

A practical guide to the MaxQuant computational platform for proteomics

Nature Protocols

4, 698-705

DOI: [10.1038/nprot.2009.36](https://doi.org/10.1038/nprot.2009.36)

Citation Report

#	ARTICLE	IF	CITATIONS
5	Studies of physiologic tremor in the dog. <i>Neurology</i> , 1964, 14, 50-50.	1.1	11
6	Tandem Affinity Purification of Ciliopathy-Associated Protein Complexes. <i>Methods in Cell Biology</i> , 2009, 91, 143-160.	1.1	19
7	Unbiased RNA-protein interaction screen by quantitative proteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10626-10631.	7.1	124
8	A Dual Pressure Linear Ion Trap Orbitrap Instrument with Very High Sequencing Speed. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2759-2769.	3.8	398
9	The B-lymphoid Grb2 interaction code. <i>Immunological Reviews</i> , 2009, 232, 135-149.	6.0	38
10	Computational principles of determining and improving mass precision and accuracy for proteome measurements in an Orbitrap. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 1477-1485.	2.8	65
11	Recent Applications of Phosphoproteomics. <i>Current Proteomics</i> , 2010, 7, 168-176.	0.3	2
12	Establishment of a Protein Frequency Library and Its Application in the Reliable Identification of Specific Protein Interaction Partners. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 861-879.	3.8	63
13	Quantitation in Mass-Spectrometry-Based Proteomics. <i>Annual Review of Plant Biology</i> , 2010, 61, 491-516.	18.7	301
14	Proteomic basics – quantification and post-translational modifications of proteins: The 3rd European Summer School in Kloster Neustift. <i>Journal of Proteomics</i> , 2010, 73, 697-700.	2.4	0
15	New Developments of Quantitative Mass Spectrometry-based Proteomics. <i>Chinese Journal of Analytical Chemistry</i> , 2010, 38, 434-441.	1.7	5
16	p53-Dependent subcellular proteome localization following DNA damage. <i>Proteomics</i> , 2010, 10, 4087-4097.	2.2	51
17	<i>Bacillus subtilis</i> BY-kinase PtkA controls enzyme activity and localization of its protein substrates. <i>Molecular Microbiology</i> , 2010, 77, 287-299.	2.5	60
18	Proteomics: a pragmatic perspective. <i>Nature Biotechnology</i> , 2010, 28, 695-709.	17.5	374
19	SUMOylation of the GTPase Rac1 is required for optimal cell migration. <i>Nature Cell Biology</i> , 2010, 12, 1078-1085.	10.3	149
20	High-stringency tandem affinity purification of proteins conjugated to ubiquitin-like moieties. <i>Nature Protocols</i> , 2010, 5, 873-882.	12.0	16
21	Quantitative Phosphoproteomics Dissection of Seven-transmembrane Receptor Signaling Using Full and Biased Agonists. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1540-1553.	3.8	135
22	The Rapamycin-sensitive Phosphoproteome Reveals That TOR Controls Protein Kinase A Toward Some But Not All Substrates. <i>Molecular Biology of the Cell</i> , 2010, 21, 3475-3486.	2.1	226

#	ARTICLE	IF	CITATIONS
23	The SILAC Fly Allows for Accurate Protein Quantification in Vivo. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2173-2183.	3.8	150
24	Proteomics on an Orbitrap Benchtop Mass Spectrometer Using All-ion Fragmentation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2252-2261.	3.8	213
25	Dynamics of the Skeletal Muscle Secretome during Myoblast Differentiation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2482-2496.	3.8	248
26	Quantitative phosphoproteomics. <i>Cell Cycle</i> , 2010, 9, 3479-3484.	2.6	7
27	Proteogenomics of <i>Pristionchus pacificus</i> reveals distinct proteome structure of nematode models. <i>Genome Research</i> , 2010, 20, 837-846.	5.5	155
28	Synaptonemal Complex Protein SYCP3 Exists in Two Isoforms Showing Different Conservation in Mammalian Evolution. <i>Cytogenetic and Genome Research</i> , 2010, 128, 162-168.	1.1	14
29	Proteome, Phosphoproteome, and N-Glycoproteome Are Quantitatively Preserved in Formalin-Fixed Paraffin-Embedded Tissue and Analyzable by High-Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2010, 9, 3688-3700.	3.7	219
30	Approaches and Applications of Quantitative LC-MS for Proteomics and Activomics. <i>Methods in Molecular Biology</i> , 2010, 658, 3-17.	0.9	10
31	A Quantitative Proteomics Analysis of Subcellular Proteome Localization and Changes Induced by DNA Damage. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 457-470.	3.8	164
32	Differential Phosphoproteomics of Fibroblast Growth Factor Signaling: Identification of Src Family Kinase-Mediated Phosphorylation Events. <i>Journal of Proteome Research</i> , 2010, 9, 2317-2328.	3.7	46
33	Quantitative Proteomics Reveals a "Poised Quiescence" Cellular State after Triggering the DNA Replication Origin Activation Checkpoint. <i>Journal of Proteome Research</i> , 2010, 9, 5445-5460.	3.7	6
34	A Fully Automated System with Online Sample Loading, Isotope Dimethyl Labeling and Multidimensional Separation for High-Throughput Quantitative Proteome Analysis. <i>Analytical Chemistry</i> , 2010, 82, 3007-3015.	6.5	66
35	Phosphopeptide Analysis Reveals Two Discrete Clusters of Phosphorylation in the N-Terminus and the Roc Domain of the Parkinson-Disease Associated Protein Kinase LRRK2. <i>Journal of Proteome Research</i> , 2010, 9, 1738-1745.	3.7	132
36	Yeast Expression Proteomics by High-Resolution Mass Spectrometry. <i>Methods in Enzymology</i> , 2010, 470, 259-280.	1.0	8
37	Site-Specific Identification of SUMO-2 Targets in Cells Reveals an Inverted SUMOylation Motif and a Hydrophobic Cluster SUMOylation Motif. <i>Molecular Cell</i> , 2010, 39, 641-652.	9.7	255
38	HSP90 and Its R2TP/Prefoldin-like Cochaperone Are Involved in the Cytoplasmic Assembly of RNA Polymerase II. <i>Molecular Cell</i> , 2010, 39, 912-924.	9.7	246
39	Protein Quantitation Using Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2010, 673, 211-222.	0.9	59
40	Bioinformatics for LC-MS/MS-Based Proteomics. <i>Methods in Molecular Biology</i> , 2010, 658, 61-91.	0.9	22

#	ARTICLE	IF	CITATIONS
41	Antimicrobial Activity of Lipophilic Avian Eggshell Surface Extracts. <i>Journal of Agricultural and Food Chemistry</i> , 2010, 58, 10156-10161.	5.2	20
42	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) Applied to Quantitative Proteomics of <i>Bacillus subtilis</i> . <i>Journal of Proteome Research</i> , 2010, 9, 3638-3646.	3.7	108
43	Quantitative analysis of the secretion of the MCP family of chemokines by muscle cells. <i>Molecular BioSystems</i> , 2011, 7, 311-321.	2.9	41
44	Ulk1-mediated phosphorylation of AMPK constitutes a negative regulatory feedback loop. <i>Autophagy</i> , 2011, 7, 696-706.	9.1	220
45	Pulsed Stable Isotope Labeling of Amino Acids in Cell Culture Uncovers the Dynamic Interactions between HIV-1 and the Monocyte-Derived Macrophage. <i>Journal of Proteome Research</i> , 2011, 10, 2852-2862.	3.7	20
46	Deep and Highly Sensitive Proteome Coverage by LC-MS/MS Without Prefractionation. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003699.	3.8	311
47	GeLCMS for In-Depth Protein Characterization and Advanced Analysis of Proteomes. <i>Methods in Molecular Biology</i> , 2011, 753, 143-155.	0.9	36
48	Proteome-Wide Mapping of the <i>Drosophila</i> Acetylome Demonstrates a High Degree of Conservation of Lysine Acetylation. <i>Science Signaling</i> , 2011, 4, ra48.	3.6	243
49	A Case Study on the Comparison of Different Software Tools for Automated Quantification of Peptides. <i>Methods in Molecular Biology</i> , 2011, 753, 373-398.	0.9	14
50	Uncovering Ubiquitin and Ubiquitin-like Signaling Networks. <i>Chemical Reviews</i> , 2011, 111, 7923-7940.	47.7	91
52	Quantitative Analysis of the Intra- and Inter-Individual Variability of the Normal Urinary Proteome. <i>Journal of Proteome Research</i> , 2011, 10, 637-645.	3.7	215
53	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
54	Analytical Aspects of Proteomics: 2009–2010. <i>Analytical Chemistry</i> , 2011, 83, 4407-4426.	6.5	28
55	Shotgun proteomic analysis of the unicellular alga <i>Ostreococcus tauri</i> . <i>Journal of Proteomics</i> , 2011, 74, 2060-2070.	2.4	56
56	Conserved and Unique Features of the Maize (<i>Zea mays</i> L.) Root Hair Proteome. <i>Journal of Proteome Research</i> , 2011, 10, 2525-2537.	3.7	41
57	Extracting gene function from protein–protein interactions using Quantitative BAC Interactomics (QUBIC). <i>Methods</i> , 2011, 53, 453-459.	3.8	96
58	Analyzing protein–protein interactions by quantitative mass spectrometry. <i>Methods</i> , 2011, 54, 387-395.	3.8	60
59	Unraveling the dynamics of protein interactions with quantitative mass spectrometry. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2011, 46, 216-228.	5.2	25

#	ARTICLE	IF	CITATIONS
60	Proteomics moves from expression to turnover: update and future perspective. Expert Review of Proteomics, 2011, 8, 325-334.	3.0	26
61	Trends and Developments in Bioinformatics in 2010: Prospects and Perspectives. Yearbook of Medical Informatics, 2011, 20, 146-155.	1.0	0
62	Quantitative Proteomics Identify Novel miR-155 Target Proteins. PLoS ONE, 2011, 6, e22146.	2.5	28
63	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) – an Introduction for Biologists. Current Proteomics, 2011, 8, 2-16.	0.3	4
64	Use of stable isotope labeling by amino acids in cell culture as a spike-in standard in quantitative proteomics. Nature Protocols, 2011, 6, 147-157.	12.0	265
65	Interleukin-2 signaling pathway analysis by quantitative phosphoproteomics. Journal of Proteomics, 2011, 75, 177-191.	2.4	42
66	Proteomic biosignatures for monocyte–macrophage differentiation. Cellular Immunology, 2011, 271, 239-255.	3.0	18
67	In Vivo Quantitative Proteomics: The SILAC Mouse. Methods in Molecular Biology, 2011, 757, 435-450.	0.9	77
68	Analysis of Phosphoproteomics Data. Methods in Molecular Biology, 2011, 696, 41-57.	0.9	12
69	Viruses and microRNAs: a toolbox for systematic analysis. Wiley Interdisciplinary Reviews RNA, 2011, 2, 787-801.	6.4	8
70	Software Lock Mass by Two-Dimensional Minimization of Peptide Mass Errors. Journal of the American Society for Mass Spectrometry, 2011, 22, 1373-1380.	2.8	138
71	Evaluating the potential of a novel oral lesion exudate collection method coupled with mass spectrometry-based proteomics for oral cancer biomarker discovery. Clinical Proteomics, 2011, 8, 13.	2.1	12
72	Catch me if you can: Mass spectrometry–based phosphoproteomics and quantification strategies. Proteomics, 2011, 11, 554-570.	2.2	90
73	Global identification of miR-373-regulated genes in breast cancer by quantitative proteomics. Proteomics, 2011, 11, 912-920.	2.2	78
74	A systematic analysis of the effects of increasing degrees of serum immunodepletion in terms of depth of coverage and other key aspects in top-down and bottom-up proteomic analyses. Proteomics, 2011, 11, 2222-2235.	2.2	64
75	MassChroQ: A versatile tool for mass spectrometry quantification. Proteomics, 2011, 11, 3572-3577.	2.2	255
76	Complex phosphorylation dynamics control the composition of the Syk interactome in B cells. European Journal of Immunology, 2011, 41, 1550-1562.	2.9	38
77	Monitoring cytoplasmic protein complexes with blue native gel electrophoresis and stable isotope labelling with amino acids in cell culture: Analysis of changes in the 20S proteasome. Electrophoresis, 2011, 32, 1819-1823.	2.4	7

#	ARTICLE	IF	CITATIONS
78	B Cell Receptor-Mediated Antigen Gathering Requires Ubiquitin Ligase Cbl and Adaptors Grb2 and Dok-3 to Recruit Dynein to the Signaling Microcluster. <i>Immunity</i> , 2011, 34, 905-918.	14.3	88
79	Preventing arginine-to-proline conversion in a cell-line-independent manner during cell cultivation under stable isotope labeling by amino acids in cell culture (SILAC) conditions. <i>Analytical Biochemistry</i> , 2011, 412, 123-125.	2.4	50
80	Quantitative Shotgun Proteomics Using a Uniform 15N-Labeled Standard to Monitor Proteome Dynamics in Time Course Experiments Reveals New Insights into the Heat Stress Response of <i>Chlamydomonas reinhardtii</i> . <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.004739.	3.8	83
81	Quantitative Proteomics and Transcriptomics Addressing the Estrogen Receptor Subtype-mediated Effects in T47D Breast Cancer Cells Exposed to the Phytoestrogen Genistein. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.002170.	3.8	40
82	Proteomics in the microbial sciences. <i>Bioengineered Bugs</i> , 2011, 2, 17-30.	1.7	21
83	A Screen for Novel Phosphoinositide 3-kinase Effector Proteins. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003178.	3.8	26
84	Identification and characterization of a novel ubiquitous nucleolar protein $\hat{\alpha}$ NARR $\hat{\alpha}$ ™ encoded by a gene overlapping the rab34 oncogene. <i>Nucleic Acids Research</i> , 2011, 39, 7103-7113.	14.5	10
85	Global Phosphoproteome Profiling Reveals Unanticipated Networks Responsive to Cisplatin Treatment of Embryonic Stem Cells. <i>Molecular and Cellular Biology</i> , 2011, 31, 4964-4977.	2.3	56
86	Chromatin Affinity Purification and Quantitative Mass Spectrometry Defining the Interactome of Histone Modification Patterns. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.005371.	3.8	74
87	The B-cell antigen receptor signals through a preformed transducer module of SLP65 and CIN85. <i>EMBO Journal</i> , 2011, 30, 3620-3634.	7.8	64
88	Protein Kinase C and NF- $\hat{\kappa}$ B $\hat{\alpha}$ €“Dependent CD4 Downregulation in Macrophages Induced by T Cell-Derived Soluble Factors: Consequences for HIV-1 Infection. <i>Journal of Immunology</i> , 2011, 187, 748-759.	0.8	12
89	Mass Spectrometric-Based Quantitative Proteomics Using SILAC. <i>Methods in Enzymology</i> , 2011, 500, 133-150.	1.0	20
90	Quantitative in vivo Analyses Reveal Calcium-dependent Phosphorylation Sites and Identifies a Novel Component of the Toxoplasma Invasion Motor Complex. <i>PLoS Pathogens</i> , 2011, 7, e1002222.	4.7	85
91	The Salivary Secretome of the Tsetse Fly <i>Glossina pallidipes</i> (Diptera: Glossinidae) Infected by Salivary Gland Hypertrophy Virus. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1371.	3.0	21
92	CYK4 inhibits Rac1-dependent PAK1 and ARHGEF7 effector pathways during cytokinesis. <i>Journal of Cell Biology</i> , 2012, 198, 865-880.	5.2	111
93	The Archaeal Proteasome Is Regulated by a Network of AAA ATPases. <i>Journal of Biological Chemistry</i> , 2012, 287, 39254-39262.	3.4	42
94	Quantitative Proteomics Profiling of Murine Mammary Gland Cells Unravels Impact of Annexin-1 on DNA Damage Response, Cell Adhesion, and Migration. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 381-393.	3.8	43
95	Modulation of Neuronal Pentraxin 1 Expression in Rat Pancreatic $\hat{\beta}$ 2-Cells Submitted to Chronic Glucotoxic Stress. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 244-254.	3.8	21

#	ARTICLE	IF	CITATIONS
96	A Quantitative Spatial Proteomics Analysis of Proteome Turnover in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.011429.	3.8	332
97	Quantitative Proteomics Reveals Regulation of Karyopherin Subunit Alpha-2 (KPNA2) and Its Potential Novel Cargo Proteins in Nonsmall Cell Lung Cancer. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1105-1122.	3.8	72
98	GIT1 Phosphorylation on Serine 46 by PKD3 Regulates Paxillin Trafficking and Cellular Protrusive Activity. <i>Journal of Biological Chemistry</i> , 2012, 287, 34604-34613.	3.4	23
99	Systematic Analysis of Protein Pools, Isoforms, and Modifications Affecting Turnover and Subcellular Localization. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013680.	3.8	48
100	System Response of Metabolic Networks in <i>Chlamydomonas reinhardtii</i> to Total Available Ammonium. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 973-988.	3.8	93
101	Global Quantitative Phosphoproteome Analysis of Human Tumor Xenografts Treated with a CD44 Antagonist. <i>Cancer Research</i> , 2012, 72, 4329-4339.	0.9	33
102	High Mass Accuracy Phosphopeptide Identification Using Tandem Mass Spectra. <i>International Journal of Proteomics</i> , 2012, 2012, 1-5.	2.0	4
103	Precision, Proteome Coverage, and Dynamic Range of Arabidopsis Proteome Profiling Using ¹⁵ N Metabolic Labeling and Label-free Approaches. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 619-628.	3.8	16
104	Proteome-wide Analysis of Lysine Acetylation Suggests its Broad Regulatory Scope in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1510-1522.	3.8	255
105	Mitochondrial Quality Control Mediated by PINK1 and Parkin: Links to Parkinsonism. <i>Cold Spring Harbor Perspectives in Biology</i> , 2012, 4, a011338-a011338.	5.5	273
106	Fast-Forward Genetics Identifies Plant CPL Phosphatases as Regulators of miRNA Processing Factor HYL1. <i>Cell</i> , 2012, 151, 859-870.	28.9	219
107	Detection and Quantitation of SUMO Chains by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2012, 832, 239-247.	0.9	8
108	Mediator Phosphorylation Prevents Stress Response Transcription During Non-stress Conditions. <i>Journal of Biological Chemistry</i> , 2012, 287, 44017-44026.	3.4	33
109	Urinary secretion and extracellular aggregation of mutant uromodulin isoforms. <i>Kidney International</i> , 2012, 81, 769-778.	5.2	20
110	Proteomics Pipeline for Biomarker Discovery of Laser Capture Microdissected Breast Cancer Tissue. <i>Journal of Mammary Gland Biology and Neoplasia</i> , 2012, 17, 155-164.	2.7	72
111	Data extraction from proteomics raw data: An evaluation of nine tandem MS tools using a large Orbitrap data set. <i>Journal of Proteomics</i> , 2012, 75, 5293-5303.	2.4	22
112	Quantitative proteomics reveals novel functions of osteoclast-associated receptor in STAT signaling and cell adhesion in human endothelial cells. <i>Journal of Molecular and Cellular Cardiology</i> , 2012, 53, 829-837.	1.9	15
113	Quantitative proteomic analysis of yeast DNA replication proteins. <i>Methods</i> , 2012, 57, 196-202.	3.8	20

#	ARTICLE	IF	CITATIONS
114	Comparative and Targeted Proteomic Analyses of Urinary Microparticles from Bladder Cancer and Hernia Patients. <i>Journal of Proteome Research</i> , 2012, 11, 5611-5629.	3.7	185
115	Delicate Analysis of Post-Translational Modifications on Dishevelled 3. <i>Journal of Proteome Research</i> , 2012, 11, 3829-3837.	3.7	12
116	Proteomic Plasma Membrane Profiling Reveals an Essential Role for gp96 in the Cell Surface Expression of LDLR Family Members, Including the LDL Receptor and LRP6. <i>Journal of Proteome Research</i> , 2012, 11, 1475-1484.	3.7	68
117	C-Terminal Heat Shock Protein 90 Inhibitor Decreases Hyperglycemia-induced Oxidative Stress and Improves Mitochondrial Bioenergetics in Sensory Neurons. <i>Journal of Proteome Research</i> , 2012, 11, 2581-2593.	3.7	47
118	Triple SILAC to Determine Stimulus Specific Interactions in the Wnt Pathway. <i>Journal of Proteome Research</i> , 2012, 11, 982-994.	3.7	63
119	Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC)-based Quantitative Proteomics Study of a Thyroid Hormone-regulated Secretome in Human Hepatoma Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.011270.	3.8	31
120	Quantitative Proteomic Analysis of Membrane Proteins Involved in Astroglial Differentiation of Neural Stem Cells by SILAC Labeling Coupled with LC-MS/MS. <i>Journal of Proteome Research</i> , 2012, 11, 829-838.	3.7	25
121	Identifying Cellular Targets of Small-Molecule Probes and Drugs with Biochemical Enrichment and SILAC. <i>Methods in Molecular Biology</i> , 2012, 803, 129-140.	0.9	25
122	Proteomic Analysis of Mitotic RNA Polymerase II Reveals Novel Interactors and Association With Proteins Dysfunctional in Disease. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.011767.	3.8	13
123	Toward objective evaluation of proteomic algorithms. <i>Nature Methods</i> , 2012, 9, 455-456.	19.0	35
124	In Vivo Quantitative Proteome Profiling: Planning and Evaluation of SILAC Experiments. <i>Methods in Molecular Biology</i> , 2012, 893, 175-199.	0.9	15
125	Systems-wide analysis of ubiquitylation dynamics reveals a key role for PAF15 ubiquitylation in DNA-damage bypass. <i>Nature Cell Biology</i> , 2012, 14, 1089-1098.	10.3	234
126	Temporal Profiling and Pulsed SILAC Labeling Identify Novel Secreted Proteins During Ex Vivo Osteoblast Differentiation of Human Stromal Stem Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 989-1007.	3.8	75
127	Analysis of protein mixtures from whole-cell extracts by single-run nanoLC-MS/MS using ultralong gradients. <i>Nature Protocols</i> , 2012, 7, 882-890.	12.0	106
128	Phosphotyrosine mediated protein interactions of the discoidin domain receptor 1. <i>Journal of Proteomics</i> , 2012, 75, 3465-3477.	2.4	63
129	Quantitative proteomic analysis of human osteoblast-like MG-63 cells in response to bioinert implant material titanium and polyetheretherketone. <i>Journal of Proteomics</i> , 2012, 75, 3560-3573.	2.4	45
130	Improved characterization of the insulin secretory granule proteomes. <i>Journal of Proteomics</i> , 2012, 75, 4620-4631.	2.4	46
131	In-depth proteomic analysis of a mollusc shell: acid-soluble and acid-insoluble matrix of the limpet <i>Lottia gigantea</i> . <i>Proteome Science</i> , 2012, 10, 28.	1.7	79

#	ARTICLE	IF	CITATIONS
132	UV-sensitive syndrome protein UVSSA recruits USP7 to regulate transcription-coupled repair. <i>Nature Genetics</i> , 2012, 44, 598-602.	21.4	213
133	Proteomics-based identification of low-abundance signaling and regulatory protein complexes in native plant tissues. <i>Nature Protocols</i> , 2012, 7, 2144-2158.	12.0	90
134	Highly Efficient Extraction of Cellular Nucleic Acid Associated Proteins in Vitro with Magnetic Oxidized Carbon Nanotubes. <i>Analytical Chemistry</i> , 2012, 84, 10454-10462.	6.5	22
135	Measuring Phosphorylation-Specific Changes in Response to Kinase Inhibitors in Mammalian Cells Using Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2012, 795, 217-231.	0.9	2
136	Analysis of the <i>Plasmodium falciparum</i> proteasome using Blue Native PAGE and label-free quantitative mass spectrometry. <i>Amino Acids</i> , 2012, 43, 1119-1129.	2.7	20
137	Proteome Alterations in Primary Human Alveolar Macrophages in Response to Influenza A Virus Infection. <i>Journal of Proteome Research</i> , 2012, 11, 4091-4101.	3.7	38
138	SILEC: a protocol for generating and using isotopically labeled coenzyme A mass spectrometry standards. <i>Nature Protocols</i> , 2012, 7, 1-11.	12.0	61
139	SILAC for the Study of Mammalian Cell Lines and Yeast Protein Complexes. <i>Methods in Molecular Biology</i> , 2012, 893, 201-221.	0.9	18
140	Quantitative Analysis of S-Nitrosylated Proteins. <i>Methods in Molecular Biology</i> , 2012, 893, 405-416.	0.9	7
141	Mass spectrometry-based phosphoproteomics in cancer research. <i>Frontiers in Biology</i> , 2012, 7, 566-586.	0.7	1
142	Quantitative Methods in Proteomics. <i>Methods in Molecular Biology</i> , 2012, , .	0.9	8
143	A Critical Appraisal of Techniques, Software Packages, and Standards for Quantitative Proteomic Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 431-442.	2.0	50
144	Identifying Chromatin Readers Using a SILAC-Based Histone Peptide Pull-Down Approach. <i>Methods in Enzymology</i> , 2012, 512, 137-160.	1.0	14
145	Quantitative maps of protein phosphorylation sites across 14 different rat organs and tissues. <i>Nature Communications</i> , 2012, 3, 876.	12.8	307
146	IsoQuant: A Software Tool for Stable Isotope Labeling by Amino Acids in Cell Culture-Based Mass Spectrometry Quantitation. <i>Analytical Chemistry</i> , 2012, 84, 4535-4543.	6.5	21
147	Integrin and Cell Adhesion Molecules. <i>Methods in Molecular Biology</i> , 2012, , .	0.9	2
148	Determining In Vivo Phosphorylation Sites Using Mass Spectrometry. <i>Current Protocols in Molecular Biology</i> , 2012, 98, Unit18.19.1-27.	2.9	27
150	1D and 2D annotation enrichment: a statistical method integrating quantitative proteomics with complementary high-throughput data. <i>BMC Bioinformatics</i> , 2012, 13, S12.	2.6	542

#	ARTICLE	IF	CITATIONS
151	Quantitative proteomics reveals altered expression of extracellular matrix related proteins of human primary dermal fibroblasts in response to sulfated hyaluronan and collagen applied as artificial extracellular matrix. <i>Journal of Materials Science: Materials in Medicine</i> , 2012, 23, 3053-3065.	3.6	13
152	Kinase Inhibitors. <i>Methods in Molecular Biology</i> , 2012, , .	0.9	2
153	Characterization of the Phosphoproteome in SLE Patients. <i>PLoS ONE</i> , 2012, 7, e53129.	2.5	7
155	Quantitative Proteomics for Investigation of Secreted Factors: Focus on Muscle Secretome. , 2012, , .		0
157	Workflow for analysis of high mass accuracy salivary data set using <sc>M</sc>ax<sc>Q</sc>uant and <sc>P</sc>rotein<sc>P</sc>ilot search algorithm. <i>Proteomics</i> , 2012, 12, 1726-1730.	2.2	20
158	Resolving protein interactions and complexes by affinity purification followed by labelâ€based quantitative mass spectrometry. <i>Proteomics</i> , 2012, 12, 1623-1638.	2.2	48
159	Direct comparison of <sc>MS</sc>â€based labelâ€free and <sc>SILAC</sc> quantitative proteome profiling strategies in primary retinal <sc>M</sc>Ã¼ller cells. <i>Proteomics</i> , 2012, 12, 1902-1911.	2.2	114
160	SIRT1 Negatively Regulates the Activities, Functions, and Protein Levels of hMOF and TIP60. <i>Molecular and Cellular Biology</i> , 2012, 32, 2823-2836.	2.3	81
161	Mitochondrial proteomicsâ€a tool for the study of metabolic disorders. <i>Journal of Inherited Metabolic Disease</i> , 2012, 35, 715-726.	3.6	44
162	Cold acclimation induces changes in Arabidopsis tonoplast protein abundance and activity and alters phosphorylation of tonoplast monosaccharide transporters. <i>Plant Journal</i> , 2012, 69, 529-541.	5.7	116
163	Mass spectrometry-based identification and characterisation of lysine and arginine methylation in the human proteome. <i>Molecular BioSystems</i> , 2013, 9, 2231.	2.9	141
164	Molecular Dermatology. <i>Methods in Molecular Biology</i> , 2013, , .	0.9	4
165	Cell Senescence. <i>Methods in Molecular Biology</i> , 2013, , .	0.9	4
166	Gene Regulation. <i>Methods in Molecular Biology</i> , 2013, , .	0.9	1
167	Chronic high glucose induced INS-1Î² cell mitochondrial dysfunction: A comparative mitochondrial proteome with SILAC. <i>Proteomics</i> , 2013, 13, 3030-3039.	2.2	16
169	Na ⁺ /K ⁺ -ATPase Is a New Interacting Partner for the Neuronal Glycine Transporter GlyT2 That Downregulates Its Expression In Vitro and In Vivo. <i>Journal of Neuroscience</i> , 2013, 33, 14269-14281.	3.6	35
170	Time-resolved quantitative proteomics implicates the core snRNP protein, SmB, together with the Survival of Motor Neuron protein, in neural trafficking. <i>Journal of Cell Science</i> , 2014, 127, 812-27.	2.0	15
171	Evaluation of <i>Drosophila</i> Metabolic Labeling Strategies for <i>in Vivo</i> Quantitative Proteomic Analyses with Applications to Early Pupa Formation and Amino Acid Starvation. <i>Journal of Proteome Research</i> , 2013, 12, 2138-2150.	3.7	13

#	ARTICLE	IF	CITATIONS
172	Argonaute2 Regulates the Pancreatic Î²-Cell Secretome. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1214-1225.	3.8	42
173	The proteome of the calcified layer organic matrix of turkey (<i>Meleagris gallopavo</i>) eggshell. <i>Proteome Science</i> , 2013, 11, 40.	1.7	41
174	TIMP-1 Increases Expression and Phosphorylation of Proteins Associated with Drug Resistance in Breast Cancer Cells. <i>Journal of Proteome Research</i> , 2013, 12, 4136-4151.	3.7	36
175	Yeast ribosomal protein L7 and its homologue Rlp7 are simultaneously present at distinct sites on pre-60S ribosomal particles. <i>Nucleic Acids Research</i> , 2013, 41, 9461-9470.	14.5	22
176	Redox Proteomics: Chemical Principles, Methodological Approaches and Biological/Biomedical Promises. <i>Chemical Reviews</i> , 2013, 113, 596-698.	47.7	222
177	System-wide identification of RNA-binding proteins by interactome capture. <i>Nature Protocols</i> , 2013, 8, 491-500.	12.0	176
178	The emerging field of chemo- and pharmacoproteomics. <i>Proteomics - Clinical Applications</i> , 2013, 7, 171-180.	1.6	15
179	An immunoaffinity purification method for the proteomic analysis of ubiquitinated protein complexes. <i>Analytical Biochemistry</i> , 2013, 440, 227-236.	2.4	25
180	Analysis of the STAT3 interactome using in-situ biotinylation and SILAC. <i>Journal of Proteomics</i> , 2013, 94, 370-386.	2.4	10
181	Retinoic acid-induced protein 3: Identification and characterisation of a novel prognostic colon cancer biomarker. <i>European Journal of Cancer</i> , 2013, 49, 531-539.	2.8	39
182	The Human Diabetes Proteome Project (HDPP): From network biology to targets for therapies and prevention. <i>Translational Proteomics</i> , 2013, 1, 3-11.	1.2	18
183	Comparative proteome approach demonstrates that platelet-derived growth factor C and D efficiently induce proliferation while maintaining multipotency of hMSCs. <i>Experimental Cell Research</i> , 2013, 319, 2649-2662.	2.6	11
184	The proteome of Toll-like receptor 3-stimulated human immortalized fibroblasts: Implications for susceptibility to herpes simplex virus encephalitis. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 131, 1157-1166.	2.9	12
186	Protein Analysis by Shotgun/Bottom-up Proteomics. <i>Chemical Reviews</i> , 2013, 113, 2343-2394.	47.7	1,171
187	Circadian acetylome reveals regulation of mitochondrial metabolic pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3339-3344.	7.1	133
188	Protein lysine acetylation analysis: current MS-based proteomic technologies. <i>Analyst</i> , 2013, 138, 1628.	3.5	34
190	Identifying Specific Protein-DNA Interactions Using SILAC-Based Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2013, 977, 137-157.	0.9	21
191	Bioanalysis of Eukaryotic Organelles. <i>Chemical Reviews</i> , 2013, 113, 2733-2811.	47.7	110

#	ARTICLE	IF	CITATIONS
192	Secretome Analyses of $\hat{1}^2$ Stimulated Hippocampal Astrocytes Reveal that CXCL10 is Involved in Astrocyte Migration. <i>Journal of Proteome Research</i> , 2013, 12, 832-843.	3.7	30
193	In vitro bioactivity and biocompatibility evaluation of bulk nanostructured titanium in osteoblast-like cells by quantitative proteomic analysis. <i>Journal of Materials Chemistry B</i> , 2013, 1, 1926.	5.8	10
194	Global Dynamics of the <i>Escherichia coli</i> Proteome and Phosphoproteome During Growth in Minimal Medium. <i>Journal of Proteome Research</i> , 2013, 12, 2611-2621.	3.7	110
195	Protein tyrosine phosphatase SHP2/PTPN11 mistargeting as a consequence of SH2-domain point mutations associated with Noonan Syndrome and leukemia. <i>Journal of Proteomics</i> , 2013, 84, 132-147.	2.4	18
196	Global Protein Quantification of Mouse Heart Tissue Based on the SILAC Mouse. <i>Methods in Molecular Biology</i> , 2013, 1005, 39-52.	0.9	13
197	High Performance Computational Analysis of Large-scale Proteome Data Sets to Assess Incremental Contribution to Coverage of the Human Genome. <i>Journal of Proteome Research</i> , 2013, 12, 2858-2868.	3.7	43
198	Citric Acid-Assisted Two-Step Enrichment with TiO_2 Enhances the Separation of Multi- and Monophosphorylated Peptides and Increases Phosphoprotein Profiling. <i>Journal of Proteome Research</i> , 2013, 12, 2467-2476.	3.7	28
199	Relative quantification of proteasome activity by activity-based protein profiling and LC-MS/MS. <i>Nature Protocols</i> , 2013, 8, 1155-1168.	12.0	77
200	$\hat{1}^21$ - and $\hat{1}^2v$ -class integrins cooperate to regulate myosin $\hat{1}^1$ during rigidity sensing of fibronectin-based microenvironments. <i>Nature Cell Biology</i> , 2013, 15, 625-636.	10.3	386
201	Global protein phosphorylation dynamics during deoxynivalenol-induced ribotoxic stress response in the macrophage. <i>Toxicology and Applied Pharmacology</i> , 2013, 268, 201-211.	2.8	38
202	Unbiased Characterization of the Senescence-Associated Secretome Using SILAC-Based Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2013, 965, 175-184.	0.9	13
203	Quantitative Proteomic Characterization of Ethanol-Responsive Pathways in Rat Microglial Cells. <i>Journal of Proteome Research</i> , 2013, 12, 2067-2077.	3.7	34
204	Aurora B suppresses microtubule dynamics and limits central spindle size by locally activating KIF4A. <i>Journal of Cell Biology</i> , 2013, 202, 605-621.	5.2	117
205	A quantitative telomeric chromatin isolation protocol identifies different telomeric states. <i>Nature Communications</i> , 2013, 4, 2848.	12.8	95
206	Quantitative Proteome Analysis of Alveolar Type-II Cells Reveals a Connection of Integrin Receptor Subunits Beta 2/6 and WNT Signaling. <i>Journal of Proteome Research</i> , 2013, 12, 5598-5608.	3.7	10
207	Sulfated Hyaluronan Containing Collagen Matrices Enhance Cell-Matrix-Interaction, Endocytosis, and Osteogenic Differentiation of Human Mesenchymal Stromal Cells. <i>Journal of Proteome Research</i> , 2013, 12, 378-389.	3.7	62
208	Identification of a Metabolizing Enzyme in Human Kidney by Proteomic Correlation Profiling. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2313-2323.	3.8	15
209	Serum aminoacylase-1 is a novel biomarker with potential prognostic utility for long-term outcome in patients with delayed graft function following renal transplantation. <i>Kidney International</i> , 2013, 84, 1214-1225.	5.2	47

#	ARTICLE	IF	CITATIONS
210	A SILAC-based Approach Identifies Substrates of Caspase-dependent Cleavage upon TRAIL-induced Apoptosis. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1436-1450.	3.8	27
211	Insm1 controls development of pituitary endocrine cells and requires a SNAG domain for function and for recruitment of histone-modifying factors. <i>Development (Cambridge)</i> , 2013, 140, 4947-4958.	2.5	46
212	Integrative Omics Approach Discovers Dynamic and Regulatory Features of Bacterial Stress Responses. <i>PLoS Genetics</i> , 2013, 9, e1003576.	3.5	57
213	Mechanisms of Human Adenovirus Inactivation by Sunlight and UVC Light as Examined by Quantitative PCR and Quantitative Proteomics. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1325-1332.	3.1	59
214	Stable Isotope Labeling in Zebrafish Allows in Vivo Monitoring of Cardiac Morphogenesis. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1502-1512.	3.8	22
215	Interaction of bacterial fatty-acid-displaced regulators with DNA is interrupted by tyrosine phosphorylation in the helix-turn-helix domain. <i>Nucleic Acids Research</i> , 2013, 41, 9371-9381.	14.5	28
216	Quantitative Fragmentome Mapping Reveals Novel, Domain-specific Partners for the Modular Protein RepoMan (Recruits PP1 Onto Mitotic Chromatin at Anaphase). <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1468-1486.	3.8	24
217	Activated Cyclin-Dependent Kinase 5 Promotes Microglial Phagocytosis of Fibrillar β -Amyloid by Up-regulating Lipoprotein Lipase Expression. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2833-2844.	3.8	51
218	Early Phosphoproteomic Changes in the Mouse Spleen During Deoxynivalenol-Induced Ribotoxic Stress. <i>Toxicological Sciences</i> , 2013, 135, 129-143.	3.1	24
219	Activin A Suppresses Osteoblast Mineralization Capacity by Altering Extracellular Matrix (ECM) Composition and Impairing Matrix Vesicle (MV) Production. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2890-2900.	3.8	57
220	Protein Sets Define Disease States and Predict In Vivo Effects of Drug Treatment. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1965-1979.	3.8	29
221	MiR-26b is down-regulated in carcinoma-associated fibroblasts from ER-positive breast cancers leading to enhanced cell migration and invasion. <i>Journal of Pathology</i> , 2013, 231, 388-399.	4.5	103
222	The Impact of Computer Science in Molecular Medicine: Enabling High- Throughput Research. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 526-575.	2.1	13
223	Novel Binding Partners and Differentially Regulated Phosphorylation Sites Clarify Eps8 as a Multi-Functional Adaptor. <i>PLoS ONE</i> , 2013, 8, e61513.	2.5	12
224	Direct Detection of Alternative Open Reading Frames Translation Products in Human Significantly Expands the Proteome. <i>PLoS ONE</i> , 2013, 8, e70698.	2.5	192
225	Quantitative-Proteomic Comparison of Alpha and Beta Cells to Uncover Novel Targets for Lineage Reprogramming. <i>PLoS ONE</i> , 2014, 9, e95194.	2.5	27
226	Identification of a Novel Neurotrophic Factor from Primary Retinal Müller Cells Using Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC). <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2371-2381.	3.8	17
227	Proteomic Survey Reveals Altered Energetic Patterns and Metabolic Failure Prior to Retinal Degeneration. <i>Journal of Neuroscience</i> , 2014, 34, 2797-2812.	3.6	25

#	ARTICLE	IF	CITATIONS
228	The PI3-kinase isoform p110 β is essential for cell transformation induced by the D816V mutant of c-Kit in a lipid-kinase-independent manner. <i>Oncogene</i> , 2014, 33, 5360-5369.	5.9	15
229	A cluster of methylations in the domain IV of 25S rRNA is required for ribosome stability. <i>Rna</i> , 2014, 20, 1632-1644.	3.5	64
230	Identifying Nuclear Protein-Protein Interactions Using GFP Affinity Purification and SILAC-Based Quantitative Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2014, 1188, 207-226.	0.9	29
231	Interplay of the Serine/Threonine-Kinase StkP and the Paralogs DivIVA and GpsB in Pneumococcal Cell Elongation and Division. <i>PLoS Genetics</i> , 2014, 10, e1004275.	3.5	166
232	Characterization of the surfaceome of the metal-reducing bacterium <i>Desulfotomaculum reducens</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 432.	3.5	22
233	The PhoP-Dependent ncRNA Mcr7 Modulates the TAT Secretion System in <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2014, 10, e1004183.	4.7	127
234	A systems-wide screen identifies substrates of the SCF β -TrCP ubiquitin ligase. <i>Science Signaling</i> , 2014, 7, rs8.	3.6	49
235	CPF-Associated Phosphatase Activity Opposes Condensin-Mediated Chromosome Condensation. <i>PLoS Genetics</i> , 2014, 10, e1004415.	3.5	49
238	A Horizontally Acquired Transcription Factor Coordinates <i>Salmonella</i> Adaptations to Host Microenvironments. <i>MBio</i> , 2014, 5, e01727-14.	4.1	19
239	Quantitative Proteomic Analysis of Compartmentalized Signaling Networks. <i>Methods in Enzymology</i> , 2014, 535, 309-325.	1.0	2
240	Basal Activity of a PARP1-NuA4 Complex Varies Dramatically across Cancer Cell Lines. <i>Cell Reports</i> , 2014, 8, 1808-1818.	6.4	16
241	KIF4A and PP2A β form a spatially restricted feedback loop opposing Aurora B at the anaphase central spindle. <i>Journal of Cell Biology</i> , 2014, 207, 683-693.	5.2	70
242	Global profiling of co- and post-translationally N-myristoylated proteomes in human cells. <i>Nature Communications</i> , 2014, 5, 4919.	12.8	199
243	E-cadherin interactome complexity and robustness resolved by quantitative proteomics. <i>Science Signaling</i> , 2014, 7, rs7.	3.6	160
244	O-linked glycosylation sites profiling in <i>Mycobacterium tuberculosis</i> culture filtrate proteins. <i>Journal of Proteomics</i> , 2014, 97, 296-306.	2.4	47
245	Herpes Simplex Virus. <i>Methods in Molecular Biology</i> , 2014, , .	0.9	1
246	Bioinformatics Tools to Identify and Quantify Proteins Using Mass Spectrometry Data. <i>Advances in Protein Chemistry and Structural Biology</i> , 2014, 94, 1-17.	2.3	10
247	Proteomic profiles of human lung adeno and squamous cell carcinoma using super-SILAC and label-free quantification approaches. <i>Proteomics</i> , 2014, 14, 795-803.	2.2	24

#	ARTICLE	IF	CITATIONS
248	Dynamic Changes in Ribosome-Associated Proteome and Phosphoproteome During Deoxynivalenol-Induced Translation Inhibition and Ribotoxic Stress. <i>Toxicological Sciences</i> , 2014, 138, 217-233.	3.1	38
249	Comparative interactomes of <i>SIRT6</i> and <i>SIRT7</i> : Implication of functional links to aging. <i>Proteomics</i> , 2014, 14, 1610-1622.	2.2	69
250	Identification of Bioactivating Enzymes Involved in the Hydrolysis of Laninamivir Octanoate, a Long-Acting Neuraminidase Inhibitor, in Human Pulmonary Tissue. <i>Drug Metabolism and Disposition</i> , 2014, 42, 1031-1038.	3.3	13
251	Urine Sample Preparation in 96-Well Filter Plates for Quantitative Clinical Proteomics. <i>Analytical Chemistry</i> , 2014, 86, 5470-5477.	6.5	85
252	Glutamine methylation in histone H2A is an RNA-polymerase-I-dedicated modification. <i>Nature</i> , 2014, 505, 564-568.	27.8	186
253	Citrullination regulates pluripotency and histone H1 binding to chromatin. <i>Nature</i> , 2014, 507, 104-108.	27.8	358
254	Collective migration of cancer-associated fibroblasts is enhanced by overexpression of tight junction-associated proteins claudin-1 and occludin. <i>Molecular Oncology</i> , 2014, 8, 178-195.	4.6	43
255	Proteomic and 3D structure analyses highlight the C/D box snoRNP assembly mechanism and its control. <i>Journal of Cell Biology</i> , 2014, 207, 463-480.	5.2	57
256	Quantitative Mass Spectrometry Reveals Plasticity of Metabolic Networks in <i>Mycobacterium smegmatis</i> . <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3014-3028.	3.8	29
257	The role of the plexin-A2 receptor in semaphorin-3A and semaphorin-3B signal transduction. <i>Journal of Cell Science</i> , 2014, 127, 5240-52.	2.0	32
258	Online Quantitative Proteomics <i>p</i> -Value Calculator for Permutation-Based Statistical Testing of Peptide Ratios. <i>Journal of Proteome Research</i> , 2014, 13, 4184-4191.	3.7	26
259	Global characterization of the oocyte-to-embryo transition in <i>C. elegans</i> uncovers a novel mRNA clearance mechanism. <i>EMBO Journal</i> , 2014, 33, 1751-1766.	7.8	68
260	Systematic Nucleo-Cytoplasmic Trafficking of Proteins Following Exposure of MCF7 Breast Cancer Cells to Estradiol. <i>Journal of Proteome Research</i> , 2014, 13, 1112-1127.	3.7	15
261	The human mitotic kinesin KIF18A binds protein phosphatase 1 (PP1) through a highly conserved docking motif. <i>Biochemical and Biophysical Research Communications</i> , 2014, 453, 432-437.	2.1	26
262	Current advances in systems and integrative biology. <i>Computational and Structural Biotechnology Journal</i> , 2014, 11, 35-46.	4.1	29
263	Quantitative Proteomic Analysis of Host-virus Interactions Reveals a Role for Golgi Brefeldin A Resistance Factor 1 (GBF1) in Dengue Infection. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2836-2854.	3.8	49
264	Quantitative phosphoproteomics reveals novel phosphorylation events in insulin signaling regulated by protein phosphatase 1 regulatory subunit 12A. <i>Journal of Proteomics</i> , 2014, 109, 63-75.	2.4	26
265	Large-Scale Proteome Quantification of Hepatocellular Carcinoma Tissues by a Three-Dimensional Liquid Chromatography Strategy Integrated with Sample Preparation. <i>Journal of Proteome Research</i> , 2014, 13, 3645-3654.	3.7	22

#	ARTICLE	IF	CITATIONS
266	Improved bottomâ€cup strategy to efficiently separate hypermodified histone peptides through ultraâ€HPLC separation on a bench top Orbitrap instrument. <i>Proteomics</i> , 2014, 14, 2212-2225.	2.2	28
267	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC). <i>Methods in Molecular Biology</i> , 2014, , .	0.9	2
268	Effect of Embryonic Development on the Chicken Egg Yolk Plasma Proteome after 12 Days of Incubation. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 2531-2540.	5.2	34
269	Dissecting the Subcellular Compartmentation of Proteins and Metabolites in Arabidopsis Leaves Using Non-aqueous Fractionation. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2246-2259.	3.8	58
270	Quantitative Phosphoproteome Analysis of <i>Bacillus subtilis</i> Reveals Novel Substrates of the Kinase PrkC and Phosphatase PrpC. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1965-1978.	3.8	81
271	The proteomic response in glioblastoma in young patients. <i>Journal of Neuro-Oncology</i> , 2014, 119, 79-89.	2.9	14
273	Characterization of the pigmented shell-forming proteome of the common grove snail <i>Cepaea nemoralis</i> . <i>BMC Genomics</i> , 2014, 15, 249.	2.8	76
274	In Vivo Quantitative Proteomics for the Study of Oncometabolism. <i>Methods in Enzymology</i> , 2014, 543, 235-259.	1.0	3
275	Chromatin enrichment for proteomics. <i>Nature Protocols</i> , 2014, 9, 2090-2099.	12.0	78
276	HGF Induces Epithelial-to-Mesenchymal Transition by Modulating the Mammalian Hippo/MST2 and ISC15 Pathways. <i>Journal of Proteome Research</i> , 2014, 13, 2874-2886.	3.7	82
277	Quantitative Phosphoproteomics of Murine <i>Fmr1</i> -KO Cell Lines Provides New Insights into FMRP-Dependent Signal Transduction Mechanisms. <i>Journal of Proteome Research</i> , 2014, 13, 4388-4397.	3.7	29
278	Dissection of a Novel Autocrine Signaling Pathway via Quantitative Secretome and Interactome Mapping. <i>Journal of Proteome Research</i> , 2014, 13, 3432-3443.	3.7	5
279	Nuclear Cytoplasmic Trafficking of Proteins is a Major Response of Human Fibroblasts to Oxidative Stress. <i>Journal of Proteome Research</i> , 2014, 13, 4398-4423.	3.7	14
280	Ecto-Fc MS identifies ligand-receptor interactions through extracellular domain Fc fusion protein baits and shotgun proteomic analysis. <i>Nature Protocols</i> , 2014, 9, 2061-2074.	12.0	21
281	Novel markers of osteogenic and adipogenic differentiation of human bone marrow stromal cells identified using a quantitative proteomics approach. <i>Stem Cell Research</i> , 2014, 12, 153-165.	0.7	155
282	Conservation of mRNA and Protein Expression during Development of <i>C.Âlegans</i> . <i>Cell Reports</i> , 2014, 6, 565-577.	6.4	98
283	Mass++: A Visualization and Analysis Tool for Mass Spectrometry. <i>Journal of Proteome Research</i> , 2014, 13, 3846-3853.	3.7	45
284	Quantitative Temporal Viromics: An Approach to Investigate Host-Pathogen Interaction. <i>Cell</i> , 2014, 157, 1460-1472.	28.9	409

#	ARTICLE	IF	CITATIONS
285	Quantitative proteomics and network analysis of SSA1 and SSB1 deletion mutants reveals robustness of chaperone HSP70 network in <i>Saccharomyces cerevisiae</i> . <i>Proteomics</i> , 2015, 15, 3126-3139.	2.2	12
286	Establishment of a proteome profile and identification of molecular markers for mouse spermatogonial stem cells. <i>Journal of Cellular and Molecular Medicine</i> , 2015, 19, 521-534.	3.6	27
287	Chronic acidosis in the tumour microenvironment selects for overexpression of LAMP2 in the plasma membrane. <i>Nature Communications</i> , 2015, 6, 8752.	12.8	151
288	Identification and Quantification of K63-Ubiquitinated Proteins in Neuronal Cells by High-Resolution Mass Spectrometry. <i>Neuromethods</i> , 2015, , 111-125.	0.3	0
289	Comparative proteomic analysis of compartmentalised Ras signalling. <i>Scientific Reports</i> , 2015, 5, 17307.	3.3	10
290	Genetic variation in insulin-induced kinase signaling. <i>Molecular Systems Biology</i> , 2015, 11, 820.	7.2	14
291	Quantitative Mass Spectrometric Profiling of Cancer-cell Proteomes Derived From Liquid and Solid Tumors. <i>Journal of Visualized Experiments</i> , 2015, , e52435.	0.3	5
292	Phosphoproteomic analysis of basal and therapy-induced adaptive signaling networks in <i>BRAF</i> and <i>NRAS</i> mutant melanoma. <i>Proteomics</i> , 2015, 15, 327-339.	2.2	13
293	Evaluation of the accuracy of protein quantification using isotope TMPP-labeled peptides. <i>Proteomics</i> , 2015, 15, 2903-2909.	2.2	5
294	Proteomic screening and identification of microRNA-128 targets in glioma cells. <i>Proteomics</i> , 2015, 15, 2602-2617.	2.2	6
295	Toward improved peptide feature detection in quantitative proteomics using stable isotope labeling. <i>Proteomics - Clinical Applications</i> , 2015, 9, 706-714.	1.6	11
296	Quantitative Analysis of Differential Proteome Expression in Bladder Cancer vs. Normal Bladder Cells Using SILAC Method. <i>PLoS ONE</i> , 2015, 10, e0134727.	2.5	18
297	Label-Free Proteomics Uncovers Energy Metabolism and Focal Adhesion Regulations Responsive for Endometrium Receptivity. <i>Journal of Proteome Research</i> , 2015, 14, 1831-1842.	3.7	37
298	Prmt5 is a regulator of muscle stem cell expansion in adult mice. <i>Nature Communications</i> , 2015, 6, 7140.	12.8	98
299	Quantitative phosphoproteomics reveals crosstalk between phosphorylation and <i>O</i> -GlcNAc in the DNA damage response pathway. <i>Proteomics</i> , 2015, 15, 591-607.	2.2	60
300	Novel Molecular Insights into Classical and Alternative Activation States of Microglia as Revealed by Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC)-based Proteomics*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 3173-3184.	3.8	51
301	Novel AKT phosphorylation sites identified in the pluripotency factors OCT4, SOX2 and KLF4. <i>Cell Cycle</i> , 2015, 14, 3748-3754.	2.6	17
302	Quantitative Glycome Analysis of N-Glycan Patterns in Bladder Cancer vs Normal Bladder Cells Using an Integrated Strategy. <i>Journal of Proteome Research</i> , 2015, 14, 639-653.	3.7	60

#	ARTICLE	IF	CITATIONS
303	Quantitative Nuclear Proteomics Identifies that miR-137-mediated EZH2 Reduction Regulates Resveratrol-induced Apoptosis of Neuroblastoma Cells*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 316-328.	3.8	62
304	Dosage and Temporal Thresholds in microRNA Proteomics*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 289-302.	3.8	10
305	Proteomics reveals the importance of the dynamic redistribution of the subcellular location of proteins in breast cancer cells. <i>Expert Review of Proteomics</i> , 2015, 12, 61-74.	3.0	8
306	Quantitative Proteomics Reveals Dynamic Interaction of c-Jun N-terminal Kinase (JNK) with RNA Transport Granule Proteins Splicing Factor Proline- and Glutamine-rich (Sfpq) and Non-POU Domain-containing Octamer-binding Protein (Nono) during Neuronal Differentiation. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 50-65.	3.8	17
307	The chicken B-cell line DT40 proteome, beadome and interactomes. <i>Data in Brief</i> , 2015, 3, 29-33.	1.0	1
308	Proteomic signatures of extracellular vesicles secreted by nonmineralizing and mineralizing human osteoblasts and stimulation of tumor cell growth. <i>FASEB Journal</i> , 2015, 29, 274-285.	0.5	72
309	Phosphoproteome of the cyanobacterium <i>Synechocystis</i> sp. PCC 6803 and its dynamics during nitrogen starvation. <i>Frontiers in Microbiology</i> , 2015, 6, 248.	3.5	79
310	Investigation of heart proteome of different consomic mouse strains. Testing the effect of polymorphisms on the proteome-wide trans-variation of proteins. <i>EuPA Open Proteomics</i> , 2015, 7, 27-42.	2.5	0
311	SILAC-iPAC: A quantitative method for distinguishing genuine from non-specific components of protein complexes by parallel affinity capture. <i>Journal of Proteomics</i> , 2015, 115, 143-156.	2.4	8
312	Cmr1/WDR76 defines a nuclear genotoxic stress body linking genome integrity and protein quality control. <i>Nature Communications</i> , 2015, 6, 6533.	12.8	80
313	High mobility group protein-mediated transcription requires DNA damage marker $\hat{\Gamma}^3$ -H2AX. <i>Cell Research</i> , 2015, 25, 837-850.	12.0	70
314	Cells deficient in base-excision repair reveal cancer hallmarks originating from adjustments to genetic instability. <i>Nucleic Acids Research</i> , 2015, 43, 3667-3679.	14.5	39
315	Conserved <i>Streptococcus pneumoniae</i> Spirosomes Suggest a Single Type of Transformation Pilus in Competence. <i>PLoS Pathogens</i> , 2015, 11, e1004835.	4.7	26
316	Plasma Membrane Profiling Defines an Expanded Class of Cell Surface Proteins Selectively Targeted for Degradation by HCMV US2 in Cooperation with UL141. <i>PLoS Pathogens</i> , 2015, 11, e1004811.	4.7	73
317	Diagnosing inflammation and infection in the urinary system via proteomics. <i>Journal of Translational Medicine</i> , 2015, 13, 111.	4.4	47
318	Quantitative Proteomics Reveals Dynamic Interactions of the Minichromosome Maintenance Complex (MCM) in the Cellular Response to Etoposide Induced DNA Damage*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2002-2013.	3.8	37
320	Similar Neutrophil-Driven Inflammatory and Antibacterial Responses in Elderly Patients with Symptomatic and Asymptomatic Bacteriuria. <i>Infection and Immunity</i> , 2015, 83, 4142-4153.	2.2	22
321	Proteogenomic Discovery of a Small, Novel Protein in Yeast Reveals a Strategy for the Detection of Unannotated Short Open Reading Frames. <i>Journal of Proteome Research</i> , 2015, 14, 5038-5047.	3.7	25

#	ARTICLE	IF	CITATIONS
322	Parallel Accumulation–Serial Fragmentation (PASEF): Multiplying Sequencing Speed and Sensitivity by Synchronized Scans in a Trapped Ion Mobility Device. <i>Journal of Proteome Research</i> , 2015, 14, 5378-5387.	3.7	281
323	The EF-Hand Ca ²⁺ Binding Protein MICU Choreographs Mitochondrial Ca ²⁺ Dynamics in Arabidopsis. <i>Plant Cell</i> , 2015, 27, 3190-3212.	6.6	103
324	Mitotic redistribution of the mitochondrial network by Miro and Cenp-F. <i>Nature Communications</i> , 2015, 6, 8015.	12.8	84
325	Quantitative Mass Spectrometry Reveals Partial Translational Regulation for Dosage Compensation in Chicken. <i>Molecular Biology and Evolution</i> , 2015, 32, 2716-2725.	8.9	45
326	Phosphoproteomic Analysis of Aurora Kinase Inhibition in Monopolar Cytokinesis. <i>Journal of Proteome Research</i> , 2015, 14, 4087-4098.	3.7	14
327	Thermal proteome profiling for unbiased identification of direct and indirect drug targets using multiplexed quantitative mass spectrometry. <i>Nature Protocols</i> , 2015, 10, 1567-1593.	12.0	481
328	Quantitative analysis of glycans, related genes, and proteins in two human bone marrow stromal cell lines using an integrated strategy. <i>Experimental Hematology</i> , 2015, 43, 760-769.e7.	0.4	7
329	Beyond single modification: Reanalysis of the acetylproteome of human sperm reveals widespread multiple modifications. <i>Journal of Proteomics</i> , 2015, 126, 296-302.	2.4	11
330	Quantitative comparison of a human cancer cell surface proteome between interphase and mitosis. <i>EMBO Journal</i> , 2015, 34, 251-265.	7.8	41
331	Delineating monoclonal antibody specificity by mass spectrometry. <i>Journal of Proteomics</i> , 2015, 114, 115-124.	2.4	8
332	From pathways to networks: Connecting dots by establishing protein–protein interaction networks in signaling pathways using affinity purification and mass spectrometry. <i>Proteomics</i> , 2015, 15, 188-202.	2.2	20
333	PIPINO: A Software Package to Facilitate the Identification of Protein-Protein Interactions from Affinity Purification Mass Spectrometry Data. <i>BioMed Research International</i> , 2016, 2016, 1-13.	1.9	0
334	Quantitative Proteomic Analysis of Venoms from Russian Vipers of Pelias Group: Phospholipases A2 are the Main Venom Components. <i>Toxins</i> , 2016, 8, 105.	3.4	32
335	Tyrosine 601 of <i>Bacillus subtilis</i> DnaK Undergoes Phosphorylation and Is Crucial for Chaperone Activity and Heat Shock Survival–. <i>Frontiers in Microbiology</i> , 2016, 7, 533.	3.5	13
336	Plasma Membrane Profiling Reveals Upregulation of ABCA1 by Infected Macrophages Leading to Restriction of Mycobacterial Growth. <i>Frontiers in Microbiology</i> , 2016, 7, 1086.	3.5	17
337	Quantitative Proteomic Analysis of Germination of <i>Nosema bombycis</i> Spores under Extremely Alkaline Conditions. <i>Frontiers in Microbiology</i> , 2016, 7, 1459.	3.5	29
338	Post-translational Serine/Threonine Phosphorylation and Lysine Acetylation: A Novel Regulatory Aspect of the Global Nitrogen Response Regulator GlnR in <i>S. coelicolor</i> M145. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 38.	3.5	48
339	Comprehensive Identification of Immunodominant Proteins of <i>Brucella abortus</i> and <i>Brucella melitensis</i> Using Antibodies in the Sera from Naturally Infected Hosts. <i>International Journal of Molecular Sciences</i> , 2016, 17, 659.	4.1	24

#	ARTICLE	IF	CITATIONS
340	Quantitative Analysis of Differential Proteome Expression in Epithelial-to-Mesenchymal Transition of Bladder Epithelial Cells Using SILAC Method. <i>Molecules</i> , 2016, 21, 84.	3.8	10
341	Biochemical and cellular characterization of transcription factors binding to the hyperconserved core promoter-associated M4 motif. <i>BMC Genomics</i> , 2016, 17, 693.	2.8	11
342	Global Lysine Acetylome Analysis of Desiccated Somatic Embryos of <i>Picea asperata</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1927.	3.6	14
343	Cytoskeleton-centric protein transportation by exosomes transforms tumor-favorable macrophages. <i>Oncotarget</i> , 2016, 7, 67387-67402.	1.8	56
345	Determining synthesis rates of individual proteins in zebrafish (<i>Danio rerio</i>) with low levels of a stable isotope labelled amino acid. <i>Proteomics</i> , 2016, 16, 1398-1406.	2.2	2
346	An interaction proteomics survey of transcription factor binding at recurrent TERT promoter mutations. <i>Proteomics</i> , 2016, 16, 417-426.	2.2	50
347	Quantitative Phosphoproteomic Study Reveals that Protein Kinase A Regulates Neural Stem Cell Differentiation Through Phosphorylation of Catenin Beta-1 and Glycogen Synthase Kinase 3 β . <i>Stem Cells</i> , 2016, 34, 2090-2101.	3.2	17
348	Interactomic analysis of REST/NRSF and implications of its functional links with the transcription suppressor TRIM28 during neuronal differentiation. <i>Scientific Reports</i> , 2016, 6, 39049.	3.3	20
349	Interconnection of post-transcriptional regulation: The RNA-binding protein Hfq is a novel target of the Lon protease in <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2016, 6, 26811.	3.3	31
350	STAGE-digging: A novel in-gel digestion processing for proteomics samples. <i>Journal of Proteomics</i> , 2016, 140, 48-54.	2.4	18
351	Programmed Cell Death. <i>Methods in Molecular Biology</i> , 2016, , .	0.9	8
352	An RNA matchmaker protein regulates the activity of the long noncoding RNA HOTAIR. <i>Rna</i> , 2016, 22, 995-1010.	3.5	55
353	Proteomic Profiling of Cell Death: Stable Isotope Labeling and Mass Spectrometry Analysis. <i>Methods in Molecular Biology</i> , 2016, 1419, 277-286.	0.9	0
354	Freezing effects on the acute myeloid leukemia cell proteome and phosphoproteome revealed using optimal quantitative workflows. <i>Journal of Proteomics</i> , 2016, 145, 214-225.	2.4	35
355	Unsupervised Identification of Isotope-Labeled Peptides. <i>Analytical Chemistry</i> , 2016, 88, 6092-6099.	6.5	1
356	Comparative interactomics analysis of different ALS-associated proteins identifies converging molecular pathways. <i>Acta Neuropathologica</i> , 2016, 132, 175-196.	7.7	113
357	Spatial Cross-Talk between Oxidative Stress and DNA Replication in Human Fibroblasts. <i>Journal of Proteome Research</i> , 2016, 15, 1907-1938.	3.7	4
358	Quantitative proteomic analysis and comparison of two bone marrow stromal cell lines using the SILAC method. <i>Experimental Hematology</i> , 2016, 44, 1059-1071.	0.4	4

#	ARTICLE	IF	CITATIONS
359	Comprehensive Characterization of Minichromosome Maintenance Complex (MCM) Protein Interactions Using Affinity and Proximity Purifications Coupled to Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 2924-2934.	3.7	18
360	The cellular proteome is affected by a gelsolin (<i>BbGEL1</i>) during morphological transitions in aerobic surface versus liquid growth in the entomopathogenic fungus <i>Beauveria bassiana</i> . <i>Environmental Microbiology</i> , 2016, 18, 4153-4169.	3.8	30
361	Catenin delta-1 (CTNND1) phosphorylation controls the mesenchymal to epithelial transition in astrocytic tumors. <i>Human Molecular Genetics</i> , 2016, 25, 4201-4210.	2.9	10
362	Efficient Application of De Novo RNA Assemblers for Proteomics Informed by Transcriptomics. <i>Journal of Proteome Research</i> , 2016, 15, 3938-3943.	3.7	10
363	NOTCH1 mediates a switch between two distinct secretomes during senescence. <i>Nature Cell Biology</i> , 2016, 18, 979-992.	10.3	365
364	Mastitomics, the integrated omics of bovine milk in an experimental model of <i>Streptococcus uberis</i> mastitis: 2. Label-free relative quantitative proteomics. <i>Molecular BioSystems</i> , 2016, 12, 2748-2761.	2.9	45
365	Proteome-wide analysis of arginine monomethylation reveals widespread occurrence in human cells. <i>Science Signaling</i> , 2016, 9, rs9.	3.6	241
366	The MaxQuant computational platform for mass spectrometry-based shotgun proteomics. <i>Nature Protocols</i> , 2016, 11, 2301-2319.	12.0	3,353
367	Comprehensive profiling of lysine acetylproteome analysis reveals diverse functions of lysine acetylation in common wheat. <i>Scientific Reports</i> , 2016, 6, 21069.	3.3	87
368	Response of Human Osteoblast to n-HA/PEEK Quantitative Proteomic Study of Bio-effects of Nano-Hydroxyapatite Composite. <i>Scientific Reports</i> , 2016, 6, 22832.	3.3	31
369	Protein translation occurs in platelet concentrates despite riboflavin/UV light pathogen inactivation treatment. <i>Proteomics - Clinical Applications</i> , 2016, 10, 839-850.	1.6	16
370	Cholesterol biosynthesis pathway as a novel mechanism of resistance to estrogen deprivation in estrogen receptor-positive breast cancer. <i>Breast Cancer Research</i> , 2016, 18, 58.	5.0	98
371	Investigation of urine proteome of preterm newborns with respiratory pathologies. <i>Journal of Proteomics</i> , 2016, 149, 31-37.	2.4	11
372	Identification of Caspase-6 as a New Regulator of Alternatively Activated Macrophages. <i>Journal of Biological Chemistry</i> , 2016, 291, 17450-17466.	3.4	17
373	Elevated Plasma Cardiac Troponin T Levels Caused by Skeletal Muscle Damage in Pompe Disease. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 6-13.	5.1	70
374	Reliable FASP-based procedures for optimal quantitative proteomic and phosphoproteomic analysis on samples from acute myeloid leukemia patients. <i>Biological Procedures Online</i> , 2016, 18, 13.	2.9	48
375	Analysis of the Protein Kinase A-Regulated Proteome of <i>Cryptococcus neoformans</i> Identifies a Role for the Ubiquitin-Proteasome Pathway in Capsule Formation. <i>MBio</i> , 2016, 7, e01862-15.	4.1	62
376	Quantitative phosphoproteomics reveals genistein as a modulator of cell cycle and DNA damage response pathways in triple-negative breast cancer cells. <i>International Journal of Oncology</i> , 2016, 48, 1016-1028.	3.3	41

#	ARTICLE	IF	CITATIONS
377	Identification of a Novel Function of Adipocyte Plasma Membrane-Associated Protein (APMAP) in Gestational Diabetes Mellitus by Proteomic Analysis of Omental Adipose Tissue. <i>Journal of Proteome Research</i> , 2016, 15, 628-637.	3.7	25
378	Development of Online pH Gradient-Eluted Strong Cation Exchange Nanoelectrospray-Tandem Mass Spectrometry for Proteomic Analysis Facilitating Basic and Histidine-Containing Peptides Identification. <i>Analytical Chemistry</i> , 2016, 88, 583-591.	6.5	12
379	Integrated analysis of shotgun proteomic data with PatternLab for proteomics 4.0. <i>Nature Protocols</i> , 2016, 11, 102-117.	12.0	257
380	Isolation of the protein and RNA content of active sites of transcription from mammalian cells. <i>Nature Protocols</i> , 2016, 11, 553-565.	12.0	20
381	Integrated genomics and proteomics define huntingtin CAG lengthâ€“dependent networks in mice. <i>Nature Neuroscience</i> , 2016, 19, 623-633.	14.8	342
382	Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. <i>Data in Brief</i> , 2016, 6, 286-294.	1.0	30
383	Mte1 interacts with Mph1 and promotes crossover recombination and telomere maintenance. <i>Genes and Development</i> , 2016, 30, 700-717.	5.9	27
384	Quantitative Phosphotyrosine Profiling of Patient-Derived Xenografts Identifies Therapeutic Targets in Pediatric Leukemia. <i>Cancer Research</i> , 2016, 76, 2766-2777.	0.9	16
385	PRIDE Inspector Toolsuite: Moving Toward a Universal Visualization Tool for Proteomics Data Standard Formats and Quality Assessment of ProteomeXchange Datasets. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 305-317.	3.8	140
386	Generating Sample-Specific Databases for Mass Spectrometry-Based Proteomic Analysis by Using RNA Sequencing. <i>Methods in Molecular Biology</i> , 2016, 1394, 219-232.	0.9	4
388	Exploring G protein-coupled receptor signaling networks using SILAC-based phosphoproteomics. <i>Methods</i> , 2016, 92, 36-50.	3.8	23
389	Benchmarking quantitative label-free LCâ€“MS data processing workflows using a complex spiked proteomic standard dataset. <i>Journal of Proteomics</i> , 2016, 132, 51-62.	2.4	68
390	CK1Î´ activity is modulated by CDK2/E- and CDK5/p35-mediated phosphorylation. <i>Amino Acids</i> , 2016, 48, 579-592.	2.7	23
391	Proteomic analysis of naturally-sourced biological scaffolds. <i>Biomaterials</i> , 2016, 75, 37-46.	11.4	115
392	Analysis of the Global Changes in SH2 Binding Properties Using Mass Spectrometry Supported by Quantitative Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) Technique. <i>Methods in Molecular Biology</i> , 2017, 1555, 419-428.	0.9	0
393	SH2 Domains. <i>Methods in Molecular Biology</i> , 2017, , .	0.9	1
394	Quantitative Proteomics Using SILAC. <i>Methods in Molecular Biology</i> , 2017, 1550, 171-184.	0.9	12
395	Mitochondria. <i>Methods in Molecular Biology</i> , 2017, , .	0.9	2

#	ARTICLE	IF	CITATIONS
396	Assessing Mitochondrial Unfolded Protein Response in Mammalian Cells. <i>Methods in Molecular Biology</i> , 2017, 1567, 363-378.	0.9	4
397	Proteomic Screen for Cellular Targets of the Vaccinia Virus F10 Protein Kinase Reveals that Phosphorylation of mDia Regulates Stress Fiber Formation. <i>Molecular and Cellular Proteomics</i> , 2017, 16, S124-S143.	3.8	8
398	Cdx2 Regulates Gene Expression through Recruitment of Brg1-associated Switch-Sucrose Non-fermentable (SWI-SNF) Chromatin Remodeling Activity. <i>Journal of Biological Chemistry</i> , 2017, 292, 3389-3399.	3.4	11
399	Proteogenomics. <i>Methods in Enzymology</i> , 2017, 585, 217-243.	1.0	6
400	Quantitative Proteomic analysis on Activated Hepatic Stellate Cells reversion Reveal STAT1 as a key regulator between Liver Fibrosis and recovery. <i>Scientific Reports</i> , 2017, 7, 44910.	3.3	19
401	Systematic analysis of the lysine acetylome reveals diverse functions of lysine acetylation in the oleaginous yeast <i>Yarrowia lipolytica</i> . <i>AMB Express</i> , 2017, 7, 94.	3.0	16
402	Identification of Chloride Intracellular Channel Protein 3 as a Novel Gene Affecting Human Bone Formation. <i>JBMR Plus</i> , 2017, 1, 16-26.	2.7	14
403	Statistical Analysis of ATM-Dependent Signaling in Quantitative Mass Spectrometry Phosphoproteomics. <i>Methods in Molecular Biology</i> , 2017, 1599, 229-244.	0.9	6
404	Mass Spectrometry-Based Proteomics for Quantifying DNA Damage-Induced Phosphorylation. <i>Methods in Molecular Biology</i> , 2017, 1599, 215-227.	0.9	14
406	tRNA-Derived RNA Fragments Associate with Human Multisynthetase Complex (MSC) and Modulate Ribosomal Protein Translation. <i>Journal of Proteome Research</i> , 2017, 16, 413-420.	3.7	72
407	Temporal profiles of plasma proteome during childhood development. <i>Journal of Proteomics</i> , 2017, 152, 321-328.	2.4	20
408	Quantitative GTPase Affinity Purification Identifies Rho Family Protein Interaction Partners. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 73-85.	3.8	20
409	Utility of high resolution accurate mass spectrometry (HRMS) in the mass isotopomer distribution analysis (MIDA) of CSF proteins modified by stable isotope labeling in mammals (SILAM) methodology applied to neurodegenerative diseases. <i>Analytical Methods</i> , 2017, 9, 3477-3484.	2.7	0
410	Identification of the adenovirus type 2 C-168 protein. <i>Virus Research</i> , 2017, 238, 110-113.	2.2	4
411	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC)-Based Quantitative Proteomics and Phosphoproteomics in Fission Yeast. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot091686.	0.3	3
412	KITD816V Induces SRC-Mediated Tyrosine Phosphorylation of MITF and Altered Transcription Program in Melanoma. <i>Molecular Cancer Research</i> , 2017, 15, 1265-1274.	3.4	15
413	The Immunosuppressant Mycophenolic Acid Alters Nucleotide and Lipid Metabolism in an Intestinal Cell Model. <i>Scientific Reports</i> , 2017, 7, 45088.	3.3	19
414	Serum estradiol levels in controlled ovarian stimulation directly affect the endometrium. <i>Journal of Molecular Endocrinology</i> , 2017, 59, 105-119.	2.5	40

#	ARTICLE	IF	CITATIONS
415	A combinatorial approach to identify calpain cleavage sites in the Machado-Joseph disease protein ataxin-3. <i>Brain</i> , 2017, 140, 1280-1299.	7.6	33
416	Profiling of Protein N-Termini and Their Modifications in Complex Samples. <i>Methods in Molecular Biology</i> , 2017, 1574, 35-50.	0.9	24
417	Mapping the secretome of human chondrogenic progenitor cells with mass spectrometry. <i>Annals of Anatomy</i> , 2017, 212, 4-10.	1.9	7
418	Quantitative Proteomic Approach Identifies Vpr Binding Protein as Novel Host Factor Supporting Influenza A Virus Infections in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 728-742.	3.8	13
419	Posttranscriptional Regulation in Adenovirus Infected Cells. <i>Journal of Proteome Research</i> , 2017, 16, 872-888.	3.7	20
420	Proteomic analysis reveals differential protein expression in variants of papillary thyroid carcinoma. <i>EuPA Open Proteomics</i> , 2017, 17, 1-6.	2.5	10
421	Polypharmacology-based ceritinib repurposing using integrated functional proteomics. <i>Nature Chemical Biology</i> , 2017, 13, 1222-1231.	8.0	60
422	Protein interaction network of alternatively spliced NudCD1 isoforms. <i>Scientific Reports</i> , 2017, 7, 12987.	3.3	12
423	Progressing neurobiological strategies against proteostasis failure: Challenges in neurodegeneration. <i>Progress in Neurobiology</i> , 2017, 159, 1-38.	5.7	27
424	Temporal characterization of the non-structural Adenovirus type 2 proteome and phosphoproteome using high-resolving mass spectrometry. <i>Virology</i> , 2017, 511, 240-248.	2.4	8
425	Proteome-Wide Analysis of N-Glycosylation Stoichiometry Using SWATH Technology. <i>Journal of Proteome Research</i> , 2017, 16, 3830-3840.	3.7	15
426	Centriolar Satellites Control GABARAP Ubiquitination and GABARAP-Mediated Autophagy. <i>Current Biology</i> , 2017, 27, 2123-2136.e7.	3.9	90
427	<i>Salmonella</i> Choleraesuis outer membrane vesicles: Proteomics and immunogenicity. <i>Journal of Basic Microbiology</i> , 2017, 57, 852-861.	3.3	14
428	Resolving Affinity Purified Protein Complexes by Blue Native PAGE and Protein Correlation Profiling. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	8
429	DNA damage-induced histone H1 ubiquitylation is mediated by HUWE1 and stimulates the RNF8-RNF168 pathway. <i>Scientific Reports</i> , 2017, 7, 15353.	3.3	54
430	Quantitative proteomic Analysis Reveals up-regulation of caveolin-1 in FOXP3-overexpressed human gastric cancer cells. <i>Scientific Reports</i> , 2017, 7, 14460.	3.3	5
431	Efficient Quantitative Comparisons of Plasma Proteomes Using Label-Free Analysis with MaxQuant. <i>Methods in Molecular Biology</i> , 2017, 1619, 339-352.	0.9	54
432	Specifying RNA-Binding Regions in Proteins by Peptide Cross-Linking and Affinity Purification. <i>Journal of Proteome Research</i> , 2017, 16, 2762-2772.	3.7	37

#	ARTICLE	IF	CITATIONS
433	Global analysis of protein lysine succinylation profiles in common wheat. <i>BMC Genomics</i> , 2017, 18, 309.	2.8	46
434	Activity-Based Protein Profiling with Natural Product-Derived Chemical Probes in Human Cell Lysates. <i>Methods in Molecular Biology</i> , 2017, 1491, 23-46.	0.9	0
435	Polyubiquitinylation Profile in Down Syndrome Brain Before and After the Development of Alzheimer Neuropathology. <i>Antioxidants and Redox Signaling</i> , 2017, 26, 280-298.	5.4	38
436	Interaction profiling of RNA-binding ubiquitin ligases reveals a link between posttranscriptional regulation and the ubiquitin system. <i>Scientific Reports</i> , 2017, 7, 16582.	3.3	17
437	Insights into the structure and assembly of a bacterial cellulose secretion system. <i>Nature Communications</i> , 2017, 8, 2065.	12.8	90
438	Phosphoproteomic analysis of the antitumor effects of ginsenoside Rg3 in human breast cancer cells. <i>Oncology Letters</i> , 2017, 15, 2889-2898.	1.8	10
439	Highly Efficient Single-Step Enrichment of Low Abundance Phosphopeptides from Plant Membrane Preparations. <i>Frontiers in Plant Science</i> , 2017, 8, 1673.	3.6	24
440	Type 1 Diabetes: Urinary Proteomics and Protein Network Analysis Support Perturbation of Lysosomal Function. <i>Theranostics</i> , 2017, 7, 2704-2717.	10.0	30
441	Conversion of Glycerol to 3-Hydroxypropanoic Acid by Genetically Engineered <i>Bacillus subtilis</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 638.	3.5	22
442	Low Concentrations of Vitamin C Reduce the Synthesis of Extracellular Polymers and Destabilize Bacterial Biofilms. <i>Frontiers in Microbiology</i> , 2017, 8, 2599.	3.5	66
443	Time-Dependent, HIV-Tat-Induced Perturbation of Human Neurons In Vitro: Towards a Model for the Molecular Pathology of HIV-Associated Neurocognitive Disorders. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 163.	2.9	6
444	Cardiac Metabolic Deregulation Induced by the Tyrosine Kinase Receptor Inhibitor Sunitinib is rescued by Endothelin Receptor Antagonism. <i>Theranostics</i> , 2017, 7, 2757-2774.	10.0	27
445	Methods to Study the BECN1 Interactome in the Course of Autophagic Responses. <i>Methods in Enzymology</i> , 2017, 587, 429-445.	1.0	7
446	Characterization of Early-Phase Neutrophil Extracellular Traps in Urinary Tract Infections. <i>PLoS Pathogens</i> , 2017, 13, e1006151.	4.7	34
447	Phosphoproteomics reveals network rewiring to a pro-adhesion state in annexin-1-deficient mammary epithelial cells. <i>Breast Cancer Research</i> , 2017, 19, 132.	5.0	13
448	Enhanced exosome secretion in Down syndrome brain - a protective mechanism to alleviate neuronal endosomal abnormalities. <i>Acta Neuropathologica Communications</i> , 2017, 5, 65.	5.2	85
449	Nanoparticle abraxane possesses impaired proliferation in A549 cells due to the underexpression of glucosamine 6-phosphate N-acetyltransferase 1 (GNPNAT1/GNA1). <i>International Journal of Nanomedicine</i> , 2017, Volume 12, 1685-1697.	6.7	32
450	Labeling Carboxyl Groups of Surface-Exposed Proteins Provides an Orthogonal Approach for Cell Surface Isolation. <i>Journal of Proteome Research</i> , 2018, 17, 1784-1793.	3.7	17

#	ARTICLE	IF	CITATIONS
451	CRISPR/Cas9-mediated Genomic Editing of Cluap1/IFT38 Reveals a New Role in Actin Arrangement. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1285-1294.	3.8	20
452	Proteome-wide identification of ubiquitin interactions using UbiA-MS. <i>Nature Protocols</i> , 2018, 13, 530-550.	12.0	454
453	Proteomic response of <i>Streptococcus pneumoniae</i> to iron limitation. <i>International Journal of Medical Microbiology</i> , 2018, 308, 713-721.	3.6	26
454	Dynamics of Zebrafish Heart Regeneration Using an HPLC-ESI-MS/MS Approach. <i>Journal of Proteome Research</i> , 2018, 17, 1300-1308.	3.7	17
455	Enhancing Membrane Protein Identification Using a Simplified Centrifugation and Detergent-Based Membrane Extraction Approach. <i>Analytical Chemistry</i> , 2018, 90, 2434-2439.	6.5	10
456	Multiplexed proteome analysis with neutron-encoded stable isotope labeling in cells and mice. <i>Nature Protocols</i> , 2018, 13, 293-306.	12.0	35
457	Extracellular Vesicles Provide a Means for Tissue Crosstalk during Exercise. <i>Cell Metabolism</i> , 2018, 27, 237-251.e4.	16.2	426
458	mRNA Cap Methyltransferase, RNMT-RAM, Promotes RNA Pol II-Dependent Transcription. <i>Cell Reports</i> , 2018, 23, 1530-1542.	6.4	36
459	Systematic analysis of the lysine malonylome in common wheat. <i>BMC Genomics</i> , 2018, 19, 209.	2.8	30
460	Proteomics Analysis of Colorectal Cancer Cells. <i>Methods in Molecular Biology</i> , 2018, 1765, 155-166.	0.9	8
461	Complementary transcriptome and proteome profiling in cabbage buds of a recessive male sterile mutant provides new insights into male reproductive development. <i>Journal of Proteomics</i> , 2018, 179, 80-91.	2.4	24
462	Open: Mucosal-luminal interface proteomics reveals biomarkers of pediatric inflammatory bowel disease-associated colitis. <i>American Journal of Gastroenterology</i> , 2018, 113, 713-724.	0.4	23
463	Evaluation of the Glypican 3 promoter for transcriptional targeting of hepatocellular carcinoma. <i>Gene Therapy</i> , 2018, 25, 115-128.	4.5	13
464	Microbial metagenome of urinary tract infection. <i>Scientific Reports</i> , 2018, 8, 4333.	3.3	93
465	microRNA-4331 Promotes Transmissible Gastroenteritis Virus (TGEV)-induced Mitochondrial Damage Via Targeting RB1, Upregulating Interleukin-1 Receptor Accessory Protein (IL1RAP), and Activating p38 MAPK Pathway In Vitro. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 190-204.	3.8	22
466	Proteome-wide lysine acetylation identification in developing rice (<i>Oryza sativa</i>) seeds and protein co-modification by acetylation, succinylation, ubiquitination, and phosphorylation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 451-463.	2.3	28
467	Quality control in mass spectrometry-based proteomics. <i>Mass Spectrometry Reviews</i> , 2018, 37, 697-711.	5.4	82
468	A mitochondrial proteomics view of complex I deficiency in <i>Candida albicans</i> . <i>Mitochondrion</i> , 2018, 38, 48-57.	3.4	24

#	ARTICLE	IF	CITATIONS
469	Comprehensive proteome analyses of lysine acetylation in tea leaves by sensing nitrogen nutrition. <i>BMC Genomics</i> , 2018, 19, 840.	2.8	31
470	Proteomics reveals ablation of PlGF increases antioxidant and neuroprotective proteins in the diabetic mouse retina. <i>Scientific Reports</i> , 2018, 8, 16728.	3.3	24
471	Destabilization of the MiniChromosome Maintenance (MCM) complex modulates the cellular response to DNA double strand breaks. <i>Cell Cycle</i> , 2018, 17, 2593-2609.	2.6	20
472	The GIS2 Gene Is Repressed by a Zinc-Regulated Bicistronic RNA in <i>Saccharomyces cerevisiae</i> . <i>Genes</i> , 2018, 9, 462.	2.4	4
473	Robust determination of differential abundance in shotgun proteomics using nonparametric statistics. <i>Molecular Omics</i> , 2018, 14, 424-436.	2.8	0
474	Phosphopeptide Enrichment from Bacterial Samples Utilizing Titanium Oxide Affinity Chromatography. <i>Methods in Molecular Biology</i> , 2018, 1841, 231-247.	0.9	1
476	The proteome of perilymph in patients with vestibular schwannoma. A possibility to identify biomarkers for tumor associated hearing loss?. <i>PLoS ONE</i> , 2018, 13, e0198442.	2.5	29
477	The proteomic study of serially passaged human skin fibroblast cells uncovers down-regulation of the chromosome condensin complex proteins involved in replicative senescence. <i>Biochemical and Biophysical Research Communications</i> , 2018, 505, 1112-1120.	2.1	6
478	SILAC-MS Profiling of Reconstituted Human Chromatin Platforms for the Study of Transcription and RNA Regulation. <i>Journal of Proteome Research</i> , 2018, 17, 3475-3484.	3.7	2
479	Absolute proteome quantification of highly purified populations of circulating reticulocytes and mature erythrocytes. <i>Blood Advances</i> , 2018, 2, 2646-2657.	5.2	69
480	p300-Mediated Lysine 2-Hydroxyisobutyrylation Regulates Glycolysis. <i>Molecular Cell</i> , 2018, 70, 663-678.e6.	9.7	126
481	Mitochondrial CoQ deficiency is a common driver of mitochondrial oxidants and insulin resistance. <i>ELife</i> , 2018, 7, .	6.0	91
482	Combined Enrichment/Enzymatic Approach To Study Tightly Clustered Multisite Phosphorylation on Ser-Rich Domains. <i>Journal of Proteome Research</i> , 2018, 17, 3050-3060.	3.7	3
483	In-depth proteomic analyses of <i>Haliotis laevigata</i> (greenlip abalone) nacre and prismatic organic shell matrix. <i>Proteome Science</i> , 2018, 16, 11.	1.7	33
484	SILAC-based quantitative proteomic analysis of the livers of spontaneous obese and diabetic rhesus monkeys. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2018, 315, E294-E306.	3.5	12
485	First comprehensive analysis of lysine acetylation in <i>Alvinocaris longirostris</i> from the deep-sea hydrothermal vents. <i>BMC Genomics</i> , 2018, 19, 352.	2.8	14
486	Proteomic Analyses of the Unexplored Sea Anemone <i>Bunodactis verrucosa</i> . <i>Marine Drugs</i> , 2018, 16, 42.	4.6	23
487	Identification of Host Defense-Related Proteins Using Label-Free Quantitative Proteomic Analysis of Milk Whey from Cows with <i>Staphylococcus aureus</i> Subclinical Mastitis. <i>International Journal of Molecular Sciences</i> , 2018, 19, 78.	4.1	28

#	ARTICLE	IF	CITATIONS
488	Preservation Method and Phosphate Buffered Saline Washing Affect the Acute Myeloid Leukemia Proteome. <i>International Journal of Molecular Sciences</i> , 2018, 19, 296.	4.1	3
489	Systematic approach for dissecting the molecular mechanisms of transcriptional regulation in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4796-E4805.	7.1	81
490	Regulation of IRE1 RNase activity by the Ribonuclease inhibitor 1 (RNH1). <i>Cell Cycle</i> , 2018, 17, 1901-1916.	2.6	9
491	Chlorosis as a Developmental Program in Cyanobacteria: The Proteomic Fundament for Survival and Awakening. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1650-1669.	3.8	47
492	Deducing the presence of proteins and proteoforms in quantitative proteomics. <i>Nature Communications</i> , 2018, 9, 2320.	12.8	23
493	Integrative Systems Biology Resources and Approaches in Disease Analytics. , 0, , .		1
494	The Queen Conch (<i>Lobatus gigas</i>) Proteome: A Valuable Tool for Biological Studies in Marine Gastropods. <i>Protein Journal</i> , 2019, 38, 628-639.	1.6	5
495	Overdosage of Balanced Protein Complexes Reduces Proliferation Rate in Aneuploid Cells. <i>Cell Systems</i> , 2019, 9, 129-142.e5.	6.2	32
496	High Constitutive Cytokine Release by Primary Human Acute Myeloid Leukemia Cells Is Associated with a Specific Intercellular Communication Phenotype. <i>Journal of Clinical Medicine</i> , 2019, 8, 970.	2.4	26
497	RIF1 promotes replication fork protection and efficient restart to maintain genome stability. <i>Nature Communications</i> , 2019, 10, 3287.	12.8	91
498	Comprehensive Analysis of the Lysine Succinylome and Protein Co-modifications in Developing Rice Seeds. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2359-2372.	3.8	22
499	An investigation into the high strength bonding technology of wafer-to-wafer with large-scale au line. <i>Journal of Physics: Conference Series</i> , 2019, 1209, 012013.	0.4	1
500	The Research on Application of Virtual Reality Technology in Museums. <i>Journal of Physics: Conference Series</i> , 2019, 1302, 042049.	0.4	7
501	Integrative proteomic and phosphoproteomic profiling of prostate cell lines. <i>PLoS ONE</i> , 2019, 14, e0224148.	2.5	14
502	Biofabrication of multiscale bone extracellular matrix scaffolds for bone tissue engineering. , 2019, 38, 168-187.		54
504	The RNA-binding ubiquitin ligase MKRN1 functions in ribosome-associated quality control of poly(A) translation. <i>Genome Biology</i> , 2019, 20, 216.	8.8	29
505	Impact of poly(A)-tail G-content on Arabidopsis PAB binding and their role in enhancing translational efficiency. <i>Genome Biology</i> , 2019, 20, 189.	8.8	49
506	At least two molecules of the RNA helicase Has1 are simultaneously present in pre-ribosomes during ribosome biogenesis. <i>Nucleic Acids Research</i> , 2019, 47, 10852-10864.	14.5	13

#	ARTICLE	IF	CITATIONS
507	The midbody interactome reveals unexpected roles for PP1 phosphatases in cytokinesis. <i>Nature Communications</i> , 2019, 10, 4513.	12.8	69
508	Multi-omic Analyses Reveal Minimal Impact of the CRISPR-Cas9 Nuclease on Cultured Human Cells. <i>Journal of Proteome Research</i> , 2019, 18, 1054-1063.	3.7	2
509	Oosporein, an abundant metabolite in <i>Beauveria caledonica</i> , with a feedback induction mechanism and a role in insect virulence. <i>Fungal Biology</i> , 2019, 123, 601-610.	2.5	31
510	On the Mechanism of Hyperthermia-Induced BRCA2 Protein Degradation. <i>Cancers</i> , 2019, 11, 97.	3.7	16
511	Quantitative Proteome Analysis Reveals Changes in the Protein Landscape During Grape Berry Development With a Focus on Vacuolar Transport Proteins. <i>Frontiers in Plant Science</i> , 2019, 10, 641.	3.6	21
512	HSF2BP Interacts with a Conserved Domain of BRCA2 and Is Required for Mouse Spermatogenesis. <i>Cell Reports</i> , 2019, 27, 3790-3798.e7.	6.4	49
513	Integrated proteomics and metabolomics analysis reveals differential lipid metabolism in human umbilical vein endothelial cells under high and low shear stress. <i>American Journal of Physiology - Cell Physiology</i> , 2019, 317, C326-C338.	4.6	21
514	Interaction of Sox2 with RNA binding proteins in mouse embryonic stem cells. <i>Experimental Cell Research</i> , 2019, 381, 129-138.	2.6	10
515	Label-Free LC-MS/MS Proteomics Analyses Reveal Proteomic Changes Accompanying <i>MSTN</i> KO in C2C12 Cells. <i>BioMed Research International</i> , 2019, 2019, 1-14.	1.9	10
516	PAD2-Mediated Citrullination Contributes to Efficient Oligodendrocyte Differentiation and Myelination. <i>Cell Reports</i> , 2019, 27, 1090-1102.e10.	6.4	59
517	Proteins that physically interact with the phosphatase Cdc14 in <i>Candida albicans</i> have diverse roles in the cell cycle. <i>Scientific Reports</i> , 2019, 9, 6258.	3.3	18
518	Identification of Filamin A Mechanobinding Partner I: Smoothelin Specifically Interacts with the Filamin A Mechanosensitive Domain 21. <i>Biochemistry</i> , 2019, 58, 4726-4736.	2.5	17
519	A New ESX-1 Substrate in <i>Mycobacterium marinum</i> That Is Required for Hemolysis but Not Host Cell Lysis. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	27
520	Surfaceome of Exosomes Secreted from the Colorectal Cancer Cell Line SW480: Peripheral and Integral Membrane Proteins Analyzed by Proteolysis and TX114. <i>Proteomics</i> , 2019, 19, e1700453.	2.2	30
521	Citrullination of HP1 ³ chromodomain affects association with chromatin. <i>Epigenetics and Chromatin</i> , 2019, 12, 21.	3.9	19
522	The long noncoding <i>scRNA</i> <i>HORAS</i> mediates castration-resistant prostate cancer survival by activating the androgen receptor transcriptional program. <i>Molecular Oncology</i> , 2019, 13, 1121-1136.	4.6	28
523	A synthetic non-histone substrate to study substrate targeting by the Gcn5 HAT and sirtuin HDACs. <i>Journal of Biological Chemistry</i> , 2019, 294, 6227-6239.	3.4	9
524	Probing H ₂ O ₂ -mediated Structural Dynamics of the Human 26S Proteasome Using Quantitative Cross-linking Mass Spectrometry (QXL-MS). <i>Molecular and Cellular Proteomics</i> , 2019, 18, 954-967.	3.8	14

#	ARTICLE	IF	CITATIONS
525	A Stress-Responsive Signaling Network Regulating Pseudohyphal Growth and Ribonucleoprotein Granule Abundance in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2019, 213, 705-720.	2.9	6
527	miR-324-5p is up regulated in end-stage osteoarthritis and regulates Indian Hedgehog signalling by differing mechanisms in human and mouse. <i>Matrix Biology</i> , 2019, 77, 87-100.	3.6	37
528	Improved SILAC method for double labeling of bacterial proteome. <i>Journal of Proteomics</i> , 2019, 194, 89-98.	2.4	5
529	Feeding cycle alters the biophysics and molecular expression of voltage-gated Na ⁺ currents in rat hippocampal CA1 neurones. <i>European Journal of Neuroscience</i> , 2019, 49, 1418-1435.	2.6	0
530	Identification and characterization of the zebra finch (<i>Taeniopygia guttata</i>) sperm proteome. <i>Journal of Proteomics</i> , 2019, 193, 192-204.	2.4	10
531	Physiological and pathophysiological characteristics of ataxin-3 isoforms. <i>Journal of Biological Chemistry</i> , 2019, 294, 644-661.	3.4	36
532	Proteogenomics in the context of the Human Proteome Project (HPP). <i>Expert Review of Proteomics</i> , 2019, 16, 267-275.	3.0	6
533	Quantitative Phosphoproteomics of Selective Autophagy Receptors. <i>Methods in Molecular Biology</i> , 2019, 1880, 691-701.	0.9	3
534	Transcriptomic and proteomic analyses reveal new insights into the regulation of immune pathways during adenovirus type 2 infection. <i>BMC Microbiology</i> , 2019, 19, 15.	3.3	10
535	Laminin β 2-enriched extracellular vesicles of oral squamous cell carcinoma cells enhance <i>in vitro</i> lymphangiogenesis <i>via</i> integrin β 3-dependent uptake by lymphatic endothelial cells. <i>International Journal of Cancer</i> , 2019, 144, 2795-2810.	5.1	45
536	microRNA-222 Attenuates Mitochondrial Dysfunction During Transmissible Gastroenteritis Virus Infection. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 51-64.	3.8	9
537	Tissue-specific extracellular matrix scaffolds for the regeneration of spatially complex musculoskeletal tissues. <i>Biomaterials</i> , 2019, 188, 63-73.	11.4	91
538	Grazing simplifies soil micro-food webs and decouples their relationships with ecosystem functions in grasslands. <i>Global Change Biology</i> , 2020, 26, 960-970.	9.5	70
539	Using affinity purification coupled with stable isotope labeling by amino acids in cell culture quantitative mass spectrometry to identify novel interactors/substrates of protein arginine methyltransferases. <i>Methods</i> , 2020, 175, 44-52.	3.8	3
540	The Implementation of Mass Spectrometry-Based Proteomics Workflows in Clinical Routines of Acute Myeloid Leukemia: Applicability and Perspectives. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6830.	4.1	11
541	NEDD4 Plays Roles in the Maintenance of Breast Cancer Stem Cell Characteristics. <i>Frontiers in Oncology</i> , 2020, 10, 1680.	2.8	20
542	The Active Constituent From <i>Gynostemma Pentaphyllum</i> Prevents Liver Fibrosis Through Regulation of the TGF- β 1/NDRG2/MAPK Axis. <i>Frontiers in Genetics</i> , 2020, 11, 594824.	2.3	9
543	Global Proteomic Analysis of Lysine Crotonylation in the Plant Pathogen <i>Botrytis cinerea</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 564350.	3.5	9

#	ARTICLE	IF	CITATIONS
544	Facilitate Angiogenesis and Neurogenesis by Growth Factors Integrated Decellularized Matrix Hydrogel. <i>Tissue Engineering - Part A</i> , 2021, 27, 771-787.	3.1	22
545	Systematic Analysis of Lysine Lactylation in the Plant Fungal Pathogen <i>Botrytis cinerea</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 594743.	3.5	47
546	Isobaric Matching between Runs and Novel PSM-Level Normalization in MaxQuant Strongly Improve Reporter Ion-Based Quantification. <i>Journal of Proteome Research</i> , 2020, 19, 3945-3954.	3.7	55
547	The FOXJ1 target <i>Cfap206</i> is required for sperm motility, mucociliary clearance of the airways and brain development. <i>Development (Cambridge)</i> , 2020, 147, .	2.5	19
548	Exercise training reverses cancer-induced oxidative stress and decrease in muscle COPS2/TRIP15/ALIEN. <i>Molecular Metabolism</i> , 2020, 39, 101012.	6.5	25
549	Differential responses to kinase inhibition in FGFR2-addicted triple negative breast cancer cells: a quantitative phosphoproteomics study. <i>Scientific Reports</i> , 2020, 10, 7950.	3.3	10
550	Ubiquitin activation is essential for schizont maturation in <i>Plasmodium falciparum</i> blood-stage development. <i>PLoS Pathogens</i> , 2020, 16, e1008640.	4.7	24
551	<i>OsCpn60¹</i> is Essential for Chloroplast Development in Rice (<i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2020, 21, 4023.	4.1	6
552	The Progression of Acute Myeloid Leukemia from First Diagnosis to Chemoresistant Relapse: A Comparison of Proteomic and Phosphoproteomic Profiles. <i>Cancers</i> , 2020, 12, 1466.	3.7	33
553	Histone H1 eviction by the histone chaperone SET reduces cell survival following DNA damage. <i>Journal of Cell Science</i> , 2020, 133, .	2.0	11
554	Proteome and Phosphoproteome Changes Associated with Prognosis in Acute Myeloid Leukemia. <i>Cancers</i> , 2020, 12, 709.	3.7	33
555	Integrative Analysis of Breast Cancer Cells Reveals an Epithelial-Mesenchymal Transition Role in Adaptation to Acidic Microenvironment. <i>Frontiers in Oncology</i> , 2020, 10, 304.	2.8	28
556	Pan-Proteomic Analysis and Elucidation of Protein Abundance among the Closely Related <i>Brucella</i> Species, <i>Brucella abortus</i> and <i>Brucella melitensis</i> . <i>Biomolecules</i> , 2020, 10, 836.	4.0	6
557	Mass Spectrometry to Study Chromatin Compaction. <i>Biology</i> , 2020, 9, 140.	2.8	2
558	Global Proteomic Analyses of STING ⁺ and ⁻ Macrophages Reveal STING and Non-STING Differentially Regulated Cellular and Molecular Pathways. <i>Proteomics - Clinical Applications</i> , 2020, 14, e1900109.	1.6	7
559	Identification of differentially activated pathways in <i>Phytophthora sojae</i> at the mycelial, cyst, and oospore stages by TMT-based quantitative proteomics analysis. <i>Journal of Proteomics</i> , 2020, 221, 103776.	2.4	8
560	Tissue- and isoform-specific protein complex analysis with natively processed bait proteins. <i>Journal of Proteomics</i> , 2021, 231, 103947.	2.4	8
561	PAR-TERRA is the main contributor to telomeric repeat-containing RNA transcripts in normal and cancer mouse cells. <i>Rna</i> , 2021, 27, 106-121.	3.5	16

#	ARTICLE	IF	CITATIONS
562	p53 activation during ribosome biogenesis regulates normal erythroid differentiation. <i>Blood</i> , 2021, 137, 89-102.	1.4	46
563	Identifying Proteinâ€“(Hydroxy)Methylated DNA Using Quantitative Interaction Proteomics. <i>Methods in Molecular Biology</i> , 2021, 2272, 209-224.	0.9	0
564	2nSILAC for Quantitative of Prototrophic Bakerâ€™s Yeast. <i>Methods in Molecular Biology</i> , 2021, 2228, 253-270.	0.9	0
565	Plant Phosphopeptide Identification and Label-Free Quantification by MaxQuant and Proteome Discoverer Software. <i>Methods in Molecular Biology</i> , 2021, 2358, 179-187.	0.9	3
566	Identification of potential candidate proteins for reprogramming spinal cord-derived astrocytes into neurons: a proteomic analysis. <i>Neural Regeneration Research</i> , 2021, 16, 2257.	3.0	5
567	Nucleotide sugar biosynthesis occurs in the glycosomes of procyclic and bloodstream form <i>Trypanosoma brucei</i> . <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009132.	3.0	9
568	Protein Complexes Form a Basis for Complex Hybrid Incompatibility. <i>Frontiers in Genetics</i> , 2021, 12, 609766.	2.3	13
569	Loss of Ciliary Gene Bbs8 Results in Physiological Defects in the Retinal Pigment Epithelium. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 607121.	3.7	12
570	Proteomic differences in the hippocampus and cortex of epilepsy brain tissue. <i>Brain Communications</i> , 2021, 3, fcab021.	3.3	22
571	The Constitutive Extracellular Protein Release by Acute Myeloid Leukemia Cellsâ€™A Proteomic Study of Patient Heterogeneity and Its Modulation by Mesenchymal Stromal Cells. <i>Cancers</i> , 2021, 13, 1509.	3.7	11
572	The consensus N glyco â€“Xâ€“S/T motif and a previously unknown N glyco â€“N â€“linked glycosylation are necessary for growth and pathogenicity of <i>Phytophthora</i> . <i>Environmental Microbiology</i> , 2021, 23, 5147-5163.	3.8	5
573	Proteomic Studies of Primary Acute Myeloid Leukemia Cells Derived from Patients Before and during Disease-Stabilizing Treatment Based on All-Trans Retinoic Acid and Valproic Acid. <i>Cancers</i> , 2021, 13, 2143.	3.7	6
575	The splicing factor XAB2 interacts with ERCC1-XPF and XPG for R-loop processing. <i>Nature Communications</i> , 2021, 12, 3153.	12.8	27
576	Biological Mechanisms Induced by Soybean Agglutinin Using an Intestinal Cell Model of Monogastric Animals. <i>Frontiers in Veterinary Science</i> , 2021, 8, 639792.	2.2	3
577	The proteome of the human endolymphatic sac endolymph. <i>Scientific Reports</i> , 2021, 11, 11850.	3.3	5
578	Proteomic strategies for characterizing ubiquitin-like modifications. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	21.2	6
579	In vivo analysis reveals that ATP-hydrolysis couples remodeling to SWI/SNF release from chromatin. <i>ELife</i> , 2021, 10, .	6.0	17
580	Effects of the Autophagy-Inhibiting Agent Chloroquine on Acute Myeloid Leukemia Cells; Characterization of Patient Heterogeneity. <i>Journal of Personalized Medicine</i> , 2021, 11, 779.	2.5	11

#	ARTICLE	IF	CITATIONS
582	Integrated Metabolomics and Proteomics Analyses in the Local Milieu of Islet Allografts in Rejection versus Tolerance. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8754.	4.1	2
583	FHL2 anchors mitochondria to actin and adapts mitochondrial dynamics to glucose supply. <i>Journal of Cell Biology</i> , 2021, 220, .	5.2	31
584	Oestrogen Activates the MAP3K1 Cascade and β -Catenin to Promote Granulosa-like Cell Fate in a Human Testis-Derived Cell Line. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10046.	4.1	0
585	Tissue-Specific Proteome and Subcellular Microscopic Analyses Reveal the Effect of High Salt Concentration on Actin Cytoskeleton and Vacuolization in Aleurone Cells during Early Germination of Barley. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9642.	4.1	9
586	Proteomic analysis of aqueous humor in canine primary angle-closure glaucoma in American Cocker Spaniel dogs. <i>Veterinary Ophthalmology</i> , 2021, 24, 520-532.	1.0	3
587	Structural determinants of peptide-dependent TAP1-TAP2 transit passage targeted by viral proteins and altered by cancer-associated mutations. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5072-5091.	4.1	9
588	Mapping Plant Phosphoproteome with Improved Tandem and Label-Free Quantification. <i>Methods in Molecular Biology</i> , 2021, 2358, 105-112.	0.9	2
589	Characterization of Extracellular HSV-1 Virions by Proteomics. <i>Methods in Molecular Biology</i> , 2014, 1144, 181-190.	0.9	13
590	SILAC Yeast: From Labeling to Comprehensive Proteome Quantification. <i>Methods in Molecular Biology</i> , 2014, 1156, 81-109.	0.9	9
591	SILAC-Based Temporal Phosphoproteomics. <i>Methods in Molecular Biology</i> , 2014, 1188, 125-148.	0.9	10
592	Analyzing the Protein Assembly and Dynamics of the Human Spliceosome with SILAC. <i>Methods in Molecular Biology</i> , 2014, 1188, 227-244.	0.9	3
593	Stable Isotope Labeling by Amino Acids Applied to Bacterial Cell Culture. <i>Methods in Molecular Biology</i> , 2014, 1188, 9-22.	0.9	25
594	Design and Application of Super-SILAC for Proteome Quantification. <i>Methods in Molecular Biology</i> , 2014, 1188, 281-291.	0.9	8
595	Identification of MicroRNA Targets by Pulsed SILAC. <i>Methods in Molecular Biology</i> , 2014, 1188, 327-349.	0.9	5
596	SILAC and Alternatives in Studying Cellular Proteomes of Plants. <i>Methods in Molecular Biology</i> , 2014, 1188, 65-83.	0.9	9
597	Stable Isotope Labeling for Proteomic Analysis of Tissues in Mouse. <i>Methods in Molecular Biology</i> , 2014, 1188, 95-106.	0.9	7
598	Combining Metabolic ^{15}N Labeling with Improved Tandem MOAC for Enhanced Probing of the Phosphoproteome. <i>Methods in Molecular Biology</i> , 2015, 1306, 81-96.	0.9	9
599	Resources for Assignment of Phosphorylation Sites on Peptides and Proteins. <i>Methods in Molecular Biology</i> , 2016, 1355, 293-306.	0.9	4

#	ARTICLE	IF	CITATIONS
600	Characterization of Extracellular HSV-1 Virions by Proteomics. <i>Methods in Molecular Biology</i> , 2020, 2060, 279-288.	0.9	9
601	Overview of Quantitative LC-MS Techniques for Proteomics and Activitomics. <i>Methods in Molecular Biology</i> , 2010, 658, 19-45.	0.9	17
602	Whole Cell Proteome Regulation by MicroRNAs Captured in a Pulsed SILAC Mass Spectrometry Approach. <i>Methods in Molecular Biology</i> , 2011, 725, 315-331.	0.9	12
603	Global Proteome Analyses of SILAC-Labeled Skin Cells. <i>Methods in Molecular Biology</i> , 2013, 961, 179-191.	0.9	11
604	Tandem Metal-Oxide Affinity Chromatography for Enhanced Depth of Phosphoproteome Analysis. <i>Methods in Molecular Biology</i> , 2014, 1072, 621-632.	0.9	10
605	SILAC-Based Quantification of Sirt1-Responsive Lysine Acetylome. <i>Methods in Molecular Biology</i> , 2013, 1077, 105-120.	0.9	11
606	Methylation of two-component response regulator MtrA in mycobacteria negatively modulates its DNA binding and transcriptional activation. <i>Biochemical Journal</i> , 2020, 477, 4473-4489.	3.7	7
612	Proteome turnover in the bloodstream and procyclic forms of <i>Trypanosoma brucei</i> measured by quantitative proteomics. <i>Wellcome Open Research</i> , 2019, 4, 152.	1.8	27
613	Tor1 and CK2 kinases control a switch between alternative ribosome biogenesis pathways in a growth-dependent manner. <i>PLoS Biology</i> , 2017, 15, e2000245.	5.6	54
614	Proteomic Changes Resulting from Gene Copy Number Variations in Cancer Cells. <i>PLoS Genetics</i> , 2010, 6, e1001090.	3.5	126
615	Large-Scale Analysis of Kinase Signaling in Yeast Pseudohyphal Development Identifies Regulation of Ribonucleoprotein Granules. <i>PLoS Genetics</i> , 2015, 11, e1005564.	3.5	24
616	Loss of the Greatwall Kinase Weakens the Spindle Assembly Checkpoint. <i>PLoS Genetics</i> , 2016, 12, e1006310.	3.5	32
617	Phosphorylation of the Yeast $\hat{\beta}$ -Tubulin Tub4 Regulates Microtubule Function. <i>PLoS ONE</i> , 2011, 6, e19700.	2.5	42
618	Pdx1 Is Post-Translationally Modified In vivo and Serine 61 Is the Principal Site of Phosphorylation. <i>PLoS ONE</i> , 2012, 7, e35233.	2.5	16
619	Analysis of Human Protein Replacement Stable Cell Lines Established using snoMEN-PR Vector. <i>PLoS ONE</i> , 2013, 8, e62305.	2.5	6
620	CK1 $\hat{\beta}$ Kinase Activity Is Modulated by Chk1-Mediated Phosphorylation. <i>PLoS ONE</i> , 2013, 8, e68803.	2.5	33
621	Differential regulation of germ line apoptosis and germ cell differentiation by CPEB family members in <i>C. elegans</i> . <i>PLoS ONE</i> , 2017, 12, e0182270.	2.5	5
622	Biological characteristics of aging in human acute myeloid leukemia cells: the possible importance of aldehyde dehydrogenase, the cytoskeleton and altered transcriptional regulation. <i>Aging</i> , 2020, 12, 24734-24777.	3.1	13

#	ARTICLE	IF	CITATIONS
623	Oncogenic epithelial cell-derived exosomes containing Rac1 and PAK2 induce angiogenesis in recipient endothelial cells. <i>Oncotarget</i> , 2016, 7, 19709-19722.	1.8	56
624	Characterization and use of HapT1-derived homologous tumors as a preclinical model to evaluate therapeutic efficacy of drugs against pancreatic tumor desmoplasia. <i>Oncotarget</i> , 0, 7, 41825-41842.	1.8	27
625	The Extracellular Bone Marrow Microenvironmentâ€™s A Proteomic Comparison of Constitutive Protein Release by In Vitro Cultured Osteoblasts and Mesenchymal Stem Cells. <i>Cancers</i> , 2021, 13, 62.	3.7	16
626	Outer Membrane Vesicles Derived from Salmonella Enteritidis Protect against the Virulent Wild-Type Strain Infection in a Mouse Model. <i>Journal of Microbiology and Biotechnology</i> , 2017, 27, 1519-1528.	2.1	22
627	Mitochondrial dysfunction remodels one-carbon metabolism in human cells. <i>ELife</i> , 2016, 5, .	6.0	332
628	Analysis of protein phosphorylation in nerve terminal reveals extensive changes in active zone proteins upon exocytosis. <i>ELife</i> , 2016, 5, .	6.0	41
629	Control of immune ligands by members of a cytomegalovirus gene expansion suppresses natural killer cell activation. <i>ELife</i> , 2017, 6, .	6.0	67
630	Deciphering the regulatory genome of Escherichia coli, one hundred promoters at a time. <i>ELife</i> , 2020, 9, .	6.0	31
631	The Na ⁺ -activated K ⁺ channel Slack contributes to synaptic development and plasticity. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 7569-7587.	5.4	4
632	Identifying the beta-site amyloid precursor protein cleaving enzyme 1 interactome through the proximity-dependent biotin identification assay. <i>Neuroscience Letters</i> , 2021, , 136302.	2.1	1
633	Development of Dual Stable Isotope Labeling by Amino Acids in Cell Culture and Application to Quantitative Proteomics. <i>Journal of the Mass Spectrometry Society of Japan</i> , 2010, 58, 81-87.	0.1	0
634	New Development of Quantitative Mass Spectrometry-Based Proteomics. <i>Chinese Journal of Analytical Chemistry</i> , 2010, 38, 434-441.	1.7	0
635	Stable Isotopic Labeling for Proteomics. , 2011, , 549-573.		2
636	Large-Scale Protein Phosphorylation Analysis by Mass Spectrometry-Based Phosphoproteomics. <i>Neuromethods</i> , 2012, , 35-46.	0.3	0
637	Dynamics of Protein Complexes Tracked by Quantitative Proteomics. , 0, , .		0
638	Proteomics Analysis of Contact-Initiated Eph Receptorâ€™s Ephrin Signaling. <i>Methods in Molecular Biology</i> , 2013, 1066, 1-16.	0.9	0
639	Large-Scale Proteome and Phosphoproteome Quantification by Using Dimethylation Isotope Labeling. <i>Springer Theses</i> , 2014, , 67-94.	0.1	0
640	SILAC-Based Quantitative Proteomics Approach to Identify Transcription Factors Interacting with a Novel Cis-Regulatory Element. <i>Journal of Proteomics and Bioinformatics</i> , 2014, 07, .	0.4	1

#	ARTICLE	IF	CITATIONS
641	Large-Scale Differential Proteome Analysis in Plasmodium falciparum Under Drug Treatment. <i>Methods in Molecular Biology</i> , 2015, 1201, 269-279.	0.9	1
642	Extracting, Enriching, and Identifying Nuclear Body Sub-Complexes Using Label-Based Quantitative Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2015, 1262, 215-238.	0.9	3
643	A Conceptual Outline for Omics Experiments Using Bioinformatics Analogies. <i>Bio-protocol</i> , 2015, 5, .	0.4	0
644	R for Proteomics. <i>New Developments in Mass Spectrometry</i> , 2016, , 321-364.	0.2	1
660	Comparative analysis of techniques to purify plasma membrane proteins. <i>Journal of Biomolecular Techniques</i> , 2010, 21, 108-15.	1.5	62
661	Quantitative proteomic analysis identifies new effectors of FOXM1 involved in breast cancer cell migration. <i>International Journal of Clinical and Experimental Pathology</i> , 2015, 8, 15836-44.	0.5	5
662	Proteomic Analysis of Mesenchymal Stromal Cell-Derived Extracellular Vesicles and Reconstructed Membrane Particles. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12935.	4.1	5
663	Quantitative Proteomics and Transcriptomics Reveals Differences in Proteins During Anthers Development in <i>Oryza longistaminata</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 744792.	3.6	3
664	Proteomic Changes of Activated Hepatic Stellate Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12782.	4.1	8
666	Proteomic and Phosphoryproteomic Investigations Reveal that Autophagy-Related Protein 1, a Protein Kinase for Autophagy Initiation, Synchronously Deploys Phosphoregulation on the Ubiquitin-Like Conjugation System in the Mycopathogen <i>Beauveria bassiana</i> . <i>MSystems</i> , 2022, 7, e0146321.	3.8	11
667	dCas9-VPR-mediated transcriptional activation of functionally equivalent genes for gene therapy. <i>Nature Protocols</i> , 2022, 17, 781-818.	12.0	11
668	Proximity Ligation Mapping of Microcephaly Associated SMPD4 Shows Association with Components of the Nuclear Pore Membrane. <i>Cells</i> , 2022, 11, 674.	4.1	3
669	Developing a Targeted Quantitative Strategy for Sulfoxide-Containing MS-Cleavable Cross-Linked Peptides to Probe Conformational Dynamics of Protein Complexes. <i>Analytical Chemistry</i> , 2022, 94, 4390-4398.	6.5	3
671	Proteome Analysis of Vacuoles Isolated from Fig (<i>Ficus carica</i> L.) Flesh during Fruit Development. <i>Plant and Cell Physiology</i> , 2022, 63, 785-801.	3.1	2
672	Quantitative Proteomic Analysis Reveals Important Roles of the Acetylation of ER-Resident Molecular Chaperones for Conidiation in <i>Fusarium oxysporum</i> . <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100231.	3.8	3
673	Altered Ca ²⁺ Homeostasis in Red Blood Cells of Polycythemia Vera Patients Following Disturbed Organelle Sorting during Terminal Erythropoiesis. <i>Cells</i> , 2022, 11, 49.	4.1	6
674	Quantitative proteomic screen identifies annexin A2 as a host target for <i>Salmonella</i> pathogenicity island-2 effectors SopD2 and PipB2. <i>Scientific Reports</i> , 2021, 11, 23630.	3.3	6
675	Biosafety and Proteome Profiles of Different Heat Inactivation Methods for <i>Mycobacterium tuberculosis</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0071621.	3.0	1

#	ARTICLE	IF	CITATIONS
720	Off-target effects of the lysosomal acid lipase inhibitors Lalistat-1 and Lalistat-2 on neutral lipid hydrolases. <i>Molecular Metabolism</i> , 2022, 61, 101510.	6.5	9
721	Advances in stable isotope labeling: dynamic labeling for spatial and temporal proteomic analysis. <i>Molecular Omics</i> , 2022, 18, 579-590.	2.8	13
722	<scpi>iTRAQ</scpi>-based quantitative proteomics reveals biomarkers/pathways in psoriasis that can predict the efficacy of methotrexate. <i>Journal of the European Academy of Dermatology and Venereology</i> , 2022, 36, 1784-1795.	2.4	6
723	Chemical Genetic Validation of CSNK2 Substrates Using an Inhibitor-Resistant Mutant in Combination with Triple SILAC Quantitative Phosphoproteomics. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	3.5	5
724	Englerin A Rewires Phosphosignaling via Hsp27 Hyperphosphorylation to Induce Cytotoxicity in Renal Cancer Cells. <i>Journal of Proteome Research</i> , 2022, 21, 1948-1960.	3.7	3
725	circEZH2 inhibits opening of mitochondrial permeability transition pore via interacting with PiC and up-regulating RSAD2. <i>Veterinary Microbiology</i> , 2022, 272, 109497.	1.9	2
726	The quantitative proteomic analysis reveals schisantherin a prevents liver fibrosis through regulating extracellular matrix organization. <i>International Journal of Mass Spectrometry</i> , 2022, 480, 116898.	1.5	1
727	Proteotoxicity caused by perturbed protein complexes underlies hybrid incompatibility in yeast. <i>Nature Communications</i> , 2022, 13, .	12.8	2
729	Direct control of lysosomal catabolic activity by mTORC1 through regulation of V-ATPase assembly. <i>Nature Communications</i> , 2022, 13, .	12.8	33
731	Synaptotagmin-13 orchestrates pancreatic endocrine cell egression and islet morphogenesis. <i>Nature Communications</i> , 2022, 13, .	12.8	9
732	Lysine acetylation plays a role in the allograft-induced stress response of the pearl oyster (<i>Pinctada</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.6	1
734	The Effect of Soybean Peptides on Improving Quality and the ACE Inhibitory Bioactivity of Extruded Rice. <i>Processes</i> , 2022, 10, 1921.	2.8	1
735	Lysosomal enzyme trafficking factor LYSET enables nutritional usage of extracellular proteins. <i>Science</i> , 2022, 378, .	12.6	28
736	Single-Cell Atlas of Patient-Derived Trophoblast Organoids in Ongoing Pregnancies. <i>Organoids</i> , 2022, 1, 106-115.	3.1	3
737	The kinesin motor KIF1C is a putative transporter of the exon junction complex in neuronal cells. <i>Rna</i> , 0, , rna.079426.122.	3.5	1
738	Mitochondrial Aconitase ACO2 Links Iron Homeostasis with Tumorigenicity in Non-“Small Cell Lung Cancer. <i>Molecular Cancer Research</i> , 2023, 21, 36-50.	3.4	3
739	Identification of novel interferon responsive protein partners of human leukocyte antigen A (HLA-A) using cross-linking mass spectrometry (CLMS) approach. <i>Scientific Reports</i> , 2022, 12, .	3.3	2
740	Effect of Insulin and Pioglitazone on Protein Phosphatase 2A Interaction Partners in Primary Human Skeletal Muscle Cells Derived from Obese Insulin-Resistant Participants. <i>ACS Omega</i> , 0, , .	3.5	1

#	ARTICLE	IF	CITATIONS
741	Use of Nuclear and Chromatin Enrichment Procedures for Quantitation of Yeast DNA Replication Proteins Using SILAC. <i>Methods in Molecular Biology</i> , 2023, , 209-218.	0.9	0
742	Antimicrobial Activity of Graphene Oxide Contributes to Alteration of Key Stress-Related and Membrane Bound Proteins. <i>International Journal of Nanomedicine</i> , 0, Volume 17, 6707-6721.	6.7	7
744	Online Alkaline-pH Reverse Phase Nanoelectrospray-Tandem Mass Spectrometry Complements Conventional Low-pH Method for Global Proteomic Analysis. <i>Journal of Proteome Research</i> , 0, , .	3.7	1
745	Identification of Filamin A Mechanobinding Partner III: SAV1 Specifically Interacts with Filamin A Mechanosensitive Domain 21. <i>Biochemistry</i> , 2023, 62, 1197-1208.	2.5	1
746	An integrated workflow for phosphopeptide identification in natural killer cells (NK-92MI) and their targets (MDA-MB-231) during immunological synapse formation. <i>STAR Protocols</i> , 2023, 4, 102104.	1.2	1
747	The force-dependent filamin A-G3BP1 interaction regulates phase-separated stress granule formation. <i>Journal of Cell Science</i> , 2023, 136, .	2.0	2
749	Rescue of Escherichia coli auxotrophy by de novo small proteins. <i>ELife</i> , 0, 12, .	6.0	7
750	Detection and Isolation of Circulating Tumor Cells from Breast Cancer Patients Using CUB Domain-Containing Protein 1. <i>Journal of Proteome Research</i> , 2023, 22, 1213-1230.	3.7	2
751	Desmosomal protein degradation as an underlying cause of arrhythmogenic cardiomyopathy. <i>Science Translational Medicine</i> , 2023, 15, .	12.4	9
752	Comparison of CX-4945 and SGC-CK2-1 as inhibitors of CSNK2 using quantitative phosphoproteomics: Triple SILAC in combination with inhibitor-resistant CSNK2. <i>Current Research in Chemical Biology</i> , 2023, 3, 100041.	2.9	5
753	Breaking spore dormancy in budding yeast transforms the cytoplasm and the solubility of the proteome. <i>PLoS Biology</i> , 2023, 21, e3002042.	5.6	7
754	Interaction of LARP4 to filamin A mechanosensing domain regulates cell migrations. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	3.7	2
755	eIF3 mRNA selectivity profiling reveals eIF3k as a cancer-relevant regulator of ribosome content. <i>EMBO Journal</i> , 2023, 42, .	7.8	0
756	The RNA-binding protein ZC3H11A interacts with the nuclear poly(A)-binding protein PABPN1 and alters polyadenylation of viral transcripts. <i>Journal of Biological Chemistry</i> , 2023, 299, 104959.	3.4	1
757	SeqWiz: a modularized toolkit for next-generation protein sequence database management and analysis. <i>BMC Bioinformatics</i> , 2023, 24, .	2.6	0
758	Graphene Oxide Attenuates Toxicity of Amyloid β Aggregates in Yeast by Promoting Disassembly and Boosting Cellular Stress Response. <i>Advanced Functional Materials</i> , 2023, 33, .	14.9	0
759	A proteomics analysis of 5xFAD mouse brain regions reveals the lysosome-associated protein Arl8b as a candidate biomarker for Alzheimer's disease. <i>Genome Medicine</i> , 2023, 15, .	8.2	2
760	Involvement of the AKT Pathway in Resistance to Erlotinib and Cabozantinib in Triple-Negative Breast Cancer Cell Lines. <i>Biomedicines</i> , 2023, 11, 2406.	3.2	0

#	ARTICLE	IF	CITATIONS
761	Melatonin decreases GSDME mediated mesothelial cell pyroptosis and prevents peritoneal fibrosis and ultrafiltration failure. <i>Science China Life Sciences</i> , 2024, 67, 360-378.	4.9	1
762	UBE2A/B is the <i>trans</i> -acting factor mediating mechanotransduction and contact inhibition. <i>Biochemical Journal</i> , 2023, 480, 1659-1674.	3.7	2
764	Genomic and Proteomic Approaches to Enhance Stress Tolerance in Plants for Creating Stress-Resilient Species. <i>Environmental Science and Engineering</i> , 2023, , 329-357.	0.2	0
765	Phosphoproteomics and Morphology of Stored Human Red Blood Cells Treated by Protein-Tyrosine-Phosphatases Inhibitor. <i>Blood Advances</i> , 0, , .	5.2	0
766	Phenotypic and proteomic characterization of the human erythroid progenitor continuum reveal dynamic changes in cell cycle and in metabolic pathways. <i>American Journal of Hematology</i> , 2024, 99, 99-112.	4.1	1
767	p97/VCP targets <i>Toxoplasma gondii</i> vacuoles for parasite restriction in interferon-stimulated human cells. <i>MSphere</i> , 0, , .	2.9	0
768	Identification and partial characterization of new cell density-dependent nucleocytoplasmic shuttling proteins and open chromatin. <i>Scientific Reports</i> , 2023, 13, .	3.3	1