

Josip Blonder

List of Publications by Year in descending order

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51
papers

2,779
citations

218677

26
h-index

197818

49
g-index

52
all docs

52
docs citations

52
times ranked

4106
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeted Mass Spectrometry Enables Quantification of Novel Pharmacodynamic Biomarkers of ATM Kinase Inhibition. <i>Cancers</i> , 2021, 13, 3843.	3.7	7
2	Comparative microsomal proteomics of a model lung cancer cell line NCI-H23 reveals distinct differences between molecular profiles of 3D and 2D cultured cells. <i>Oncotarget</i> , 2021, 12, 2022-2038.	1.8	3
3	Tissue sample preparation for proteomic analysis. , 2020, , 39-52.		1
4	Cell surface protein enrichment for biomarker and drug target discovery using mass spectrometry-based proteomics. , 2020, , 409-420.		4
5	Identification of Sec23ip, Part of 14-3-3 β Protein Network, as a Regulator of Acute Steroidogenesis in MA-10 Leydig Cells. <i>Endocrinology</i> , 2020, 161, .	2.8	6
6	Nanoparticle physicochemical properties determine the activation of intracellular complement. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2019, 17, 266-275.	3.3	22
7	Protocol for the Analysis of Laser Capture Microdissected Fresh-Frozen Tissue Homogenates by Silver-Stained 1D SDS-PAGE. <i>Methods in Molecular Biology</i> , 2018, 1723, 95-110.	0.9	2
8	Direct molecular dissection of tumor parenchyma from tumor stroma in tumor xenograft using mass spectrometry-based glycoproteomics. <i>Oncotarget</i> , 2018, 9, 26431-26452.	1.8	7
9	Preparation and Immunoaffinity Depletion of Fresh Frozen Tissue Homogenates for Mass Spectrometry-Based Proteomics in the Context of Drug Target/Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2017, 1647, 71-90.	0.9	4
10	Comparative proteomics of a model MCF10A-KRasG12V cell line reveals a distinct molecular signature of the KRasG12V cell surface. <i>Oncotarget</i> , 2016, 7, 86948-86971.	1.8	23
11	Mass spectrometry in cancer biomarker research: a case for immunodepletion of abundant blood-derived proteins from clinical tissue specimens. <i>Biomarkers in Medicine</i> , 2014, 8, 269-286.	1.4	34
12	Protein Modifications Regulate the Role of 14-3-3 β Adaptor Protein in cAMP-induced Steroidogenesis in MA-10 Leydig Cells. <i>Journal of Biological Chemistry</i> , 2014, 289, 26542-26553.	3.4	20
13	Steroidogenesis in MA-10 Mouse Leydig Cells Is Altered via Fatty Acid Import into the Mitochondria1. <i>Biology of Reproduction</i> , 2014, 91, 96.	2.7	11
14	Tissue Sample Preparation for Proteomic Analysis. , 2013, , 39-50.		3
15	Proteomic Analysis of Frozen Tissue Samples Using Laser Capture Microdissection. <i>Methods in Molecular Biology</i> , 2013, 1002, 71-83.	0.9	21
16	Trypsin-Mediated 18O/16O Labeling for Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2013, 1002, 133-149.	0.9	2
17	SASH1 Is a Scaffold Molecule in Endothelial TLR4 Signaling. <i>Journal of Immunology</i> , 2013, 191, 892-901.	0.8	51
18	Profiling the erythrocyte membrane proteome isolated from patients diagnosed with chronic obstructive pulmonary disease. <i>Journal of Proteomics</i> , 2012, 76, 259-269.	2.4	13

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19	Post-digestion ¹⁸ O Exchange/Labeling for Quantitative Shotgun Proteomics of Membrane Proteins. <i>Methods in Molecular Biology</i> , 2012, 893, 223-240.	0.9	2
20	Identification of a Dynamic Mitochondrial Protein Complex Driving Cholesterol Import, Trafficking, and Metabolism to Steroid Hormones. <i>Molecular Endocrinology</i> , 2012, 26, 1868-1882.	3.7	211
21	CD44 Promotes Intoxication by the Clostridial Iota-Family Toxins. <i>PLoS ONE</i> , 2012, 7, e51356.	2.5	47
22	Proteomic Profiling of H-Ras-G12V Induced Hypertrophic Cardiomyopathy in Transgenic Mice Using Comparative LC-MS Analysis of Thin Fresh-Frozen Tissue Sections. <i>Journal of Proteome Research</i> , 2012, 11, 1561-1570.	3.7	13
23	Molecular profiling of the human nasal epithelium: A proteomics approach. <i>Journal of Proteomics</i> , 2011, 75, 56-69.	2.4	19
24	Profiling Solid Tumor Heterogeneity by LCM and Biological MS of Fresh-Frozen Tissue Sections. <i>Methods in Molecular Biology</i> , 2011, 755, 95-106.	0.9	15
25	Optimized Method for Computing ¹⁸ O/ ¹⁶ O Ratios of Differentially Stable-Isotope Labeled Peptides in the Context of Postdigestion ¹⁸ O Exchange/Labeling. <i>Analytical Chemistry</i> , 2010, 82, 5878-5886.	6.5	22
26	Combined Blood/Tissue Analysis for Cancer Biomarker Discovery: Application to Renal Cell Carcinoma. <i>Analytical Chemistry</i> , 2010, 82, 1584-1588.	6.5	41
27	Optimization of protein solubilization for the analysis of the CD14 human monocyte membrane proteome using LC-MS/MS. <i>Journal of Proteomics</i> , 2009, 73, 112-122.	2.4	24
28	Separation, detection and quantitation of peptides by liquid chromatography and capillary electrochromatography. <i>Journal of Chromatography A</i> , 2009, 1216, 1825-1837.	3.7	56
29	Targeting and Insertion of the Cholesterol-Binding Translocator Protein into the Outer Mitochondrial Membrane. <i>Biochemistry</i> , 2009, 48, 6909-6920.	2.5	57
30	Approaching Solid Tumor Heterogeneity on a Cellular Basis by Tissue Proteomics Using Laser Capture Microdissection and Biological Mass Spectrometry. <i>Journal of Proteome Research</i> , 2009, 8, 2310-2318.	3.7	75
31	¹⁸ O Stable Isotope Labeling in MS-based Proteomics. <i>Briefings in Functional Genomics & Proteomics</i> , 2009, 8, 136-144.	3.8	105
32	Biomarker discovery: tissues versus fluids versus both. <i>Expert Review of Molecular Diagnostics</i> , 2007, 7, 473-475.	3.1	19
33	Proteomic profiling of differentiating osteoblasts. <i>Expert Review of Proteomics</i> , 2006, 3, 483-496.	3.0	21
34	Proteomic Analysis of Plasma Membrane from Hypoxia-Adapted Malignant Melanoma. <i>Journal of Proteome Research</i> , 2006, 5, 2996-3007.	3.7	62
35	Combined Chemical and Enzymatic Stable Isotope Labeling for Quantitative Profiling of Detergent-Insoluble Membrane Proteins Isolated Using Triton X-100 and Brij-96. <i>Journal of Proteome Research</i> , 2006, 5, 349-360.	3.7	52
36	Identification of membrane proteins from mammalian cell/tissue using methanol-facilitated solubilization and tryptic digestion coupled with 2D-LC-MS/MS. <i>Nature Protocols</i> , 2006, 1, 2784-2790.	12.0	100

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37	Quantitative analysis of the low molecular weight serum proteome using ¹⁸ O stable isotope labeling in a lung tumor xenograft mouse model. <i>Journal of the American Society for Mass Spectrometry</i> , 2005, 16, 1221-1230.	2.8	59
38	Quantitative Profiling of the Detergent-Resistant Membrane Proteome of Iota-b Toxin Induced Vero Cells. <i>Journal of Proteome Research</i> , 2005, 4, 523-531.	3.7	75
39	Proteomic Analysis of Lipid Microdomains from Lipopolysaccharide-Activated Human Endothelial Cells. <i>Journal of Proteome Research</i> , 2005, 4, 349-357.	3.7	45
40	Global Analysis of the Cortical Neuron Proteome. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 896-907.	3.8	58
41	A Proteomic Characterization of the Plasma Membrane of Human Epidermis by High-Throughput Mass Spectrometry. <i>Journal of Investigative Dermatology</i> , 2004, 123, 691-699.	0.7	76
42	A detergent- and cyanogen bromide-free method for integral membrane proteomics: Application to <i>Halobacterium</i> purple membranes and the human epidermal membrane proteome. <i>Proteomics</i> , 2004, 4, 31-45.	2.2	140
43	Proteomic analysis of detergent-resistant membrane rafts. <i>Electrophoresis</i> , 2004, 25, 1307-1318.	2.4	78
44	Proteomic investigation of natural killer cell microsomes using gas-phase fractionation by mass spectrometry. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004, 1698, 87-95.	2.3	21
45	Analysis of Murine Natural Killer Cell Microsomal Proteins Using Two-Dimensional Liquid Chromatography Coupled to Tandem Electrospray Ionization Mass Spectrometry. <i>Journal of Proteome Research</i> , 2004, 3, 862-870.	3.7	19
46	Characterization and quantitation of membrane proteomes using multidimensional MS-based proteomic technologies. <i>Expert Review of Proteomics</i> , 2004, 1, 153-163.	3.0	35
47	Global Analysis of the Membrane Subproteome of <i>Pseudomonas aeruginosa</i> Using Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2004, 3, 434-444.	3.7	55
48	Affinity Labeling of Highly Hydrophobic Integral Membrane Proteins for Proteome-Wide Analysis. <i>Journal of Proteome Research</i> , 2003, 2, 153-161.	3.7	81
49	On-Column Sample Enrichment for Capillary Electrophoresis Sheathless Electrospray Ionization Mass Spectrometry: A Evaluation for Peptide Analysis and Protein Identification. <i>Analytical Chemistry</i> , 2003, 75, 5984-5993.	6.5	61
50	High-Efficiency On-Line Solid-Phase Extraction Coupling to 150- μ m-i.d. Column Liquid Chromatography for Proteomic Analysis. <i>Analytical Chemistry</i> , 2003, 75, 3596-3605.	6.5	104
51	Enrichment of Integral Membrane Proteins for Proteomic Analysis Using Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2002, 1, 351-360.	3.7	226