

# Martin R Larsen

## List of Publications by Year in descending order

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Version: 2024-02-01

169  
papers

10,754  
citations

36303

51  
h-index

34986

98  
g-index

175  
all docs

175  
docs citations

175  
times ranked

13567  
citing authors

#	ARTICLE	IF	CITATIONS
1	The impact of Zika virus exposure on the placental proteomic profile. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2022, 1868, 166270.	3.8	2
2	Quantitative proteomic study reveals differential expression of matricellular proteins between fibrous dysplasia and cemento-ossifying fibroma pathogenesis. <i>Journal of Oral Pathology and Medicine</i> , 2022, 51, 405-412.	2.7	2
3	Characterization of Differentially Abundant Proteins Among <i>Leishmania (Viannia) braziliensis</i> Strains Isolated From Atypical or Typical Lesions. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 824968.	3.9	0
4	Exportin 1 modulates life span by regulating nucleolar dynamics via the autophagy protein LGG-1/GABARAP. <i>Science Advances</i> , 2022, 8, eabj1604.	10.3	5
5	Comprehensive proteomics and sialomics of the anti-proliferative activity of safranal on triple negative MDA-MB-231 breast cancer cell lines. <i>Journal of Proteomics</i> , 2022, 259, 104539.	2.4	6
6	The intrinsic and microenvironmental features of diffuse midline glioma: Implications for the development of effective immunotherapeutic treatment strategies. <i>Neuro-Oncology</i> , 2022, 24, 1408-1422.	1.2	27
7	DIPG-07. Preclinical and case study results underpinning the phase II clinical trial testing the combination of ONC201 and paxalisib for the treatment of patients with diffuse midline glioma (NCT05009992). <i>Neuro-Oncology</i> , 2022, 24, i18-i19.	1.2	0
8	Ultraviolet Photodissociation of Protonated Peptides and Proteins Can Proceed with H/D Scrambling. <i>Analytical Chemistry</i> , 2021, 93, 691-696.	6.5	8
9	Identification of SRSF10 as a regulator of SMN2-ISMN1. <i>Human Mutation</i> , 2021, 42, 246-260.	2.5	15
10	Quantitative phosphoproteomics uncovers synergy between DNA-PK and FLT3 inhibitors in acute myeloid leukaemia. <i>Leukemia</i> , 2021, 35, 1782-1787.	7.2	22
11	The phosphoproteome of rice leaves responds to water and nitrogen supply. <i>Molecular Omics</i> , 2021, 17, 706-718.	2.8	5
12	N-Glycosylation in isolated rat nerve terminals. <i>Molecular Omics</i> , 2021, 17, 517-532.	2.8	5
13	CSF proteome in multiple sclerosis subtypes related to brain lesion transcriptomes. <i>Scientific Reports</i> , 2021, 11, 4132.	3.3	10
14	A Proteomic Atlas of Lineage and Cancer-Polarized Expression Modules in Myeloid Cells Modeling Immunosuppressive Tumor-Infiltrating Subsets. <i>Journal of Personalized Medicine</i> , 2021, 11, 542.	2.5	6
15	Divalent Metal Transporter 1 Knock-Down Modulates IL-1 $\beta$ Mediated Pancreatic Beta-Cell Pro-Apoptotic Signaling Pathways through the Autophagic Machinery. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8013.	4.1	4
16	Linking inherent O-Linked Protein Glycosylation of YghJ to Increased Antigen Potential. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 705468.	3.9	3
17	Pharmacological inhibition of mitochondrial soluble adenylyl cyclase in astrocytes causes activation of cAMP-activated protein kinase and induces breakdown of glycogen. <i>Glia</i> , 2021, 69, 2828-2844.	4.9	11
18	Systems-wide analysis of glycoprotein conformational changes by limited deglycosylation assay. <i>Journal of Proteomics</i> , 2021, 248, 104355.	2.4	2

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19	HSPB1 influences mitochondrial respiration in ER-stressed beta cells. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140680.	2.3	7
20	Long Term Response to Circulating Angiogenic Cells, Unstimulated or Atherosclerotic Pre-Conditioned, in Critical Limb Ischemic Mice. <i>Biomedicines</i> , 2021, 9, 1147.	3.2	3
21	The heart arrhythmia-linked D130G calmodulin mutation causes premature inhibitory autophosphorylation of CaMKII. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2021, 1868, 119119.	4.1	3
22	Comprehensive Protocol to Simultaneously Study Protein Phosphorylation, Acetylation, and N-Linked Sialylated Glycosylation. <i>Methods in Molecular Biology</i> , 2021, 2261, 55-72.	0.9	5
23	HDL proteome remodeling associates with COVID-19 severity. <i>Journal of Clinical Lipidology</i> , 2021, 15, 796-804.	1.5	22
24	A protein-centric view of in vitro biological model systems for schizophrenia. <i>Stem Cells</i> , 2021, 39, 1569-1578.	3.2	0
25	Effect of APOB polymorphism rs562338 (G/A) on serum proteome of coronary artery disease patients: a proteogenomic approach. <i>Scientific Reports</i> , 2021, 11, 22766.	3.3	3
26	MYC regulates metabolism through vesicular transfer of glycolytic kinases. <i>Open Biology</i> , 2021, 11, 210276.	3.6	5
27	Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. <i>Nature Communications</i> , 2020, 11, 5248.	12.8	49
28	Serum Proteomics Reveals Alterations in Protease Activity, Axon Guidance, and Visual Phototransduction Pathways in Infants With In Utero Exposure to Zika Virus Without Congenital Zika Syndrome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 577819.	3.9	10
29	Cellular Imprinting Proteomics Assay: A Novel Method for Detection of Neural and Ocular Disorders Applied to Congenital Zika Virus Syndrome. <i>Journal of Proteome Research</i> , 2020, 19, 4496-4515.	3.7	20
30	Glutamate-glutamine homeostasis is perturbed in neurons and astrocytes derived from patient iPSC models of frontotemporal dementia. <i>Molecular Brain</i> , 2020, 13, 125.	2.6	36
31	Resolution of NASH and hepatic fibrosis by the GLP-1R and GCGR dual-agonist cotadutide via modulating mitochondrial function and lipogenesis. <i>Nature Metabolism</i> , 2020, 2, 413-431.	11.9	131
32	Depolarization-dependent Induction of Site-specific Changes in Sialylation on N-linked Glycoproteins in Rat Nerve Terminals. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1418-1435.	3.8	18
33	Proteomic changes during experimental de- and remyelination in the corpus callosum. <i>PLoS ONE</i> , 2020, 15, e0230249.	2.5	9
34	Characterization of Signaling Pathways Associated with Pancreatic $\beta$ -cell Adaptive Flexibility in Compensation of Obesity-linked Diabetes in db/db Mice. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 971-993.	3.8	22
35	Proteomics insights into the responses of <i>Saccharomyces cerevisiae</i> during mixed-culture alcoholic fermentation with <i>Lachancea thermotolerans</i> . <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	17
36	Proteomic Analysis of Restored Insulin Production and Trafficking in Obese Diabetic Mouse Pancreatic Islets Following Euglycemia. <i>Journal of Proteome Research</i> , 2019, 18, 3245-3258.	3.7	19

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37	PARK2 Mutation Causes Metabolic Disturbances and Impaired Survival of Human iPSC-Derived Neurons. <i>Frontiers in Cellular Neuroscience</i> , 2019, 13, 297.	3.7	47
38	A Systems-level Characterization of the Differentiation of Human Embryonic Stem Cells into Mesenchymal Stem Cells*[S]. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1950-1966.	3.8	13
39	Ageing and amyloidosis underlie the molecular and pathological alterations of tau in a mouse model of familial Alzheimer's disease. <i>Scientific Reports</i> , 2019, 9, 15758.	3.3	27
40	Proteomic signatures of neuroinflammation in Alzheimer's disease, multiple sclerosis and ischemic stroke. <i>Expert Review of Proteomics</i> , 2019, 16, 601-611.	3.0	14
41	First-trimester proteomic profiling identifies novel predictors of gestational diabetes mellitus. <i>PLoS ONE</i> , 2019, 14, e0214457.	2.5	23
42	Proteomic Profiling of Mouse Epididymosomes Reveals their Contributions to Post-testicular Sperm Maturation. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S91-S108.	3.8	111
43	Integrated Proteomics Reveals Apoptosis-related Mechanisms Associated with Placental Malaria*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 182-199.	3.8	15
44	Dynamic Changes in the Protein Localization in the Nuclear Environment in Pancreatic Î2-Cell after Brief Glucose Stimulation. <i>Journal of Proteome Research</i> , 2018, 17, 1664-1676.	3.7	6
45	Development of a Neo-Epitope Specific Assay for Serological Assessment of Type VII Collagen Turnover and Its Relevance in Fibroproliferative Disorders. <i>Assay and Drug Development Technologies</i> , 2018, 16, 123-131.	1.2	9
46	A Targeted LC-MS Strategy for Low-Abundant HLA Class-II-Presented Peptide Detection Identifies Novel Human Papillomavirus T-Cell Epitopes. <i>Proteomics</i> , 2018, 18, e1700390.	2.2	27
47	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	8.0	580
48	Characterizing disease-associated changes in post-translational modifications by mass spectrometry. <i>Expert Review of Proteomics</i> , 2018, 15, 245-258.	3.0	47
49	Characterization of Macrophage Endogenous S-Nitrosoproteome Using a Cysteine-Specific Phosphonate Adaptable Tag in Combination with TiO <sub>2</sub> Chromatography. <i>Journal of Proteome Research</i> , 2018, 17, 1172-1182.	3.7	21
50	Characterization of the Molecular Mechanisms Underlying Glucose Stimulated Insulin Secretion from Isolated Pancreatic Î2-cells Using Post-translational Modification Specific Proteomics (PTMomics). <i>Molecular and Cellular Proteomics</i> , 2018, 17, 95-110.	3.8	31
51	Diverse Protein Profiles in CNS Myeloid Cells and CNS Tissue From Lipopolysaccharide- and Vehicle-Injected APPSWE/PS1 <sup>E9</sup> Transgenic Mice Implicate Cathepsin Z in Alzheimer's Disease. <i>Frontiers in Cellular Neuroscience</i> , 2018, 12, 397.	3.7	26
52	Development of a Trypanosoma cruzi strain typing assay using MS2 peptide spectral libraries (Tc-STAMS2). <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006351.	3.0	12
53	Experimental Demyelination and Axonal Loss Are Reduced in MicroRNA-146a Deficient Mice. <i>Frontiers in Immunology</i> , 2018, 9, 490.	4.8	43
54	Omics-Based Approach Reveals Complement-Mediated Inflammation in Chronic Lymphocytic Inflammation With Pontine Perivascular Enhancement Responsive to Steroids (CLIPPERS). <i>Frontiers in Immunology</i> , 2018, 9, 741.	4.8	10

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55	Age-Dependent Changes in the Sarkosyl-Insoluble Proteome of APPSWE/PS1 <sup>E9</sup> Transgenic Mice Implicate Dysfunctional Mitochondria in the Pathogenesis of Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2018, 64, 1247-1259.	2.6	23
56	Orthologous proteins of experimental de- and remyelination are differentially regulated in the CSF proteome of multiple sclerosis subtypes. <i>PLoS ONE</i> , 2018, 13, e0202530.	2.5	28
57	NS1 codon usage adaptation to humans in pandemic Zika virus. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2018, 113, e170385.	1.6	11
58	Snake Venom Extracellular vesicles (SVEVs) reveal wide molecular and functional proteome diversity. <i>Scientific Reports</i> , 2018, 8, 12067.	3.3	20
59	Extracellular vesicles with altered tetraspanin CD9 and CD151 levels confer increased prostate cell motility and invasion. <i>Scientific Reports</i> , 2018, 8, 8822.	3.3	52
60	Quantitative Proteomics and Phosphoproteomics Analysis Revealed Different Regulatory Mechanisms of Halothane and Rendement Napole Genes in Porcine Muscle Metabolism. <i>Journal of Proteome Research</i> , 2018, 17, 2834-2849.	3.7	16
61	Distinct urinary glycoprotein signatures in prostate cancer patients. <i>Oncotarget</i> , 2018, 9, 33077-33097.	1.8	33
62	Understanding Alzheimer's disease by global quantification of protein phosphorylation and sialylated N-linked glycosylation profiles: A chance for new biomarkers in neuroproteomics?. <i>Journal of Proteomics</i> , 2017, 161, 11-25.	2.4	23
63	Elucidation of Altered Pathways in Tumor-Initiating Cells of Triple-Negative Breast Cancer: A Useful Cell Model System for Drug Screening. <i>Stem Cells</i> , 2017, 35, 1898-1912.	3.2	13
64	Novel DNA coding regions and protein arginylation reveal unexplored <i>T. cruzi</i> proteome and PTMs. <i>International Journal of Mass Spectrometry</i> , 2017, 418, 51-66.	1.5	4
65	Alterations in the Cerebral Microvascular Proteome Expression Profile After Transient Global Cerebral Ischemia in Rat. <i>Journal of Molecular Neuroscience</i> , 2017, 61, 396-411.	2.3	2
66	Proteomic Expression Changes in Large Cerebral Arteries After Experimental Subarachnoid Hemorrhage in Rat Are Regulated by the MEK-ERK1/2 Pathway. <i>Journal of Molecular Neuroscience</i> , 2017, 62, 380-394.	2.3	10
67	Convergent Akt activation drives acquired EGFR inhibitor resistance in lung cancer. <i>Nature Communications</i> , 2017, 8, 410.	12.8	117
68	TNF $\alpha$ affects CREB-mediated neuroprotective signaling pathways of synaptic plasticity in neurons as revealed by proteomics and phospho-proteomics. <i>Oncotarget</i> , 2017, 8, 60223-60242.	1.8	11
69	The Splicing Efficiency of Activating HRAS Mutations Can Determine Costello Syndrome Phenotype and Frequency in Cancer. <i>PLoS Genetics</i> , 2016, 12, e1006039.	3.5	18
70	High-performance hybrid Orbitrap mass spectrometers for quantitative proteome analysis: Observations and implications. <i>Proteomics</i> , 2016, 16, 907-914.	2.2	64
71	Detection of proteolytic signatures for Parkinson's disease. <i>Future Neurology</i> , 2016, 11, 15-32.	0.5	0
72	The Arrhythmogenic Calmodulin Mutation D129G Dysregulates Cell Growth, Calmodulin-dependent Kinase II Activity, and Cardiac Function in Zebrafish. <i>Journal of Biological Chemistry</i> , 2016, 291, 26636-26646.	3.4	24

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73	Simultaneous Enrichment of Cysteine-containing Peptides and Phosphopeptides Using a Cysteine-specific Phosphonate Adaptable Tag (CysPAT) in Combination with titanium dioxide (TiO <sub>2</sub> ) Chromatography. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3282-3296.	3.8	55
74	A novel mass spectrometric strategy <i>â€œ</i> BEMAP <i>â€™</i> reveals Extensive O-linked protein glycosylation in Enterotoxigenic <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2016, 6, 32016.	3.3	21
75	Glycomic and sialoproteomic data of gastric carcinoma cells overexpressing ST3GAL4. <i>Data in Brief</i> , 2016, 7, 814-833.	1.0	13
76	Proteomic Identification of Putative MicroRNA394 Target Genes in <i>Arabidopsis thaliana</i> Identifies Major Latex Protein Family Members Critical for Normal Development. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2033-2047.	3.8	39
77	Glycomic analysis of gastric carcinoma cells discloses glycans as modulators of RON receptor tyrosine kinase activation in cancer. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 1795-1808.	2.4	49
78	Sequential Elution from IMAC (SIMAC): An Efficient Method for Enrichment and Separation of Mono- and Multi-phosphorylated Peptides. <i>Methods in Molecular Biology</i> , 2016, 1355, 147-160.	0.9	24
79	Improving the Phosphoproteome Coverage for Limited Sample Amounts Using TiO <sub>2</sub> -SIMAC-HILIC (TiSH) Phosphopeptide Enrichment and Fractionation. <i>Methods in Molecular Biology</i> , 2016, 1355, 161-177.	0.9	28
80	Phosphopeptide Enrichment by Immobilized Metal Affinity Chromatography. <i>Methods in Molecular Biology</i> , 2016, 1355, 123-133.	0.9	39
81	The Use of Titanium Dioxide for Selective Enrichment of Phosphorylated Peptides. <i>Methods in Molecular Biology</i> , 2016, 1355, 135-146.	0.9	56
82	Chronic low-dose-rate ionising radiation affects the hippocampal phosphoproteome in the ApoE <sup>0/0</sup> Alzheimer's mouse model. <i>Oncotarget</i> , 2016, 7, 71817-71832.	1.8	38
83	An integrated proteomics approach shows synaptic plasticity changes in an APP/PS1 Alzheimer's mouse model. <i>Oncotarget</i> , 2016, 7, 33627-33648.	1.8	55
84	Proteotranscriptomic Profiling of 231-BR Breast Cancer Cells: Identification of Potential Biomarkers and Therapeutic Targets for Brain Metastasis. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2316-2330.	3.8	59
85	Unraveling incompatibility between wheat and the fungal pathogen <i>Zymoseptoria tritici</i> through apoplastic proteomics. <i>BMC Genomics</i> , 2015, 16, 362.	2.8	37
86	The mRNA decay factor PAT 1 functions in a pathway including MAP kinase 4 and immune receptor SUMM 2. <i>EMBO Journal</i> , 2015, 34, 593-608.	7.8	100
87	Optimization of calmodulin-affinity chromatography for brain and organelles. <i>EuPA Open Proteomics</i> , 2015, 8, 55-67.	2.5	1
88	Quantitative proteomics analysis of platelet-derived microparticles reveals distinct protein signatures when stimulated by different physiological agonists. <i>Journal of Proteomics</i> , 2015, 121, 56-66.	2.4	81
89	Automated N-glycan profiling of a mutant <i>Trypanosoma rangeli</i> sialidase expressed in <i>Pichia pastoris</i> , using tandem mass spectrometry and bioinformatics. <i>Glycobiology</i> , 2015, 25, 1350-1361.	2.5	6
90	Quantitative Proteome Analysis Reveals Increased Content of Basement Membrane Proteins in Arteries From Patients With Type 2 Diabetes Mellitus and Lower Levels Among Metformin Users. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 727-735.	5.1	38

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91	Integrated Solid-Phase Extractionâ€“Capillary Liquid Chromatography (speLC) Interfaced to ESIâ€“MS/MS for Fast Characterization and Quantification of Protein and Proteomes. <i>Journal of Proteome Research</i> , 2014, 13, 6169-6175.	3.7	19
92	Spatial and Temporal Effects in Protein Post-translational Modification Distributions in the Developing Mouse Brain. <i>Journal of Proteome Research</i> , 2014, 13, 260-267.	3.7	21
93	Quantitative phosphoproteomic analysis of porcine muscle within 24 h postmortem. <i>Journal of Proteomics</i> , 2014, 106, 125-139.	2.4	49
94	Plasma proteome profiling of atherosclerotic disease manifestations reveals elevated levels of the cytoskeletal protein vinculin. <i>Journal of Proteomics</i> , 2014, 101, 141-153.	2.4	37
95	Quantitative proteomics of fractionated membrane and lumen exosome proteins from isogenic metastatic and nonmetastatic bladder cancer cells reveal differential expression of EMT factors. <i>Proteomics</i> , 2014, 14, 699-712.	2.2	148
96	Comparative Proteomics and Glycoproteomics Reveal Increased N-Linked Glycosylation and Relaxed Sequon Specificity in <i>Campylobacter jejuni</i> NCTC11168 O. <i>Journal of Proteome Research</i> , 2014, 13, 5136-5150.	3.7	48
97	Diversity Within the O-linked Protein Glycosylation Systems of <i>Acinetobacter</i> Species. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2354-2370.	3.8	64
98	Structural Basis for Phosphorylation and Lysine Acetylation Cross-talk in a Kinase Motif Associated with Myocardial Ischemia and Cardioprotection. <i>Journal of Biological Chemistry</i> , 2014, 289, 25890-25906.	3.4	48
99	Neuronal process structure and growth proteins are targets of heavy PTM regulation during brain development. <i>Journal of Proteomics</i> , 2014, 101, 77-87.	2.4	12
100	Proteins differentially expressed in human beta-cells-enriched pancreatic islet cultures and human insulinomas. <i>Molecular and Cellular Endocrinology</i> , 2013, 381, 16-25.	3.2	3
101	Site-Specific Glycan-Peptide Analysis for Determination of <i>N</i> -Glycoproteome Heterogeneity. <i>Journal of Proteome Research</i> , 2013, 12, 5791-5800.	3.7	153
102	Structural analysis of glycoprotein sialylation â€“ Part I: pre-LC-MS analytical strategies. <i>RSC Advances</i> , 2013, 3, 22683.	3.6	46
103	Structural analysis of glycoprotein sialylation â€“ part II: LC-MS based detection. <i>RSC Advances</i> , 2013, 3, 22706.	3.6	81
104	Battle through Signaling between Wheat and the Fungal Pathogen <i>Septoria tritici</i> Revealed by Proteomics and Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2497-2508.	3.8	58
105	Technologies and challenges in large-scale phosphoproteomics. <i>Proteomics</i> , 2013, 13, 910-931.	2.2	142
106	Quantitative Phosphoproteomic Analysis of Early Alterations in Protein Phosphorylation by 2,3,7,8-Tetrachlorodibenzo- <i>p</i> -dioxin. <i>Journal of Proteome Research</i> , 2013, 12, 866-882.	3.7	6
107	Acute Myocardial Infarction and Pulmonary Diseases Result in Two Different Degradation Profiles of Elastin as Quantified by Two Novel ELISAs. <i>PLoS ONE</i> , 2013, 8, e60936.	2.5	19
108	Modification of the <i>Campylobacter jejuni</i> N-Linked Glycan by EptC Protein-mediated Addition of Phosphoethanolamine. <i>Journal of Biological Chemistry</i> , 2012, 287, 29384-29396.	3.4	63

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109	Modulation of Protein Phosphorylation, N-Glycosylation and Lys-Acetylation in Grape ( <i>Vitis vinifera</i> ) Mesocarp and Exocarp Owing to <i>Lobesia botrana</i> Infection. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 945-956.	3.8	118
110	A Novel Method for the Simultaneous Enrichment, Identification, and Quantification of Phosphopeptides and Sialylated Glycopeptides Applied to a Temporal Profile of Mouse Brain Development. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1191-1202.	3.8	121
111	TiSH â€” a robust and sensitive global phosphoproteomics strategy employing a combination of TiO <sub>2</sub> , SIMAC, and HILIC. <i>Journal of Proteomics</i> , 2012, 75, 5749-5761.	2.4	174
112	Performance of Isobaric and Isotopic Labeling in Quantitative Plant Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 3046-3052.	3.7	52
113	Chemical Deamidation: A Common Pitfall in Large-Scale N-Linked Glycoproteomic Mass Spectrometry-Based Analyses. <i>Journal of Proteome Research</i> , 2012, 11, 1949-1957.	3.7	151
114	Changes in phosphorylation of myofibrillar proteins during postmortem development of porcine muscle. <i>Food Chemistry</i> , 2012, 134, 1999-2006.	8.2	69
115	Purification and Identification of O-GlcNAc-Modified Peptides Using Phosphate-Based Alkyne CLICK Chemistry in Combination with Titanium Dioxide Chromatography and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2011, 10, 1449-1458.	3.7	45
116	A Novel Post-translational Modification in Nerve Terminals: O-Linked <i>N</i> -Acetylglucosamine Phosphorylation. <i>Journal of Proteome Research</i> , 2011, 10, 2725-2733.	3.7	33
117	Multidimensional Strategy for Sensitive Phosphoproteomics Incorporating Protein Prefractionation Combined with SIMAC, HILIC, and TiO <sub>2</sub> Chromatography Applied to Proximal EGF Signaling. <i>Journal of Proteome Research</i> , 2011, 10, 5383-5397.	3.7	63
118	Postmortem Changes in Pork Muscle Protein Phosphorylation in Relation to the RN Genotype. <i>Journal of Agricultural and Food Chemistry</i> , 2011, 59, 11608-11615.	5.2	36
119	Proteomics of the oxidative stress response induced by hydrogen peroxide and paraquat reveals a novel AhpC-like protein in <i>Pseudomonas aeruginosa</i> . <i>Proteomics</i> , 2011, 11, 3056-3069.	2.2	27
120	Gelatin-based phosphoproteomics analysis of sarcoplasmic proteins in postmortem porcine muscle with pH decline rate and time differences. <i>Proteomics</i> , 2011, 11, 4063-4076.	2.2	100
121	Research Resource: New and Diverse Substrates for the Insulin Receptor Isoform A Revealed by Quantitative Proteomics After Stimulation With IGF-II or Insulin. <i>Molecular Endocrinology</i> , 2011, 25, 1456-1468.	3.7	48
122	Glycoproteomic Profile in Wine: A â€”Sweetâ€” Molecular Renaissance. <i>Journal of Proteome Research</i> , 2010, 9, 6148-6159.	3.7	45
123	Quantitative iTRAQ-Based Proteomic Identification of Candidate Biomarkers for Diabetic Nephropathy in Plasma of Type 1 Diabetic Patients. <i>Clinical Proteomics</i> , 2010, 6, 105-114.	2.1	28
124	Improved accuracy of cell surface shaving proteomics in <i>Staphylococcus aureus</i> using a false-positive control. <i>Proteomics</i> , 2010, 10, 2037-2049.	2.2	86
125	Matrix metalloproteinase-9-mediated type III collagen degradation as a novel serological biochemical marker for liver fibrogenesis. <i>Liver International</i> , 2010, 30, 1293-1304.	3.9	59
126	Selective enrichment of sialic acid-containing glycopeptides using titanium dioxide chromatography with analysis by HILIC and mass spectrometry. <i>Nature Protocols</i> , 2010, 5, 1974-1982.	12.0	225



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127	Undesirable Charge-Enhancement of Isobaric Tagged Phosphopeptides Leads to Reduced Identification Efficiency. <i>Journal of Proteome Research</i> , 2010, 9, 4045-4052.	3.7	117
128	Expression, purification and characterization of the cancer-germline antigen GAGE12l: A candidate for cancer immunotherapy. <i>Protein Expression and Purification</i> , 2010, 73, 217-222.	1.3	4
129	Quantitative phosphoproteomics of depolarization-dependent protein phosphorylation in nerve terminals. <i>FASEB Journal</i> , 2010, 24, 905.2.	0.5	0
130	Analytical strategies for phosphoproteomics. <i>Proteomics</i> , 2009, 9, 1451-1468.	2.2	434
131	A phosphoproteomics approach to elucidate neuropeptide signal transduction controlling insect metamorphosis. <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 475-483.	2.7	70
132	TiO <sub>2</sub> -Based Phosphoproteomic Analysis of the Plasma Membrane and the Effects of Phosphatase Inhibitor Treatment. <i>Journal of Proteome Research</i> , 2008, 7, 3304-3313.	3.7	94
133	Characterization of the Human Cerebrospinal Fluid Phosphoproteome by Titanium Dioxide Affinity Chromatography and Mass Spectrometry. <i>Analytical Chemistry</i> , 2008, 80, 6308-6316.	6.5	56
134	SIMAC (Sequential Elution from IMAC), a Phosphoproteomics Strategy for the Rapid Separation of Monophosphorylated from Multiply Phosphorylated Peptides. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 661-671.	3.8	380
135	The in Vivo Phosphorylation Sites in Multiple Isoforms of Amphiphysin I from Rat Brain Nerve Terminals. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1146-1161.	3.8	25
136	Chapter 12 Phosphoproteomics. <i>Comprehensive Analytical Chemistry</i> , 2008, 52, 275-296.	1.3	1
137	Ser649 and Ser650 Are the Major Determinants of Protein Kinase A-Mediated Activation of Human Hormone-Sensitive Lipase against Lipid Substrates. <i>PLoS ONE</i> , 2008, 3, e3756.	2.5	49
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