Martin R Larsen

List of Publications by Citations

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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.

169 papers

8,672 citations

48 h-index

90 g-index

175 ext. papers

9,889 ext. citations

5.3 avg, IF

L-index

#	Paper	IF	Citations
169	Highly selective enrichment of phosphorylated peptides from peptide mixtures using titanium dioxide microcolumns. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 873-86	7.6	1257
168	Highly selective enrichment of phosphorylated peptides using titanium dioxide. <i>Nature Protocols</i> , 2006 , 1, 1929-35	18.8	509
167	Analytical strategies for phosphoproteomics. <i>Proteomics</i> , 2009 , 9, 1451-68	4.8	392
166	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, 661-71	7.6	355
165	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
164	Cdk5 is essential for synaptic vesicle endocytosis. <i>Nature Cell Biology</i> , 2003 , 5, 701-10	23.4	259
163	Exploring the sialiome using titanium dioxide chromatography and mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1778-87	7.6	240
162	Selective enrichment of sialic acid-containing glycopeptides using titanium dioxide chromatography with analysis by HILIC and mass spectrometry. <i>Nature Protocols</i> , 2010 , 5, 1974-82	18.8	198
161	Analysis of posttranslational modifications of proteins by tandem mass spectrometry. <i>BioTechniques</i> , 2006 , 40, 790-8	2.5	161
160	TiSHa robust and sensitive global phosphoproteomics strategy employing a combination of TiO2, SIMAC, and HILIC. <i>Journal of Proteomics</i> , 2012 , 75, 5749-61	3.9	151
159	Chemical deamidation: a common pitfall in large-scale N-linked glycoproteomic mass spectrometry-based analyses. <i>Journal of Proteome Research</i> , 2012 , 11, 1949-57	5.6	138
158	Site-specific glycan-peptide analysis for determination of N-glycoproteome heterogeneity. <i>Journal of Proteome Research</i> , 2013 , 12, 5791-800	5.6	130
157	Technologies and challenges in large-scale phosphoproteomics. <i>Proteomics</i> , 2013 , 13, 910-31	4.8	130
156	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	4.8	123
155	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-	19 ^{7.6}	121
154	The brain exocyst complex interacts with RalA in a GTP-dependent manner: identification of a novel mammalian Sec3 gene and a second Sec15 gene. <i>Journal of Biological Chemistry</i> , 2001 , 276, 29792-7	5.4	118
153	Molecular characterization of covalent complexes between tissue transglutaminase and gliadin peptides. <i>Journal of Biological Chemistry</i> , 2004 , 279, 17607-16	5.4	108

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152	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, 1191-202	7.6	100
151	Undesirable charge-enhancement of isobaric tagged phosphopeptides leads to reduced identification efficiency. <i>Journal of Proteome Research</i> , 2010 , 9, 4045-52	5.6	99
150	Modulation of protein phosphorylation, N-glycosylation and Lys-acetylation in grape (Vitis vinifera) mesocarp and exocarp owing to Lobesia botrana infection. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 945-56	7.6	97
149	TiO(2)-based phosphoproteomic analysis of the plasma membrane and the effects of phosphatase inhibitor treatment. <i>Journal of Proteome Research</i> , 2008 , 7, 3304-13	5.6	90
148	Gel-based phosphoproteomics analysis of sarcoplasmic proteins in postmortem porcine muscle with pH decline rate and time differences. <i>Proteomics</i> , 2011 , 11, 4063-76	4.8	89
147	Quorum-sensing regulation of adhesion in Serratia marcescens MG1 is surface dependent. <i>Journal of Bacteriology</i> , 2007 , 189, 2702-11	3.5	83
146	Improved detection of hydrophilic phosphopeptides using graphite powder microcolumns and mass spectrometry: evidence for in vivo doubly phosphorylated dynamin I and dynamin III. <i>Molecular and Cellular Proteomics</i> , 2004 , 3, 456-65	7.6	82
145	Convergent Akt activation drives acquired EGFR inhibitor resistance in lung cancer. <i>Nature Communications</i> , 2017 , 8, 410	17.4	80
144	Improved accuracy of cell surface shaving proteomics in Staphylococcus aureus using a false-positive control. <i>Proteomics</i> , 2010 , 10, 2037-49	4.8	77
143	Proteome analysis of Saccharomyces cerevisiae: a methodological outline. <i>Electrophoresis</i> , 1997 , 18, 13	6 1 .#2	73
142	Comparative proteome analysis of Chlamydia trachomatis serovar A, D and L2. <i>Proteomics</i> , 2002 , 2, 164	- 846 8	73
141	The mRNA decay factor PAT1 functions in a pathway including MAP kinase 4 and immune receptor SUMM2. <i>EMBO Journal</i> , 2015 , 34, 593-608	13	71
140	A phosphoproteomics approach to elucidate neuropeptide signal transduction controlling insect metamorphosis. <i>Insect Biochemistry and Molecular Biology</i> , 2009 , 39, 475-83	4.5	68
139	Identification of phosphorylation sites in protein kinase A substrates using artificial neural networks and mass spectrometry. <i>Journal of Proteome Research</i> , 2004 , 3, 426-33	5.6	67
138	Structural analysis of glycoprotein sialylation [þart II: LC-MS based detection. <i>RSC Advances</i> , 2013 , 3, 22706	3.7	66
137	Proteomic Profiling of Mouse Epididymosomes Reveals their Contributions to Post-testicular Sperm Maturation. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, S91-S108	7.6	66
136	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, 5383-97	5.6	61
135	Characterization of a secreted Chlamydia protease. <i>Cellular Microbiology</i> , 2002 , 4, 411-24	3.9	61

134	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	3.9	60
133	Changes in phosphorylation of myofibrillar proteins during postmortem development of porcine muscle. <i>Food Chemistry</i> , 2012 , 134, 1999-2006	8.5	60
132	Matrix metalloproteinase-9-mediated type III collagen degradation as a novel serological biochemical marker for liver fibrogenesis. <i>Liver International</i> , 2010 , 30, 1293-304	7.9	56
131	The phosphorylation pattern of bovine heart complex I subunits. <i>Proteomics</i> , 2007 , 7, 1575-83	4.8	55
130	Phosphorylation of dynamin I on Ser-795 by protein kinase C blocks its association with phospholipids. <i>Journal of Biological Chemistry</i> , 2000 , 275, 11610-7	5.4	55
129	Modification of the Campylobacter jejuni N-linked glycan by EptC protein-mediated addition of phosphoethanolamine. <i>Journal of Biological Chemistry</i> , 2012 , 287, 29384-96	5.4	53
128	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, 973-82	5.6	53
127	High-performance hybrid Orbitrap mass spectrometers for quantitative proteome analysis: Observations and implications. <i>Proteomics</i> , 2016 , 16, 907-14	4.8	53
126	Alterations in gamma-actin and tubulin-targeted drug resistance in childhood leukemia. <i>Journal of the National Cancer Institute</i> , 2006 , 98, 1363-74	9.7	52
125	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, 2316-30	7.6	50
124	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, 1024-35	3.6	50
123	Dynamic cofilin phosphorylation in the control of lamellipodial actin homeostasis. <i>Journal of Cell Science</i> , 2007 , 120, 1888-97	5.3	50
122	Battle through signaling between wheat and the fungal pathogen Septoria tritici revealed by proteomics and phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2497-508	7.6	49
121	Resolution of NASH and hepatic fibrosis by the GLP-1R/GcgR dual-agonist Cotadutide via modulating mitochondrial function and lipogenesis. <i>Nature Metabolism</i> , 2020 , 2, 413-431	14.6	47
120	Characterization of the human cerebrospinal fluid phosphoproteome by titanium dioxide affinity chromatography and mass spectrometry. <i>Analytical Chemistry</i> , 2008 , 80, 6308-16	7.8	47
119	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	3.7	45
118	The Use of Titanium Dioxide for Selective Enrichment of Phosphorylated Peptides. <i>Methods in Molecular Biology</i> , 2016 , 1355, 135-46	1.4	45
117	Diversity within the O-linked protein glycosylation systems of acinetobacter species. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2354-70	7.6	44

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116	chemistry in combination with titanium dioxide chromatography and mass spectrometry. <i>Journal of Proteome Research</i> , 2011 , 10, 1449-58	5.6	44	
115	The in vivo phosphorylation sites of rat brain dynamin I. <i>Journal of Biological Chemistry</i> , 2007 , 282, 1469	55.7407	43	
114	Performance of isobaric and isotopic labeling in quantitative plant proteomics. <i>Journal of Proteome Research</i> , 2012 , 11, 3046-52	5.6	42	
113	Unraveling the pathogenesis of type 1 diabetes with proteomics: present and future directions. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 441-57	7.6	41	
112	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-	-68	40	
111	Extracellular vesicles with altered tetraspanin CD9 and CD151 levels confer increased prostate cell motility and invasion. <i>Scientific Reports</i> , 2018 , 8, 8822	4.9	38	
110	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, 25890-906	5.4	38	
109	Glycoproteomic profile in wine: a ßweetRmolecular renaissance. <i>Journal of Proteome Research</i> , 2010 , 9, 6148-59	5.6	38	
108	Comparative proteomics and glycoproteomics reveal increased N-linked glycosylation and relaxed sequon specificity in Campylobacter jejuni NCTC11168 O. <i>Journal of Proteome Research</i> , 2014 , 13, 5136-	- 50 6	37	
107	Structural analysis of glycoprotein sialylation IPart I: pre-LC-MS analytical strategies. <i>RSC Advances</i> , 2013 , 3, 22683	3.7	36	
106	Simultaneous Enrichment of Cysteine-containing Peptides and Phosphopeptides Using a Cysteine-specific Phosphonate Adaptable Tag (CysPAT) in Combination with titanium dioxide (TiO2) Chromatography. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 3282-3296	7.6	36	
105	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, 1795-8	0 8	35	
104	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, 727-35		34	
103	Quantitative phosphoproteomic analysis of porcine muscle within 24 h postmortem. <i>Journal of Proteomics</i> , 2014 , 106, 125-39	3.9	34	
102	An integrated proteomics approach shows synaptic plasticity changes in an APP/PS1 Alzheimer mouse model. <i>Oncotarget</i> , 2016 , 7, 33627-48	3.3	34	
101	Characterization of differently processed forms of enolase 2 from Saccharomyces cerevisiae by two-dimensional gel electrophoresis and mass spectrometry. <i>Electrophoresis</i> , 2001 , 22, 566-75	3.6	33	
100	Postmortem changes in pork muscle protein phosphorylation in relation to the RN genotype. Journal of Agricultural and Food Chemistry, 2011 , 59, 11608-15	5.7	32	
99	Immune-mediated beta-cell destruction in vitro and in vivo-A pivotal role for galectin-3. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 344, 406-15	3.4	31	

98	Phosphorylation of both nucleoplasmin domains is required for activation of its chromatin decondensation activity. <i>Journal of Biological Chemistry</i> , 2007 , 282, 21213-21	5.4	30
97	Phosphopeptide Enrichment by Immobilized Metal Affinity Chromatography. <i>Methods in Molecular Biology</i> , 2016 , 1355, 123-33	1.4	30
96	Mutation Causes Metabolic Disturbances and Impaired Survival of Human iPSC-Derived Neurons. <i>Frontiers in Cellular Neuroscience</i> , 2019 , 13, 297	6.1	29
95	Unraveling incompatibility between wheat and the fungal pathogen Zymoseptoria tritici through apoplastic proteomics. <i>BMC Genomics</i> , 2015 , 16, 362	4.5	29
94	Plasma proteome profiling of atherosclerotic disease manifestations reveals elevated levels of the cytoskeletal protein vinculin. <i>Journal of Proteomics</i> , 2014 , 101, 141-53	3.9	29
93	Characterizing disease-associated changes in post-translational modifications by mass spectrometry. <i>Expert Review of Proteomics</i> , 2018 , 15, 245-258	4.2	28
92	Experimental Demyelination and Axonal Loss Are Reduced in MicroRNA-146a Deficient Mice. <i>Frontiers in Immunology</i> , 2018 , 9, 490	8.4	27
91	Distinct urinary glycoprotein signatures in prostate cancer patients. <i>Oncotarget</i> , 2018 , 9, 33077-33097	3.3	27
90	Proteomic Identification of Putative MicroRNA394 Target Genes in Arabidopsis thaliana Identifies Major Latex Protein Family Members Critical for Normal Development. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2033-47	7.6	26
89	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	5	26
88	Chronic low-dose-rate ionising radiation affects the hippocampal phosphoproteome in the ApoE-/-Alzheimerß mouse model. <i>Oncotarget</i> , 2016 , 7, 71817-71832	3.3	26
87	A novel post-translational modification in nerve terminals: O-linked N-acetylglucosamine phosphorylation. <i>Journal of Proteome Research</i> , 2011 , 10, 2725-33	5.6	23
86	Unravelling the role of the ToxR-like transcriptional regulator WmpR in the marine antifouling bacterium Pseudoalteromonas tunicata. <i>Microbiology (United Kingdom)</i> , 2006 , 152, 1385-1394	2.9	23
85	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, 365-73	2	23
84	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, 147-60	1.4	21
83	Improving the Phosphoproteome Coverage for Limited Sample Amounts Using TiO2-SIMAC-HILIC (TiSH) Phosphopeptide Enrichment and Fractionation. <i>Methods in Molecular Biology</i> , 2016 , 1355, 161-77	, ^{1.} 4	20
82	Characterization of the Molecular Mechanisms Underlying Glucose Stimulated Insulin Secretion from Isolated Pancreatic Etells Using Post-translational Modification Specific Proteomics (PTMomics). <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 95-110	7.6	20
81	Understanding Alzheimer disease by global quantification of protein phosphorylation and sialylated N-linked glycosylation profiles: A chance for new biomarkers in neuroproteomics?.	3.9	19

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80	Spatial and temporal effects in protein post-translational modification distributions in the developing mouse brain. <i>Journal of Proteome Research</i> , 2014 , 13, 260-7	5.6	19
79	Proteomics of the oxidative stress response induced by hydrogen peroxide and paraquat reveals a novel AhpC-like protein in Pseudomonas aeruginosa. <i>Proteomics</i> , 2011 , 11, 3056-69	4.8	19
78	The in vivo phosphorylation sites in multiple isoforms of amphiphysin I from rat brain nerve terminals. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1146-61	7.6	19
77	A Targeted LC-MS Strategy for Low-Abundant HLA Class-I-Presented Peptide Detection Identifies Novel Human Papillomavirus T-Cell Epitopes. <i>Proteomics</i> , 2018 , 18, e1700390	4.8	18
76	Integrated solid-phase extraction-capillary liquid chromatography (speLC) interfaced to ESI-MS/MS for fast characterization and quantification of protein and proteomes. <i>Journal of Proteome Research</i> , 2014 , 13, 6169-75	5.6	18
75	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	5.4	17
74	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	3.7	16
73	Phosphorylation of the regulatory beta-subunit of protein kinase CK2 by checkpoint kinase Chk1: identification of the in vitro CK2beta phosphorylation site. <i>FEBS Letters</i> , 2004 , 569, 217-23	3.8	15
72	Diverse Protein Profiles in CNS Myeloid Cells and CNS Tissue From Lipopolysaccharide- and Vehicle-Injected APP/PS1 Transgenic Mice Implicate Cathepsin Z in Alzheimer Disease. Frontiers in Cellular Neuroscience, 2018, 12, 397	6.1	15
71	First-trimester proteomic profiling identifies novel predictors of gestational diabetes mellitus. <i>PLoS ONE</i> , 2019 , 14, e0214457	3.7	14
70	A novel mass spectrometric strategy "BEMAP" reveals Extensive O-linked protein glycosylation in Enterotoxigenic Escherichia coli. <i>Scientific Reports</i> , 2016 , 6, 32016	4.9	14
69	Snake Venom Extracellular vesicles (SVEVs) reveal wide molecular and functional proteome diversity. <i>Scientific Reports</i> , 2018 , 8, 12067	4.9	14
68	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	3.7	14
67	Characterization of Macrophage Endogenous S-Nitrosoproteome Using a Cysteine-Specific Phosphonate Adaptable Tag in Combination with TiO Chromatography. <i>Journal of Proteome Research</i> , 2018 , 17, 1172-1182	5.6	13
66	Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. <i>Nature Communications</i> , 2020 , 11, 5248	17.4	13
65	Proteomics insights into the responses of Saccharomyces cerevisiae during mixed-culture alcoholic fermentation with Lachancea thermotolerans. <i>FEMS Microbiology Ecology</i> , 2019 , 95,	4.3	12
64	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	5.6	12
63	Characterization of Signaling Pathways Associated with Pancreatic Etell Adaptive Flexibility in Compensation of Obesity-linked Diabetes in Mice. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 971-993	7.6	12

62	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	5.6	11
61	The Splicing Efficiency of Activating HRAS Mutations Can Determine Costello Syndrome Phenotype and Frequency in Cancer. <i>PLoS Genetics</i> , 2016 , 12, e1006039	6	11
60	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	5.8	10
59	Neuronal process structure and growth proteins are targets of heavy PTM regulation during brain development. <i>Journal of Proteomics</i> , 2014 , 101, 77-87	3.9	10
58	Identification and characterization of a novel Chlamydia trachomatis reticulate body protein. <i>FEMS Microbiology Letters</i> , 2002 , 212, 193-202	2.9	10
57	TNF由ffects CREB-mediated neuroprotective signaling pathways of synaptic plasticity in neurons as revealed by proteomics and phospho-proteomics. <i>Oncotarget</i> , 2017 , 8, 60223-60242	3.3	10
56	Development of a Trypanosoma cruzi strain typing assay using MS2 peptide spectral libraries (Tc-STAMS2). <i>PLoS Neglected Tropical Diseases</i> , 2018 , 12, e0006351	4.8	9
55	A Systems-level Characterization of the Differentiation of Human Embryonic Stem Cells into Mesenchymal Stem Cells. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1950-1966	7.6	9
54	Integrated Proteomics Reveals Apoptosis-related Mechanisms Associated with Placental Malaria. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 182-199	7.6	9
53	Quantitative phosphoproteomics uncovers synergy between DNA-PK and FLT3 inhibitors in acute myeloid leukaemia. <i>Leukemia</i> , 2021 , 35, 1782-1787	10.7	9
52	Ageing and amyloidosis underlie the molecular and pathological alterations of tau in a mouse model of familial Alzheimerß disease. <i>Scientific Reports</i> , 2019 , 9, 15758	4.9	8
51	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	3.3	8
50	Glutamate-glutamine homeostasis is perturbed in neurons and astrocytes derived from patient iPSC models of frontotemporal dementia. <i>Molecular Brain</i> , 2020 , 13, 125	4.5	8
49	Depolarization-dependent Induction of Site-specific Changes in Sialylation on linked Glycoproteins in Rat Nerve Terminals. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 1418-1435	7.6	7
48	NS1 codon usage adaptation to humans in pandemic Zika virus. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2018 , 113, e170385	2.6	7
47	Proteomic signatures of neuroinflammation in Alzheimerß disease, multiple sclerosis and ischemic stroke. <i>Expert Review of Proteomics</i> , 2019 , 16, 601-611	4.2	6
46	Glycomic and sialoproteomic data of gastric carcinoma cells overexpressing ST3GAL4. <i>Data in Brief</i> , 2016 , 7, 814-33	1.2	6
45	Age-Dependent Changes in the Sarkosyl-Insoluble Proteome of APPSWE/PS1 E 9 Transgenic Mice Implicate Dysfunctional Mitochondria in the Pathogenesis of Alzheimer ® Disease. <i>Journal of Alzheimerls Disease</i> , 2018 , 64, 1247-1259	4.3	6

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44	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	8.4	5	
43	Quantitative phosphoproteomic analysis of early alterations in protein phosphorylation by 2,3,7,8-tetrachlorodibenzo-p-dioxin. <i>Journal of Proteome Research</i> , 2013 , 12, 866-82	5.6	5	
42	HDL proteome remodeling associates with COVID-19 severity. Journal of Clinical Lipidology, 2021,	4.9	5	
41	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, 4496-45	1 5 .6	5	
40	Proteomic changes during experimental de- and remyelination in the corpus callosum. <i>PLoS ONE</i> , 2020 , 15, e0230249	3.7	5	
39	Automated N-glycan profiling of a mutant Trypanosoma rangeli sialidase expressed in Pichia pastoris, using tandem mass spectrometry and bioinformatics. <i>Glycobiology</i> , 2015 , 25, 1350-61	5.8	4	
38	Dynamic Changes in the Protein Localization in the Nuclear Environment in Pancreatic Ecell after Brief Glucose Stimulation. <i>Journal of Proteome Research</i> , 2018 , 17, 1664-1676	5.6	4	
37	Expression, purification and characterization of the cancer-germline antigen GAGE12I: a candidate for cancer immunotherapy. <i>Protein Expression and Purification</i> , 2010 , 73, 217-22	2	4	
36	Mass spectrometric characterization of posttranslationally modified proteinsphosphorylation. <i>Methods in Molecular Biology</i> , 2004 , 251, 245-62	1.4	4	
35	Serum Proteomics Reveals Alterations in Protease Activity, Axon Guidance, and Visual Phototransduction Pathways in Infants With Exposure to Zika Virus Without Congenital Zika Syndrome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020 , 10, 577819	5.9	4	
34	Pharmacological inhibition of mitochondrial soluble adenylyl cyclase in astrocytes causes activation of AMP-activated protein kinase and induces breakdown of glycogen. <i>Glia</i> , 2021 , 69, 2828-2844	9	4	
33	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	2.1	3	
32	Proteins differentially expressed in human beta-cells-enriched pancreatic islet cultures and human insulinomas. <i>Molecular and Cellular Endocrinology</i> , 2013 , 381, 16-25	4.4	3	
31	Identification of SRSF10 as a regulator of SMN2 ISS-N1. Human Mutation, 2021, 42, 246-260	4.7	3	
30	Novel DNA coding regions and protein arginylation reveal unexplored T. cruzi proteome and PTMs. <i>International Journal of Mass Spectrometry</i> , 2017 , 418, 51-66	1.9	2	
29	Genistein-induced proteome changes in the human endometrial carcinoma cell line, ishikawa. <i>Clinical Proteomics</i> , 2006 , 2, 153-167	5	2	
28	Ultraviolet Photodissociation of Protonated Peptides and Proteins Can Proceed with H/D Scrambling. <i>Analytical Chemistry</i> , 2021 , 93, 691-696	7.8	2	
27	CSF proteome in multiple sclerosis subtypes related to brain lesion transcriptomes. <i>Scientific Reports</i> , 2021 , 11, 4132	4.9	2	

26	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	3.3	1
25	Optimization of calmodulin-affinity chromatography for brain and organelles. <i>EuPA Open Proteomics</i> , 2015 , 8, 55-67	0.1	1
24	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,	3.6	1
23	Divalent Metal Transporter 1 Knock-Down Modulates IL-1 Mediated Pancreatic Beta-Cell Pro-Apoptotic Signaling Pathways through the Autophagic Machinery. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
22	The phosphoproteome of rice leaves responds to water and nitrogen supply. <i>Molecular Omics</i> , 2021 , 17, 706-718	4.4	1
21	N-Glycosylation in isolated rat nerve terminals. <i>Molecular Omics</i> , 2021 , 17, 517-532	4.4	1
20	Systems-wide analysis of glycoprotein conformational changes by limited deglycosylation assay. Journal of Proteomics, 2021 , 248, 104355	3.9	1
19	Long Term Response to Circulating Angiogenic Cells, Unstimulated or Atherosclerotic Pre-Conditioned, in Critical Limb Ischemic Mice. <i>Biomedicines</i> , 2021 , 9,	4.8	1
18	The heart arrhythmia-linked D130G calmodulin mutation causes premature inhibitory autophosphorylation of CaMKII. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2021 , 1868, 119	149	1
17	Comprehensive Protocol to Simultaneously Study Protein Phosphorylation, Acetylation, and N-Linked Sialylated Glycosylation. <i>Methods in Molecular Biology</i> , 2021 , 2261, 55-72	1.4	1
16	Comparative proteome analysis of Chlamydia trachomatis serovar A, D and L2 2002 , 2, 164		1
15	Chapter 12 Phosphoproteomics. Comprehensive Analytical Chemistry, 2008, 52, 275-296	1.9	O
14	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 ,	3.3	0
13	MYC regulates metabolism through vesicular transfer of glycolytic kinases. <i>Open Biology</i> , 2021 , 11, 210	2 7 6	O
12	HSPB1 influences mitochondrial respiration in ER-stressed beta cells. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021 , 1869, 140680	4	O
11	Exportin 1 modulates life span by regulating nucleolar dynamics via the autophagy protein LGG-1/GABARAP <i>Science Advances</i> , 2022 , 8, eabj1604	14.3	O
10	Comprehensive proteomics and sialiomics 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	3.9	0
9	Post-Translational Modifications317-342		

LIST OF PUBLICATIONS

8 A protein-centric view of in vitro biological model systems for schizophrenia. Stem Cells, 2021, 39, 1569-15878

7	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	4.9
6	Quantitative phosphoproteomics of depolarization-dependent protein phosphorylation in nerve terminals. <i>FASEB Journal</i> , 2010 , 24, 905.2	0.9
5	Detection of proteolytic signatures for Parkinson® disease. Future Neurology, 2016, 11, 15-32	1.5
4	Linking inherent O-Linked Protein Glycosylation of YghJ to Increased Antigen Potential. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 705468	5.9
3	The impact of Zika virus exposure on the placental proteomic profile. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2022 , 1868, 166270	6.9
2	Characterization of Differentially Abundant Proteins Among Strains Isolated From Atypical or Typical Lesions <i>Frontiers in Cellular and Infection Microbiology</i> , 2022 , 12, 824968	5.9
1	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). Neuro-Oncology 2022, 24, i18-i19	1