

Jakob Bunkenborg

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

57
papers

6,216
citations

29
h-index

58
g-index

58
ext. papers

6,700
ext. citations

8.4
avg, IF

5.02
L-index

#	Paper	IF	Citations
57	Characterization of a novel + 70Da modification in rhGM-CSF expressed in E. coli using chemical assays in combination with mass spectrometry. <i>Amino Acids</i> , 2021 , 1	3.5	0
56	Magnitude of Ubiquitination Determines the Fate of Epidermal Growth Factor Receptor Upon Ligand Stimulation. <i>Journal of Molecular Biology</i> , 2021 , 433, 167240	6.5	1
55	Interpretation of Tandem Mass Spectra of Posttranslationally Modified Peptides. <i>Methods in Molecular Biology</i> , 2020 , 2051, 199-230	1.4	
54	Introduction to Mass Spectrometry-Based Proteomics. <i>Methods in Molecular Biology</i> , 2020 , 2051, 1-58	1.4	5
53	Genomic adaptations of the green alga <i>Dunaliella salina</i> to life under high salinity. <i>Algal Research</i> , 2020 , 50, 101990	5	5
52	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	3.7	21
51	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	2	10
50	Discrimination of Isoleucine and Leucine by Dimethylation-Assisted MS3. <i>Analytical Chemistry</i> , 2018 , 90, 9055-9059	7.8	6
49	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	4.7	4
48	Covalent perturbation as a tool for validation of identifications and PTM mapping applied to bovine alpha-crystallin. <i>Proteomics</i> , 2016 , 16, 545-53	4.8	2
47	Centrosomes. Regulated assembly of a supramolecular centrosome scaffold in vitro. <i>Science</i> , 2015 , 348, 808-12	33.3	125
46	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	5.4	3
45	S100A11 is required for efficient plasma membrane repair and survival of invasive cancer cells. <i>Nature Communications</i> , 2014 , 5, 3795	17.4	124
44	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, 2696-703	5.6	29
43	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, 2984-92	3.5	26
42	Inducing autophagy: a comparative phosphoproteomic study of the cellular response to ammonia and rapamycin. <i>Autophagy</i> , 2014 , 10, 339-55	10.2	57
41	Identification of thioredoxin target disulfides using isotope-coded affinity tags. <i>Methods in Molecular Biology</i> , 2014 , 1072, 677-85	1.4	2

40	The human cap-binding complex is functionally connected to the nuclear RNA exosome. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 1367-76	17.6	157
39	The barley grain thioredoxin system - an update. <i>Frontiers in Plant Science</i> , 2013 , 4, 151	6.2	7
38	Introduction to mass spectrometry-based proteomics. <i>Methods in Molecular Biology</i> , 2013 , 1007, 1-45	1.4	19
37	Cutting edge proteomics: benchmarking of six commercial trypsins. <i>Journal of Proteome Research</i> , 2013 , 12, 3631-41	5.6	30
36	Interpretation of tandem mass spectra of posttranslationally modified peptides. <i>Methods in Molecular Biology</i> , 2013 , 1007, 139-71	1.4	2
35	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, 5293-303	3.9	16
34	Friend or food: different cues to the autophagosomal proteome. <i>Autophagy</i> , 2012 , 8, 995-6	10.2	3
33	Identification of autophagosome-associated proteins and regulators by quantitative proteomic analysis and genetic screens. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.014035	7.6	99
32	ErbB2-associated changes in the lysosomal proteome. <i>Proteomics</i> , 2011 , 11, 2830-8	4.8	21
31	Site-specific phosphorylation dynamics of the nuclear proteome during the DNA damage response. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1314-23	7.6	195
30	MSQuant, an open source platform for mass spectrometry-based quantitative proteomics. <i>Journal of Proteome Research</i> , 2010 , 9, 393-403	5.6	225
29	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	7.9	82
28	SIRT3 deacetylates mitochondrial 3-hydroxy-3-methylglutaryl CoA synthase 2 and regulates ketone body production. <i>Cell Metabolism</i> , 2010 , 12, 654-61	24.6	357
27	Identification of thioredoxin target disulfides in proteins released from barley aleurone layers. <i>Journal of Proteomics</i> , 2010 , 73, 1133-6	3.9	20
26	The minotaur proteome: avoiding cross-species identifications deriving from bovine serum in cell culture models. <i>Proteomics</i> , 2010 , 10, 3040-4	4.8	36
25	Identification of thioredoxin disulfide targets using a quantitative proteomics approach based on isotope-coded affinity tags. <i>Journal of Proteome Research</i> , 2008 , 7, 5270-6	5.6	97
24	An enzymatic deglycosylation scheme enabling identification of core fucosylated N-glycans and O-glycosylation site mapping of human plasma proteins. <i>Journal of Proteome Research</i> , 2007 , 6, 3021-31	5.6	106
23	Modification-Specific Proteomic Analysis of Glycoproteins in Human Body Fluids by Mass Spectrometry 2007 , 107-128		3

22	Quantitative proteomic assessment of very early cellular signaling events. <i>Nature Biotechnology</i> , 2007 , 25, 566-8	44.5	103
21	A mass spectrometry-friendly database for cSNP identification. <i>Nature Methods</i> , 2007 , 4, 465-6	21.6	57
20	Interpretation of collision-induced fragmentation tandem mass spectra of posttranslationally modified peptides. <i>Methods in Molecular Biology</i> , 2007 , 367, 169-94	1.4	
19	Quantitation of multisite EGF receptor phosphorylation using mass spectrometry and a novel normalization approach. <i>Journal of Proteome Research</i> , 2007 , 6, 2768-85	5.6	26
18	Mammalian Sir2 homolog SIRT3 regulates global mitochondrial lysine acetylation. <i>Molecular and Cellular Biology</i> , 2007 , 27, 8807-14	4.8	940
17	On-bead chemical synthesis and display of phosphopeptides for affinity pull-down proteomics. <i>ChemBioChem</i> , 2006 , 7, 623-30	3.8	13
16	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	11.5	564
15	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, 935-43	5.6	106
14	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, 2338-47	5.6	119
13	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, 1578-86 ^{2.2}	2.2	48
12	A proteomic analysis of human hemodialysis fluid. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 637-50	7.6	55
11	A proteomic analysis of human bile. <i>Molecular and Cellular Proteomics</i> , 2004 , 3, 715-28	7.6	130
10	Screening for N-glycosylated proteins by liquid chromatography mass spectrometry. <i>Proteomics</i> , 2004 , 4, 454-65	4.8	175
9	Database-independent, database-dependent, and extended interpretation of peptide mass spectra in VEMS V2.0. <i>Proteomics</i> , 2004 , 4, 2583-93	4.8	56
8	Comprehensive proteomic analysis of human pancreatic juice. <i>Journal of Proteome Research</i> , 2004 , 3, 1042-55	5.6	173
7	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, 556-66	5.6	425
6	Identification of a gene causing human cytochrome c oxidase deficiency by integrative genomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 605-10	11.5	472
5	Integrated analysis of protein composition, tissue diversity, and gene regulation in mouse mitochondria. <i>Cell</i> , 2003 , 115, 629-40	56.2	742

4	NMR characterization of the DNA binding properties of a novel Hoechst 33258 analogue peptide building block. <i>Bioconjugate Chemistry</i> , 2002 , 13, 927-36	6.3	10
3	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, 4792-802	16.4	52
2	Concerted intercalation and minor groove recognition of DNA by a homodimeric thiazole orange dye. <i>Bioconjugate Chemistry</i> , 2000 , 11, 861-7	6.3	29
1	On the sequence selective bis-intercalation of a homodimeric thiazole orange dye in DNA. <i>Bioconjugate Chemistry</i> , 1999 , 10, 824-31	6.3	26