Plant Science</i> , 2013, 4, 151.	3.6	7
20	Introduction to Mass Spectrometry-Based Proteomics. <i>Methods in Molecular Biology</i> , 2013, 1007, 1-45.	0.9	26
21	Cutting Edge Proteomics: Benchmarking of Six Commercial Trypsins. <i>Journal of Proteome Research</i> , 2013, 12, 3631-3641.	3.7	35
22	Interpretation of Tandem Mass Spectra of Posttranslationally Modified Peptides. <i>Methods in Molecular Biology</i> , 2013, 1007, 139-171.	0.9	3
23	Friend or food. <i>Autophagy</i> , 2012, 8, 995-996.	9.1	4
24	Identification of Autophagosome-associated Proteins and Regulators by Quantitative Proteomic Analysis and Genetic Screens. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014035.	3.8	118
25	Data extraction from proteomics raw data: An evaluation of nine tandem MS tools using a large Orbitrap data set. <i>Journal of Proteomics</i> , 2012, 75, 5293-5303.	2.4	22
26	ErbB2-associated changes in the lysosomal proteome. <i>Proteomics</i> , 2011, 11, 2830-2838.	2.2	23
27	Identification of thioredoxin target disulfides in proteins released from barley aleurone layers. <i>Journal of Proteomics</i> , 2010, 73, 1133-1136.	2.4	23
28	The minotaur proteome: Avoiding cross-species identifications deriving from bovine serum in cell culture models. <i>Proteomics</i> , 2010, 10, 3040-3044.	2.2	42
29	Site-specific Phosphorylation Dynamics of the Nuclear Proteome during the DNA Damage Response. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1314-1323.	3.8	225
30	MSQuant, an Open Source Platform for Mass Spectrometry-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 393-403.	3.7	237
31	Up-regulated Proteins in the Fluid Bathing the Tumour Cell Microenvironment as Potential Serological Markers for Early Detection of Cancer of the Breast. <i>Molecular Oncology</i> , 2010, 4, 65-89.	4.6	88
32	SIRT3 Deacetylates Mitochondrial 3-Hydroxy-3-Methylglutaryl CoA Synthase 2 and Regulates Ketone Body Production. <i>Cell Metabolism</i> , 2010, 12, 654-661.	16.2	418
33	Identification of Thioredoxin Disulfide Targets Using a Quantitative Proteomics Approach Based on Isotope-Coded Affinity Tags. <i>Journal of Proteome Research</i> , 2008, 7, 5270-5276.	3.7	109
34	Interpretation of Collision-Induced Fragmentation Tandem Mass Spectra of Posttranslationally Modified Peptides. , 2007, 367, 169-194.		0
35	Quantitation of Multisite EGF Receptor Phosphorylation Using Mass Spectrometry and a Novel Normalization Approach. <i>Journal of Proteome Research</i> , 2007, 6, 2768-2785.	3.7	27
36	Mammalian Sir2 Homolog SIRT3 Regulates Global Mitochondrial Lysine Acetylation. <i>Molecular and Cellular Biology</i> , 2007, 27, 8807-8814.	2.3	1,097

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37	An Enzymatic Deglycosylation Scheme Enabling Identification of Core Fucosylated <i>N</i> -Glycans and O-Glycosylation Site Mapping of Human Plasma Proteins. <i>Journal of Proteome Research</i> , 2007, 6, 3021-3031.	3.7	117
38	Modification-Specific Proteomic Analysis of Glycoproteins in Human Body Fluids by Mass Spectrometry. , 2007, , 107-128.		3
39	Quantitative proteomic assessment of very early cellular signaling events. <i>Nature Biotechnology</i> , 2007, 25, 566-568.	17.5	110
40	A mass spectrometry-friendly database for cSNP identification. <i>Nature Methods</i> , 2007, 4, 465-466.	19.0	72
41	Modification-Specific Proteomics of Plasma Membrane Proteins: Identification and Characterization of Glycosylphosphatidylinositol-Anchored Proteins Released upon Phospholipase D Treatment. <i>Journal of Proteome Research</i> , 2006, 5, 935-943.	3.7	111
42	On-Bead Chemical Synthesis and Display of Phosphopeptides for Affinity Pull-Down Proteomics. <i>ChemBioChem</i> , 2006, 7, 623-630.	2.6	15
43	Reversible lysine acetylation controls the activity of the mitochondrial enzyme acetyl-CoA synthetase 2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10224-10229.	7.1	642
44	Serum protein profiling by miniaturized solid-phase extraction and matrix-assisted laser desorption/ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2005, 19, 1578-1586.	1.5	50
45	A Proteomic Analysis of Human Hemodialysis Fluid. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 637-650.	3.8	60
46	VEMS 3.0: Algorithms and Computational Tools for Tandem Mass Spectrometry Based Identification of Post-translational Modifications in Proteins. <i>Journal of Proteome Research</i> , 2005, 4, 2338-2347.	3.7	126
47	A Proteomic Analysis of Human Bile. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 715-728.	3.8	142
48	Screening for N-glycosylated proteins by liquid chromatography mass spectrometry. <i>Proteomics</i> , 2004, 4, 454-465.	2.2	185
49	Database-independent, database-dependent, and extended interpretation of peptide mass spectra in VEMS V2.0. <i>Proteomics</i> , 2004, 4, 2583-2593.	2.2	60
50	Comprehensive Proteomic Analysis of Human Pancreatic Juice. <i>Journal of Proteome Research</i> , 2004, 3, 1042-1055.	3.7	194
51	A New Strategy for Identification of N-Glycosylated Proteins and Unambiguous Assignment of Their Glycosylation Sites Using HILIC Enrichment and Partial Deglycosylation. <i>Journal of Proteome Research</i> , 2004, 3, 556-566.	3.7	452
52	Integrated Analysis of Protein Composition, Tissue Diversity, and Gene Regulation in Mouse Mitochondria. <i>Cell</i> , 2003, 115, 629-640.	28.9	815
53	Identification of a gene causing human cytochrome <i>c</i> oxidase deficiency by integrative genomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 605-610.	7.1	526
54	NMR Characterization of the DNA Binding Properties of a Novel Hoechst 33258 Analogue Peptide Building Block. <i>Bioconjugate Chemistry</i> , 2002, 13, 927-936.	3.6	10

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55	Comparison of Aqueous Molecular Dynamics with NMR Relaxation and Residual Dipolar Couplings Favors Internal Motion in a Mannose Oligosaccharide. <i>Journal of the American Chemical Society</i> , 2001, 123, 4792-4802.	13.7	54
56	Concerted Intercalation and Minor Groove Recognition of DNA by a Homodimeric Thiazole Orange Dye. <i>Bioconjugate Chemistry</i> , 2000, 11, 861-867.	3.6	33
57	On the Sequence Selective Bis-Intercalation of a Homodimeric Thiazole Orange Dye in DNA. <i>Bioconjugate Chemistry</i> , 1999, 10, 824-831.	3.6	27