

Martin R Larsen

List of Publications by Year in descending order

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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	Highly Selective Enrichment of Phosphorylated Peptides from Peptide Mixtures Using Titanium Dioxide Microcolumns. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 873-886.	3.8	1,356
2	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	8.0	580
3	Highly selective enrichment of phosphorylated peptides using titanium dioxide. <i>Nature Protocols</i> , 2006, 1, 1929-1935.	12.0	565
4	Analytical strategies for phosphoproteomics. <i>Proteomics</i> , 2009, 9, 1451-1468.	2.2	434
5	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
6	Cdk5 is essential for synaptic vesicle endocytosis. <i>Nature Cell Biology</i> , 2003, 5, 701-710.	10.3	290
7	Exploring the Sialome Using Titanium Dioxide Chromatography and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1778-1787.	3.8	256
8	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
9	Analysis of posttranslational modifications of proteins by tandem mass spectrometry. <i>BioTechniques</i> , 2006, 40, 790-798.	1.8	201
10	TiSH – a robust and sensitive global phosphoproteomics strategy employing a combination of TiO ₂ , SIMAC, and HILIC. <i>Journal of Proteomics</i> , 2012, 75, 5749-5761.	2.4	174
11	Site-Specific Glycan-Peptide Analysis for Determination of N-Glycoproteome Heterogeneity. <i>Journal of Proteome Research</i> , 2013, 12, 5791-5800.	3.7	153
12	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
13	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
14	Technologies and challenges in large-scale phosphoproteomics. <i>Proteomics</i> , 2013, 13, 910-931.	2.2	142
15	Molecular Characterization of Covalent Complexes between Tissue Transglutaminase and Gliadin Peptides. <i>Journal of Biological Chemistry</i> , 2004, 279, 17607-17616.	3.4	136
16	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
17	Characterization of Gel-separated Glycoproteins Using Two-step Proteolytic Digestion Combined with Sequential Microcolumns and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 107-119.	3.8	130
18	The Brain Exocyst Complex Interacts with RalA in a GTP-dependent Manner. <i>Journal of Biological Chemistry</i> , 2001, 276, 29792-29797.	3.4	128

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19	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
20	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
21	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
22	Convergent Akt activation drives acquired EGFR inhibitor resistance in lung cancer. <i>Nature Communications</i> , 2017, 8, 410.	12.8	117
23	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
24	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
25	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
26	Quorum-Sensing Regulation of Adhesion in <i>Serratia marcescens</i> MG1 Is Surface Dependent. <i>Journal of Bacteriology</i> , 2007, 189, 2702-2711.	2.2	95
27	TiO ₂ -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
28	Improved Detection of Hydrophilic Phosphopeptides Using Graphite Powder Microcolumns and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 456-465.	3.8	91
29	Identification of Phosphorylation Sites in Protein Kinase A Substrates Using Artificial Neural Networks and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2004, 3, 426-433.	3.7	88
30	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
31	Proteome analysis of <i>Saccharomyces cerevisiae</i> : A methodological outline. <i>Electrophoresis</i> , 1997, 18, 1361-1372.	2.4	82
32	Dynamic cofilin phosphorylation in the control of lamellipodial actin homeostasis. <i>Journal of Cell Science</i> , 2007, 120, 1888-1897.	2.0	82
33	Structural analysis of glycoprotein sialylation – part II: LC-MS based detection. <i>RSC Advances</i> , 2013, 3, 22706.	3.6	81
34	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
35	Comparative proteome analysis of <i>Chlamydia trachomatis</i> serovar A, D and L2. <i>Proteomics</i> , 2002, 2, 164-186.	2.2	77
36	Characterization of a secreted <i>Chlamydia</i> protease. <i>Cellular Microbiology</i> , 2002, 4, 411-424.	2.1	75

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37	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
38	Changes in phosphorylation of myofibrillar proteins during postmortem development of porcine muscle. <i>Food Chemistry</i> , 2012, 134, 1999-2006.	8.2	69
39	Phosphorylation of Dynamin I on Ser-795 by Protein Kinase C Blocks Its Association with Phospholipids. <i>Journal of Biological Chemistry</i> , 2000, 275, 11610-11617.	3.4	65
40	Diversity Within the O-linked Protein Glycosylation Systems of Acinetobacter Species. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2354-2370.	3.8	64
41	High-performance hybrid Orbitrap mass spectrometers for quantitative proteome analysis: Observations and implications. <i>Proteomics</i> , 2016, 16, 907-914.	2.2	64
42	Multidimensional Strategy for Sensitive Phosphoproteomics Incorporating Protein Prefractionation Combined with SIMAC, HILIC, and TiO ₂ Chromatography Applied to Proximal EGF Signaling. <i>Journal of Proteome Research</i> , 2011, 10, 5383-5397.	3.7	63
43	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
44	The phosphorylation pattern of bovine heart complex I subunits. <i>Proteomics</i> , 2007, 7, 1575-1583.	2.2	60
45	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
46	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
47	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
48	Novel Protein Phosphorylation Site Identification in Spinach Stroma Membranes by Titanium Dioxide Microcolumns and Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2006, 5, 973-982.	3.7	57
49	Alterations in β -Actin and Tubulin-Targeted Drug Resistance in Childhood Leukemia. <i>Journal of the National Cancer Institute</i> , 2006, 98, 1363-1374.	6.3	57
50	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
51	The Use of Titanium Dioxide for Selective Enrichment of Phosphorylated Peptides. <i>Methods in Molecular Biology</i> , 2016, 1355, 135-146.	0.9	56
52	Simultaneous Enrichment of Cysteine-containing Peptides and Phosphopeptides Using a Cysteine-specific Phosphonate Adaptable Tag (CysPAT) in Combination with titanium dioxide (TiO ₂) Chromatography. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3282-3296.	3.8	55
53	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
54	Correlation of acidic and basic carrier ampholyte and immobilized pH gradient two-dimensional gel electrophoresis patterns based on mass spectrometric protein identification. <i>Electrophoresis</i> , 1998, 19, 1024-1035.	2.4	53

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55	Performance of Isobaric and Isotopic Labeling in Quantitative Plant Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 3046-3052.	3.7	52
56	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
57	Quantitative phosphoproteomic analysis of porcine muscle within 24 h postmortem. <i>Journal of Proteomics</i> , 2014, 106, 125-139.	2.4	49
58	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
59	Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. <i>Nature Communications</i> , 2020, 11, 5248.	12.8	49
60	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
61	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
62	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
63	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
64	Unraveling the Pathogenesis of Type 1 Diabetes with Proteomics: Present And Future Directions. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 441-457.	3.8	47
65	Characterizing disease-associated changes in post-translational modifications by mass spectrometry. <i>Expert Review of Proteomics</i> , 2018, 15, 245-258.	3.0	47
66	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
67	Structural analysis of glycoprotein sialylation – Part I: pre-LC-MS analytical strategies. <i>RSC Advances</i> , 2013, 3, 22683.	3.6	46
68	The in Vivo Phosphorylation Sites of Rat Brain Dynamin I*. <i>Journal of Biological Chemistry</i> , 2007, 282, 14695-14707.	3.4	45
69	Glycoproteomic Profile in Wine: A “Sweet” Molecular Renaissance. <i>Journal of Proteome Research</i> , 2010, 9, 6148-6159.	3.7	45
70	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
71	Experimental Demyelination and Axonal Loss Are Reduced in MicroRNA-146a Deficient Mice. <i>Frontiers in Immunology</i> , 2018, 9, 490.	4.8	43
72	Characterization of differently processed forms of enolase 2 from <i>Saccharomyces cerevisiae</i> by two-dimensional gel electrophoresis and mass spectrometry. <i>Electrophoresis</i> , 2001, 22, 566-575.	2.4	42

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73	Immune-mediated β 2-cell destruction in vitro and in vivo—A pivotal role for galectin-3. <i>Biochemical and Biophysical Research Communications</i> , 2006, 344, 406-415.	2.1	41
74	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
75	Phosphopeptide Enrichment by Immobilized Metal Affinity Chromatography. <i>Methods in Molecular Biology</i> , 2016, 1355, 123-133.	0.9	39
76	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
77	Chronic low-dose-rate ionising radiation affects the hippocampal phosphoproteome in the ApoE ^{0/0} Alzheimer's mouse model. <i>Oncotarget</i> , 2016, 7, 71817-71832.	1.8	38
78	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
79	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
80	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
81	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
82	A Novel Post-translational Modification in Nerve Terminals: O-Linked N-Acetylglucosamine Phosphorylation. <i>Journal of Proteome Research</i> , 2011, 10, 2725-2733.	3.7	33
83	Distinct urinary glycoprotein signatures in prostate cancer patients. <i>Oncotarget</i> , 2018, 9, 33077-33097.	1.8	33
84	Phosphorylation of Both Nucleoplasmin Domains Is Required for Activation of Its Chromatin Decondensation Activity. <i>Journal of Biological Chemistry</i> , 2007, 282, 21213-21221.	3.4	32
85	Characterization of the Molecular Mechanisms Underlying Glucose Stimulated Insulin Secretion from Isolated Pancreatic β 2-cells Using Post-translational Modification Specific Proteomics (PTMomics). <i>Molecular and Cellular Proteomics</i> , 2018, 17, 95-110.	3.8	31
86	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
87	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
88	Improving the Phosphoproteome Coverage for Limited Sample Amounts Using TiO ₂ -SIMAC-HILIC (TiSH) Phosphopeptide Enrichment and Fractionation. <i>Methods in Molecular Biology</i> , 2016, 1355, 161-177.	0.9	28
89	Unravelling the role of the ToxR-like transcriptional regulator WmpR in the marine antifouling bacterium <i>Pseudoalteromonas tunicata</i> . <i>Microbiology (United Kingdom)</i> , 2006, 152, 1385-1394.	1.8	27
90	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

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91	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
92	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
93	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
94	Diverse Protein Profiles in CNS Myeloid Cells and CNS Tissue From Lipopolysaccharide- and Vehicle-Injected APPSWE/PS1 ^{E9} Transgenic Mice Implicate Cathepsin Z in Alzheimer's Disease. <i>Frontiers in Cellular Neuroscience</i> , 2018, 12, 397.	3.7	26
95	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
96	Characterization of Purified Recombinant Bet v 1 with Authentic N-Terminus, Cloned in Fusion with Maltose-Binding Protein. <i>Protein Expression and Purification</i> , 1996, 8, 365-373.	1.3	24
97	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
98	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
99	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
100	Age-Dependent Changes in the Sarkosyl-Insoluble Proteome of APPSWE/PS1 ^{E9} 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
101	First-trimester proteomic profiling identifies novel predictors of gestational diabetes mellitus. <i>PLoS ONE</i> , 2019, 14, e0214457.	2.5	23
102	Characterization of Signaling Pathways Associated with Pancreatic Î2-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
103	Quantitative phosphoproteomics uncovers synergy between DNA-PK and FLT3 inhibitors in acute myeloid leukaemia. <i>Leukemia</i> , 2021, 35, 1782-1787.	7.2	22
104	HDL proteome remodeling associates with COVID-19 severity. <i>Journal of Clinical Lipidology</i> , 2021, 15, 796-804.	1.5	22
105	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
106	A novel mass spectrometric strategy -BEMAP- reveals Extensive O-linked protein glycosylation in Enterotoxigenic Escherichia coli. <i>Scientific Reports</i> , 2016, 6, 32016.	3.3	21
107	Characterization of Macrophage Endogenous S-Nitrosoproteome Using a Cysteine-Specific Phosphonate Adaptable Tag in Combination with TiO ₂ Chromatography. <i>Journal of Proteome Research</i> , 2018, 17, 1172-1182.	3.7	21
108	Snake Venom Extracellular vesicles (SVEVs) reveal wide molecular and functional proteome diversity. <i>Scientific Reports</i> , 2018, 8, 12067.	3.3	20

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109	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
110	Phosphorylation of the regulatory \hat{I}^2 -subunit of protein kinase CK2 by checkpoint kinase Chk1: identification of the in vitro CK2 \hat{I}^2 phosphorylation site. <i>FEBS Letters</i> , 2004, 569, 217-223.	2.8	19
111	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
112	Integrated Solid-Phase Extraction \hat{I}^2 Capillary Liquid Chromatography (speLC) Interfaced to ESI \hat{I}^2 MS/MS for Fast Characterization and Quantification of Protein and Proteomes. <i>Journal of Proteome Research</i> , 2014, 13, 6169-6175.	3.7	19
113	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
114	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
115	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
116	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
117	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
118	Integrated Proteomics Reveals Apoptosis-related Mechanisms Associated with Placental Malaria*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 182-199.	3.8	15
119	Identification of SRSF10 as a regulator of <i>SMN2</i> ISS \hat{I}^2 N1. <i>Human Mutation</i> , 2021, 42, 246-260.	2.5	15
120	Proteomic signatures of neuroinflammation in Alzheimer \hat{I}^2 Ms disease, multiple sclerosis and ischemic stroke. <i>Expert Review of Proteomics</i> , 2019, 16, 601-611.	3.0	14
121	Glycomic and sialoproteomic data of gastric carcinoma cells overexpressing ST3GAL4. <i>Data in Brief</i> , 2016, 7, 814-833.	1.0	13
122	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
123	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
124	Identification and characterization of a novel <i>Chlamydia trachomatis</i> reticulate body protein. <i>FEMS Microbiology Letters</i> , 2002, 212, 193-202.	1.8	12
125	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
126	Development of a <i>Trypanosoma cruzi</i> strain typing assay using MS2 peptide spectral libraries (Tc-STAMS2). <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006351.	3.0	12

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127	NS1 codon usage adaptation to humans in pandemic Zika virus. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2018, 113, e170385.	1.6	11
128	Pharmacological inhibition of mitochondrial soluble adenylyl cyclase in astrocytes causes activation of α -activated protein kinase and induces breakdown of glycogen. <i>Glia</i> , 2021, 69, 2828-2844.	4.9	11
129	TNF \pm 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
130	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
131	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
132	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
133	CSF proteome in multiple sclerosis subtypes related to brain lesion transcriptomes. <i>Scientific Reports</i> , 2021, 11, 4132.	3.3	10
134	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
135	Proteomic changes during experimental de- and remyelination in the corpus callosum. <i>PLoS ONE</i> , 2020, 15, e0230249.	2.5	9
136	Ultraviolet Photodissociation of Protonated Peptides and Proteins Can Proceed with H/D Scrambling. <i>Analytical Chemistry</i> , 2021, 93, 691-696.	6.5	8
137	HSPB1 influences mitochondrial respiration in ER-stressed beta cells. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140680.	2.3	7
138	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
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