

Kris Gevaert

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4424548/publications.pdf>

Version: 2024-02-01

411
papers

27,373
citations

4136

87
h-index

10152

140
g-index

441
all docs

441
docs citations

441
times ranked

36641
citing authors

#	ARTICLE	IF	CITATIONS
1	Improved visualization of protein consensus sequences by iceLogo. <i>Nature Methods</i> , 2009, 6, 786-787.	9.0	664
2	Exploring proteomes and analyzing protein processing by mass spectrometric identification of sorted N-terminal peptides. <i>Nature Biotechnology</i> , 2003, 21, 566-569.	9.4	573
3	PRIDE: The proteomics identifications database. <i>Proteomics</i> , 2005, 5, 3537-3545.	1.3	553
4	LNCipedia: a database for annotated human lncRNA transcript sequences and structures. <i>Nucleic Acids Research</i> , 2013, 41, D246-D251.	6.5	488
5	Melanoma addiction to the long non-coding RNA SAMMSON. <i>Nature</i> , 2016, 531, 518-522.	13.7	488
6	Proteomics analyses reveal the evolutionary conservation and divergence of N-terminal acetyltransferases from yeast and humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8157-8162.	3.3	472
7	Global Analysis of the Mitochondrial N-Proteome Identifies a Processing Peptidase Critical for Protein Stability. <i>Cell</i> , 2009, 139, 428-439.	13.5	434
8	Cdc42 induces filopodia by promoting the formation of an IRSp53:Mena complex. <i>Current Biology</i> , 2001, 11, 1645-1655.	1.8	357
9	Morphological and biochemical characterization of a human liver in a uPA-SCID mouse chimera. <i>Hepatology</i> , 2005, 41, 847-856.	3.6	351
10	Protein identification methods in proteomics. <i>Electrophoresis</i> , 2000, 21, 1145-1154.	1.3	328
11	LRRK2 Controls an EndoA Phosphorylation Cycle in Synaptic Endocytosis. <i>Neuron</i> , 2012, 75, 1008-1021.	3.8	312
12	The serine protease Omi/HtrA2 is released from mitochondria during apoptosis. Omi interacts with caspase-inhibitor XIAP and induces enhanced caspase activity. <i>Cell Death and Differentiation</i> , 2002, 9, 20-26.	5.0	308
13	PINK1 Loss-of-Function Mutations Affect Mitochondrial Complex I Activity via NdufA10 Ubiquinone Uncoupling. <i>Science</i> , 2014, 344, 203-207.	6.0	300
14	Endonuclease G: a mitochondrial protein released in apoptosis and involved in caspase-independent DNA degradation. <i>Cell Death and Differentiation</i> , 2001, 8, 1136-1142.	5.0	298
15	The miR-17-92 MicroRNA Cluster Regulates Multiple Components of the TGF- β Pathway in Neuroblastoma. <i>Molecular Cell</i> , 2010, 40, 762-773.	4.5	279
16	Targeted Peptidecentric Proteomics Reveals Caspase-7 as a Substrate of the Caspase-1 Inflammasomes. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2350-2363.	2.5	276
17	Caspase-14 protects against epidermal UVB photodamage and water loss. <i>Nature Cell Biology</i> , 2007, 9, 666-674.	4.6	266
18	The deubiquitinase USP15 antagonizes Parkin-mediated mitochondrial ubiquitination and mitophagy. <i>Human Molecular Genetics</i> , 2014, 23, 5227-5242.	1.4	264

#	ARTICLE	IF	CITATIONS
19	Identification of a novel mechanism of bloodâ€‘brain communication during peripheral inflammation via choroid plexusâ€‘derived extracellular vesicles. <i>EMBO Molecular Medicine</i> , 2016, 8, 1162-1183.	3.3	259
20	Protein N-terminal acetyltransferases: when the start matters. <i>Trends in Biochemical Sciences</i> , 2012, 37, 152-161.	3.7	252
21	Rac/Cdc42 and p65PAK Regulate the Microtubule-destabilizing Protein Stathmin through Phosphorylation at Serine 16. <i>Journal of Biological Chemistry</i> , 2001, 276, 1677-1680.	1.6	246
22	Parkin Interacts with Ambra1 to Induce Mitophagy. <i>Journal of Neuroscience</i> , 2011, 31, 10249-10261.	1.7	239
23	The TPLATE Adaptor Complex Drives Clathrin-Mediated Endocytosis in Plants. <i>Cell</i> , 2014, 156, 691-704.	13.5	238
24	Chromatographic Isolation of Methionine-containing Peptides for Gel-free Proteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 896-903.	2.5	219
25	ANGUSTIFOLIA3 Binds to SWI/SNF Chromatin Remodeling Complexes to Regulate Transcription during <i>Arabidopsis</i> Leaf Development. <i>Plant Cell</i> , 2014, 26, 210-229.	3.1	219
26	Caspase-specific and nonspecific in vivo protein processing during Fas-induced apoptosis. <i>Nature Methods</i> , 2005, 2, 771-777.	9.0	208
27	Capturing the phosphorylation and protein interaction landscape of the plant TOR kinase. <i>Nature Plants</i> , 2019, 5, 316-327.	4.7	205
28	<i>Listeria monocytogenes</i> impairs SUMOylation for efficient infection. <i>Nature</i> , 2010, 464, 1192-1195.	13.7	201
29	Protein Language: Post-Translational Modifications Talking to Each Other. <i>Trends in Plant Science</i> , 2018, 23, 1068-1080.	4.3	199
30	T-cell receptor-induced JNK activation requires proteolytic inactivation of CYLD by MALT1. <i>EMBO Journal</i> , 2011, 30, 1742-1752.	3.5	196
31	Confounding factors of ultrafiltration and protein analysis in extracellular vesicle research. <i>Scientific Reports</i> , 2017, 7, 2704.	1.6	181
32	N-terminal acetylome analyses and functional insights of the N-terminal acetyltransferase NatB. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12449-12454.	3.3	175
33	Damage on plants activates Ca ²⁺ -dependent metacaspases for release of immunomodulatory peptides. <i>Science</i> , 2019, 363, .	6.0	170
34	Caspase-14 Is Required for Filaggrin Degradation to Natural Moisturizing Factors in the Skin. <i>Journal of Investigative Dermatology</i> , 2011, 131, 2233-2241.	0.3	167
35	Selecting protein N-terminal peptides by combined fractional diagonal chromatography. <i>Nature Protocols</i> , 2011, 6, 1130-1141.	5.5	164
36	Sulfenome mining in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11545-11550.	3.3	163

#	ARTICLE	IF	CITATIONS
37	NatF Contributes to an Evolutionary Shift in Protein N-Terminal Acetylation and Is Important for Normal Chromosome Segregation. <i>PLoS Genetics</i> , 2011, 7, e1002169.	1.5	161
38	Toll-like Receptor 4 Engagement on Dendritic Cells Restrains Phago-Lysosome Fusion and Promotes Cross-Presentation of Antigens. <i>Immunity</i> , 2015, 43, 1087-1100.	6.6	160
39	An improved toolbox to unravel the plant cellular machinery by tandem affinity purification of Arabidopsis protein complexes. <i>Nature Protocols</i> , 2015, 10, 169-187.	5.5	160
40	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	9.4	155
41	Deep Proteome Coverage Based on Ribosome Profiling Aids Mass Spectrometry-based Protein and Peptide Discovery and Provides Evidence of Alternative Translation Products and Near-cognate Translation Initiation Events*. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1780-1790.	2.5	154
42	Dynamic Changes in ANGUSTIFOLIA3 Complex Composition Reveal a Growth Regulatory Mechanism in the Maize Leaf. <i>Plant Cell</i> , 2015, 27, 1605-1619.	3.1	154
43	Impairment of Angiogenesis by Fatty Acid Synthase Inhibition Involves mTOR Malonylation. <i>Cell Metabolism</i> , 2018, 28, 866-880.e15.	7.2	154
44	The Neural Cell Adhesion Molecules L1 and CHL1 Are Cleaved by BACE1 Protease in Vivo. <i>Journal of Biological Chemistry</i> , 2012, 287, 25927-25940.	1.6	152
45	Synaptogyrin-3 Mediates Presynaptic Dysfunction Induced by Tau. <i>Neuron</i> , 2018, 97, 823-835.e8.	3.8	151
46	NAA80 is actinâ€™s N-terminal acetyltransferase and regulates cytoskeleton assembly and cell motility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4399-4404.	3.3	150
47	Identification and Functional Characterization of N-Terminally Acetylated Proteins in <i>Drosophila melanogaster</i> . <i>PLoS Biology</i> , 2009, 7, e1000236.	2.6	149
48	DBToolkit: processing protein databases for peptide-centric proteomics. <i>Bioinformatics</i> , 2005, 21, 3584-3585.	1.8	148
49	Improved recovery of proteomeâ€™informative, protein Nâ€™terminal peptides by combined fractional diagonal chromatography (COFRADIC). <i>Proteomics</i> , 2008, 8, 1362-1370.	1.3	144
50	A protein phosphatase 2A complex spatially controls plant cell division. <i>Nature Communications</i> , 2013, 4, 1863.	5.8	138
51	Multiple mechanisms limit meiotic crossovers: TOP3Î± and two BLM homologs antagonize crossovers in parallel to FANCM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4713-4718.	3.3	138
52	The ROS Wheel: Refining ROS Transcriptional Footprints. <i>Plant Physiology</i> , 2016, 171, 1720-1733.	2.3	137
53	Citrullinated Glucose-Regulated Protein 78 Is an Autoantigen in Type 1 Diabetes. <i>Diabetes</i> , 2015, 64, 573-586.	0.3	136
54	LRRK2 functions in synaptic vesicle endocytosis through a kinase-dependent mechanism. <i>Journal of Cell Science</i> , 2015, 128, 541â€“52.	1.2	134

#	ARTICLE	IF	CITATIONS
55	Mutations in LZTR1 drive human disease by dysregulating RAS ubiquitination. <i>Science</i> , 2018, 362, 1177-1182.	6.0	133
56	A Plant Plasma Membrane H ⁺ -ATPase Expressed in Yeast Is Activated by Phosphorylation at Its Penultimate Residue and Binding of 14-3-3 Regulatory Proteins in the Absence of Fusaric Acid. <i>Journal of Biological Chemistry</i> , 2000, 275, 17762-17770.	1.6	131
57	FYVE1/FREE1 Interacts with the PYL4 ABA Receptor and Mediates Its Delivery to the Vacuolar Degradation Pathway. <i>Plant Cell</i> , 2016, 28, 2291-2311.	3.1	129
58	Proteome-derived Peptide Libraries Allow Detailed Analysis of the Substrate Specificities of N ^ε -acetyltransferases and Point to hNaa10p as the Post-translational Actin N ^ε -acetyltransferase. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.004580.	2.5	127
59	The human platelet proteome mapped by peptide-centric proteomics: A functional protein profile. <i>Proteomics</i> , 2005, 5, 3193-3204.	1.3	126
60	Global Differential Non-Gel Proteomics by Quantitative and Stable Labeling of Tryptic Peptides with Oxygen-18. <i>Journal of Proteome Research</i> , 2004, 3, 786-791.	1.8	125
61	Stable isotopic labeling in proteomics. <i>Proteomics</i> , 2008, 8, 4873-4885.	1.3	125
62	Analysis of the β -secretase interactome and validation of its association with tetraspanin-enriched microdomains. <i>Nature Cell Biology</i> , 2009, 11, 1340-1346.	4.6	121
63	Chronic Kidney Disease Circulating Calciprotein Particles and Extracellular Vesicles Promote Vascular Calcification. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018, 38, 575-587.	1.1	121
64	SitePredicting the cleavage of proteinase substrates. <i>Trends in Biochemical Sciences</i> , 2009, 34, 319-323.	3.7	119
65	Look Closely, the Beautiful May Be Small: Precursor-Derived Peptides in Plants. <i>Annual Review of Plant Biology</i> , 2019, 70, 153-186.	8.6	119
66	A Repressor Protein Complex Regulates Leaf Growth in Arabidopsis. <i>Plant Cell</i> , 2015, 27, 2273-2287.	3.1	118
67	Listeria comet tails: the actin-based motility machinery at work. <i>Trends in Cell Biology</i> , 2008, 18, 220-227.	3.6	117
68	Redox Proteomics of Protein-bound Methionine Oxidation. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006866.	2.5	117
69	Genetic predisposition for beta cell fragility underlies type 1 and type 2 diabetes. <i>Nature Genetics</i> , 2016, 48, 519-527.	9.4	117
70	Matrix metalloproteinase 13 modulates intestinal epithelial barrier integrity in inflammatory diseases by activating TNF. <i>EMBO Molecular Medicine</i> , 2013, 5, 1000-1016.	3.3	114
71	The Chaperone-Like Protein HYPK Acts Together with NatA in Cotranslational N-Terminal Acetylation and Prevention of Huntingtin Aggregation. <i>Molecular and Cellular Biology</i> , 2010, 30, 1898-1909.	1.1	113
72	Proteome-wide Identification of HtrA2/Omi Substrates. <i>Journal of Proteome Research</i> , 2007, 6, 1006-1015.	1.8	111

#	ARTICLE	IF	CITATIONS
73	Large-Scale Identification of N-Terminal Peptides in the Halophilic Archaea <i>Halobacterium salinarum</i> and <i>Natronomonas pharaonis</i> . <i>Journal of Proteome Research</i> , 2007, 6, 2195-2204.	1.8	109
74	The <i>Arabidopsis</i> METACASPASE9 Degradome. <i>Plant Cell</i> , 2013, 25, 2831-2847.	3.1	109
75	Mining for protein S-sulfenylation in <i>Arabidopsis</i> uncovers redox-sensitive sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21256-21261.	3.3	107
76	Complementary positional proteomics for screening substrates of endo- and exoproteases. <i>Nature Methods</i> , 2010, 7, 512-515.	9.0	106
77	An Organellar N ⁶ -Acetyltransferase, Naa60, Acetylates Cytosolic N Termini of Transmembrane Proteins and Maintains Golgi Integrity. <i>Cell Reports</i> , 2015, 10, 1362-1374.	2.9	105
78	Proteome analysis of the <i>Chlamydia pneumoniae</i> elementary body. <i>Electrophoresis</i> , 2001, 22, 1204-1223.	1.3	104
79	Cysteines under ROS attack in plants: a proteomics view. <i>Journal of Experimental Botany</i> , 2015, 66, 2935-2944.	2.4	103
80	Variable Glutamine-Rich Repeats Modulate Transcription Factor Activity. <i>Molecular Cell</i> , 2015, 59, 615-627.	4.5	103
81	The Human N-Alpha-Acetyltransferase 40 (hNaa40p/hNatD) Is Conserved from Yeast and N-Terminally Acetylates Histones H2A and H4. <i>PLoS ONE</i> , 2011, 6, e24713.	1.1	102
82	Biochemical and cellular analysis of Ogden syndrome reveals downstream Nt-acetylation defects. <i>Human Molecular Genetics</i> , 2015, 24, 1956-1976.	1.4	97
83	Zebrafish Collagen Type I: Molecular and Biochemical Characterization of the Major Structural Protein in Bone and Skin. <i>Scientific Reports</i> , 2016, 6, 21540.	1.6	97
84	The Plant PTM Viewer, a central resource for exploring plant protein modifications. <i>Plant Journal</i> , 2019, 99, 752-762.	2.8	97
85	The generation and use of recombinant extracellular vesicles as biological reference material. <i>Nature Communications</i> , 2019, 10, 3288.	5.8	96
86	Analysis of Protein Processing by N-terminal Proteomics Reveals Novel Species-specific Substrate Determinants of Granzyme B Orthologs. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 258-272.	2.5	95
87	Small Heat-Shock Protein HSPB1 Mutants Stabilize Microtubules in Charcot-Marie-Tooth Neuropathy. <i>Journal of Neuroscience</i> , 2011, 31, 15320-15328.	1.7	95
88	Reversible labeling of cysteine-containing peptides allows their specific chromatographic isolation for non-gel proteome studies. <i>Proteomics</i> , 2004, 4, 897-908.	1.3	93
89	Cells Lacking F-Actin are Genetically Reprogrammed and Maintain Conditional Migratory Capacity*. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 255-271.	2.5	93
90	A novel approach to analyze lysosomal dysfunctions through subcellular proteomics and lipidomics: the case of NPC1 deficiency. <i>Scientific Reports</i> , 2017, 7, 41408.	1.6	93

#	ARTICLE	IF	CITATIONS
91	Tumor necrosis factor-induced modulation of glyoxalase I activities through phosphorylation by PKA results in cell death and is accompanied by the formation of a specific methylglyoxal-derived AGE. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 949-954.	3.3	92
92	A nanobody targeting the F-actin capping protein CapG restrains breast cancer metastasis. <i>Breast Cancer Research</i> , 2013, 15, R116.	2.2	91
93	cIAP1/2 Are Direct E3 Ligases Conjugating Diverse Types of Ubiquitin Chains to Receptor Interacting Proteins Kinases 1 to 4 (RIP1-4). <i>PLoS ONE</i> , 2011, 6, e22356.	1.1	91
94	The deubiquitylase USP33 discriminates between RALB functions in autophagy and innate immune response. <i>Nature Cell Biology</i> , 2013, 15, 1220-1230.	4.6	89
95	Feeling the Heat: Searching for Plant Thermosensors. <i>Trends in Plant Science</i> , 2019, 24, 210-219.	4.3	89
96	Protein Methionine Sulfoxide Dynamics in <i>Arabidopsis thaliana</i> under Oxidative Stress. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1217-1229.	2.5	88
97	The mTOR and PP2A Pathways Regulate PHD2 Phosphorylation to Fine-Tune HIF1 α Levels and Colorectal Cancer Cell Survival under Hypoxia. <i>Cell Reports</i> , 2017, 18, 1699-1712.	2.9	88
98	Constitutively active LVR8 photoreceptor variant in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20326-20331.	3.3	87
99	Proteome studies of bacterial antibiotic resistance mechanisms. <i>Journal of Proteomics</i> , 2014, 97, 88-99.	1.2	86
100	Disruption of endocytosis through chemical inhibition of clathrin heavy chain function. <i>Nature Chemical Biology</i> , 2019, 15, 641-649.	3.9	86
101	A la carte proteomics with an emphasis on gel-free techniques. <i>Proteomics</i> , 2007, 7, 2698-2718.	1.3	85
102	In Vitro and in Vivo Protein-bound Tyrosine Nitration Characterized by Diagonal Chromatography. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2642-2652.	2.5	85
103	It's Time for Some "Site" Seeing: Novel Tools to Monitor the Ubiquitin Landscape in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2016, 28, 6-16.	3.1	84
104	GRIM REAPER peptide binds to receptor kinase PRK5 to trigger cell death in <i>Arabidopsis</i> . <i>EMBO Journal</i> , 2015, 34, 55-66.	3.5	83
105	Proteomic Identification of Cysteine Cathepsin Substrates Shed from the Surface of Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2213-2228.	2.5	82
106	Peptide-level Robust Ridge Regression Improves Estimation, Sensitivity, and Specificity in Data-dependent Quantitative Label-free Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 657-668.	2.5	82
107	CEP5 and XIP1/CEPR1 regulate lateral root initiation in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2016, 67, 4889-4899.	2.4	81
108	FIGL1 and its novel partner FLIP form a conserved complex that regulates homologous recombination. <i>PLoS Genetics</i> , 2018, 14, e1007317.	1.5	81

#	ARTICLE	IF	CITATIONS
109	A matrix-assisted laser desorption ionization post-source decay (MALDI-PSD) analysis of proteins released from isolated liver mitochondria treated with recombinant truncated Bid. <i>Cell Death and Differentiation</i> , 2002, 9, 301-308.	5.0	79
110	Positional proteomics reveals differences in N-terminal proteoform stability. <i>Molecular Systems Biology</i> , 2016, 12, 858.	3.2	79
111	Functional characterization of the Arabidopsis transcription factor bZIP29 reveals its role in leaf and root development. <i>Journal of Experimental Botany</i> , 2016, 67, 5825-5840.	2.4	78
112	Comparative proteome analysis of <i>Chlamydia trachomatis</i> serovar A, D and L2. <i>Proteomics</i> , 2002, 2, 164-186.	1.3	77
113	Recessive osteogenesis imperfecta caused by LEPRE1 mutations: clinical documentation and identification of the splice form responsible for prolyl 3-hydroxylation. <i>Journal of Medical Genetics</i> , 2009, 46, 233-241.	1.5	77
114	Improving the reliability and throughput of mass spectrometry-based proteomics by spectrum quality filtering. <i>Proteomics</i> , 2006, 6, 2086-2094.	1.3	76
115	The RING E3 Ligase KEEP ON GOING Modulates JASMONATE ZIM-DOMAIN12 Stability. <i>Plant Physiology</i> , 2015, 169, 1405-1417.	2.3	76
116	Exploring the protein-protein interaction landscape in plants. <i>Plant, Cell and Environment</i> , 2019, 42, 387-409.	2.8	76
117	Characterization of a secreted <i>Chlamydia</i> protease. <i>Cellular Microbiology</i> , 2002, 4, 411-424.	1.1	75
118	ms_lims, a simple yet powerful open source laboratory information management system for MS-driven proteomics. <i>Proteomics</i> , 2010, 10, 1261-1264.	1.3	73
119	Experimental design and data-analysis in label-free quantitative LC/MS proteomics: A tutorial with MSqRob. <i>Journal of Proteomics</i> , 2018, 171, 23-36.	1.2	72
120	EXPANSIN A1-mediated radial swelling of pericycle cells positions anticlinal cell divisions during lateral root initiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8597-8602.	3.3	71
121	Classification and Nomenclature of Metacaspases and Paracaspases: No More Confusion with Caspases. <i>Molecular Cell</i> , 2020, 77, 927-929.	4.5	71
122	Diagonal reverse-phase chromatography applications in peptide-centric proteomics: Ahead of catalogue-omics?. <i>Analytical Biochemistry</i> , 2005, 345, 18-29.	1.1	70
123	The MAGUK Protein MPP7 Binds to the Polarity Protein hDlg1 and Facilitates Epithelial Tight Junction Formation. <i>Molecular Biology of the Cell</i> , 2007, 18, 1744-1755.	0.9	70
124	Protein alpha-N-acetylation studied by N-terminomics. <i>FEBS Journal</i> , 2011, 278, 3822-3834.	2.2	70
125	DYN-2 Based Identification of Arabidopsis Sulfenomes*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1183-1200.	2.5	70
126	A peptide concentration and purification method for protein characterization in the subpicomole range using matrix assisted laser desorption/ionization-postsource decay (MALDI-PSD) sequencing. <i>Electrophoresis</i> , 1998, 19, 909-917.	1.3	67

#	ARTICLE	IF	CITATIONS
127	Protein identification based on matrix assisted laser desorption/ionization-post source decay-mass spectrometry. <i>Electrophoresis</i> , 2001, 22, 1645-1651.	1.3	67
128	A proteogenomics approach integrating proteomics and ribosome profiling increases the efficiency of protein identification and enables the discovery of alternative translation start sites. <i>Proteomics</i> , 2014, 14, 2688-2698.	1.3	66
129	Global phosphoproteome analysis on human HepG2 hepatocytes using reversed-phase diagonal LC. <i>Proteomics</i> , 2005, 5, 3589-3599.	1.3	65
130	Proteome-wide Substrate Analysis Indicates Substrate Exclusion as a Mechanism to Generate Caspase-7 Versus Caspase-3 Specificity. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2700-2714.	2.5	64
131	Angiotensin I-Converting Enzyme Inhibitory Activity of Gelatin Hydrolysates and Identification of Bioactive Peptides. <i>Journal of Agricultural and Food Chemistry</i> , 2011, 59, 552-558.	2.4	64
132	De novo design of a biologically active amyloid. <i>Science</i> , 2016, 354, .	6.0	63
133	DET1-mediated degradation of a SAGA-like deubiquitination module controls H2Bub homeostasis. <i>ELife</i> , 2018, 7, .	2.8	63
134	SnRK2 Protein Kinases and mRNA Decapping Machinery Control Root Development and Response to Salt. <i>Plant Physiology</i> , 2020, 182, 361-377.	2.3	62
135	Diversity in Protein Glycosylation among Insect Species. <i>PLoS ONE</i> , 2011, 6, e16682.	1.1	62
136	Structural analysis and identification of gel-purified proteins, available in the femtomole range, using a novel computer program for peptide sequence assignment, by matrix-assisted laser desorption ionization reflectron time-of-flight mass spectrometry. <i>Electrophoresis</i> , 1996, 17, 918-924.	1.3	61
137	Strigolactones, karrikins and beyond. <i>Plant, Cell and Environment</i> , 2017, 40, 1691-1703.	2.8	61
138	Ectopic application of the repressive histone modification H3K9me2 establishes post-zygotic reproductive isolation in <i>Arabidopsis thaliana</i> . <i>Genes and Development</i> , 2017, 31, 1272-1287.	2.7	61
139	Distinct branches of the N-end rule pathway modulate the plant immune response. <i>New Phytologist</i> , 2019, 221, 988-1000.	3.5	59
140	Proteome-wide Characterization of N-Glycosylation Events by Diagonal Chromatography. <i>Journal of Proteome Research</i> , 2006, 5, 2438-2447.	1.8	57
141	A COFRADIC Protocol To Study Protein Ubiquitination. <i>Journal of Proteome Research</i> , 2014, 13, 3107-3113.	1.8	57
142	A review of COFRADIC techniques targeting protein N-terminal acetylation. <i>BMC Proceedings</i> , 2009, 3, S6.	1.8	56
143	A protein-protein interaction map of the TNF-induced NF- κ B signal transduction pathway. <i>Scientific Data</i> , 2018, 5, 180289.	2.4	56
144	MS-driven protease substrate degradomics. <i>Proteomics</i> , 2010, 10, 1284-1296.	1.3	55

#	ARTICLE	IF	CITATIONS
145	The Non-JAZ TIFY Protein TIFY8 from <i>Arabidopsis thaliana</i> Is a Transcriptional Repressor. <i>PLoS ONE</i> , 2014, 9, e84891.	1.1	55
146	Drugging the catalytically inactive state of RET kinase in RET-rearranged tumors. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	55
147	Developmental Plasticity at High Temperature. <i>Plant Physiology</i> , 2019, 181, 399-411.	2.3	55
148	Peptides adsorbed on reverse-phase chromatographic beads as targets for femtomole sequencing by post-source decay matrix assisted laser desorption ionization-reflectron time of flight mass spectrometry (MALDI-RETTOF-MS). <i>Electrophoresis</i> , 1997, 18, 2950-2960.	1.3	54
149	Plant proteins under oxidative attack. <i>Proteomics</i> , 2013, 13, 932-940.	1.3	54
150	N-terminal Proteomics Assisted Profiling of the Unexplored Translation Initiation Landscape in <i>Arabidopsis thaliana</i> . <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1064-1080.	2.5	54
151	The transcriptional repressor complex FRS7-FRS12 regulates flowering time and growth in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2017, 8, 15235.	5.8	54
152	Do we want our data raw? Including binary mass spectrometry data in public proteomics data repositories. <i>Proteomics</i> , 2005, 5, 3501-3505.	1.3	53
153	The Transcriptional Repressor Glis2 Is a Novel Binding Partner for p120 Catenin. <i>Molecular Biology of the Cell</i> , 2007, 18, 1918-1927.	0.9	53
154	Bioinformatics Analysis of a <i>Saccharomyces cerevisiae</i> N-Terminal Proteome Provides Evidence of Alternative Translation Initiation and Post-Translational N-Terminal Acetylation. <i>Journal of Proteome Research</i> , 2011, 10, 3578-3589.	1.8	53
155	A complex interaction pattern of CIS and SOCS2 with the leptin receptor. <i>Journal of Cell Science</i> , 2006, 119, 2214-2224.	1.2	52
156	The iceLogo web server and SOAP service for determining protein consensus sequences. <i>Nucleic Acids Research</i> , 2015, 43, W543-W546.	6.5	52
157	An Agarose-Based Gel-Concentration System for Microsequence and Mass Spectrometric Characterization of Proteins Previously Purified in Polyacrylamide Gels Starting at Low Picomole Levels. <i>FEBS Journal</i> , 1995, 230, 258-265.	0.2	51
158	A Quantitative Proteomics Design for Systematic Identification of Protease Cleavage Events. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2327-2333.	2.5	51
159	Câ€terminomics: Targeted analysis of natural and posttranslationally modified protein and peptide Câ€termini. <i>Proteomics</i> , 2015, 15, 903-914.	1.3	51
160	Mapping Proteolytic Processing in the Secretome of Gastric Cancer-Associated Myofibroblasts Reveals Activation of MMP-1, MMP-2, and MMP-3. <i>Journal of Proteome Research</i> , 2013, 12, 3413-3422.	1.8	50
161	Up-to-Date Workflow for Plant (Phospho)proteomics Identifies Differential Drought-Responsive Phosphorylation Events in Maize Leaves. <i>Journal of Proteome Research</i> , 2016, 15, 4304-4317.	1.8	50
162	Pick a Tag and Explore the Functions of Your Pet Protein. <i>Trends in Biotechnology</i> , 2019, 37, 1078-1090.	4.9	50

#	ARTICLE	IF	CITATIONS
163	Peptizer, a Tool for Assessing False Positive Peptide Identifications and Manually Validating Selected Results. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2364-2372.	2.5	49
164	A <i>Saccharomyces cerevisiae</i> Model Reveals In Vivo Functional Impairment of the Ogden Syndrome N-Terminal Acetyltransferase NAA10 Ser37Pro Mutant. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2031-2041.	2.5	49
165	N-terminal acetylome analysis reveals the specificity of Naa50 (Nat5) and suggests a kinetic competition between N-terminal acetyltransferases and methionine aminopeptidases. <i>Proteomics</i> , 2015, 15, 2436-2446.	1.3	49
166	MascotDatfile: An open-source library to fully parse and analyse MASCOT MS/MS search results. <i>Proteomics</i> , 2007, 7, 364-366.	1.3	48
167	Vaccination with an <i>Ostertagia ostertagi</i> Polyprotein Allergen Protects Calves against Homologous Challenge Infection. <i>Infection and Immunity</i> , 2004, 72, 2995-3001.	1.0	47
168	Identification of <i>Chlamydia trachomatis</i> CT621, a protein delivered through the type III secretion system to the host cell cytoplasm and nucleus. <i>FEMS Immunology and Medical Microbiology</i> , 2009, 57, 46-58.	2.7	47
169	Interaction of the Tobacco Lectin with Histone Proteins. <i>Plant Physiology</i> , 2011, 155, 1091-1102.	2.3	47
170	Vaccination against <i>Ostertagia ostertagi</i> with subfractions of the protective ES-thiol fraction. <i>Veterinary Parasitology</i> , 2007, 149, 239-245.	0.7	46
171	A Role for Human N-alpha Acetyltransferase 30 (Naa30) in Maintaining Mitochondrial Integrity. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3361-3372.	2.5	46
172	A fast and convenient MALDI-MS based proteomic approach: identification of components scaffolded by the actin cytoskeleton of activated human thrombocytes. <i>Journal of Biotechnology</i> , 2000, 78, 259-269.	1.9	44
173	Fast profiling of protease specificity reveals similar substrate specificities for cathepsins K, L and S. <i>Proteomics</i> , 2015, 15, 2479-2490.	1.3	44
174	Protein aggregation as an antibiotic design strategy. <i>Molecular Microbiology</i> , 2016, 99, 849-865.	1.2	44
175	Noncoding after All: Biases in Proteomics Data Do Not Explain Observed Absence of lncRNA Translation Products. <i>Journal of Proteome Research</i> , 2017, 16, 2508-2515.	1.8	44
176	The expression, processing and localization of polymorphic membrane proteins in <i>Chlamydia pneumoniae</i> strain CWL029. <i>BMC Microbiology</i> , 2002, 2, 36.	1.3	43
177	PP2A-3 interacts with ACR4 and regulates formative cell division in the <i>Arabidopsis</i> root. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1447-1452.	3.3	43
178	Activation-associated secreted proteins are the most abundant antigens in a host protective fraction from <i>Ostertagia ostertagi</i> . <i>Molecular and Biochemical Parasitology</i> , 2003, 128, 111-114.	0.5	42
179	Identification and Characterization of Immunogenic Proteins of <i>Mycoplasma genitalium</i> . <i>Vaccine Journal</i> , 2006, 13, 913-922.	3.2	42
180	Chitinase-like Proteins are Candidate Biomarkers for Sepsis-induced Acute Kidney Injury. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013094.	2.5	42

#	ARTICLE	IF	CITATIONS
181	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	2.5	42
182	Targeted Proteomics for Studying Pathogenic Bacteria. <i>Proteomics</i> , 2019, 19, e1800435.	1.3	42
183	Improved tandem mass spectrometric characterization of 3-nitrotyrosine sites in peptides. <i>Rapid Communications in Mass Spectrometry</i> , 2006, 20, 2885-2893.	0.7	41
184	Mechanistic insight into taxol-induced cell death. <i>Oncogene</i> , 2008, 27, 4580-4591.	2.6	41
185	Proteomics methods to study methionine oxidation. <i>Mass Spectrometry Reviews</i> , 2014, 33, 147-156.	2.8	41
186	Trapping mammalian protein complexes in viral particles. <i>Nature Communications</i> , 2016, 7, 11416.	5.8	41
187	Caspase substrates: easily caught in deep waters?. <i>Trends in Biotechnology</i> , 2009, 27, 680-688.	4.9	40
188	Rover: A tool to visualize and validate quantitative proteomics data from different sources. <i>Proteomics</i> , 2010, 10, 1226-1229.	1.3	40
189	thermo-msf-parser: An Open Source Java Library to Parse and Visualize Thermo Proteome Discoverer <i><i>msf</i></i> Files. <i>Journal of Proteome Research</i> , 2011, 10, 3840-3843.	1.8	40
190	Proteome-derived Peptide Libraries to Study the Substrate Specificity Profiles of Carboxypeptidases. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2096-2110.	2.5	40
191	ADAM30 Downregulates APP-Linked Defects Through Cathepsin D Activation in Alzheimer's Disease. <i>EBioMedicine</i> , 2016, 9, 278-292.	2.7	40
192	The calcium-binding protein p54/NEFA is a novel luminal resident of medial Golgi cisternae that traffics independently of mannosidase II. <i>European Journal of Cell Biology</i> , 2002, 81, 87-100.	1.6	39
193	N-terminal acetylation and other functions of N ^ε -acetyltransferases. <i>Biological Chemistry</i> , 2012, 393, 291-298.	1.2	39
194	Linking functions: an additional role for an intrinsically disordered linker domain in the transcriptional coactivator CBP. <i>Scientific Reports</i> , 2017, 7, 4676.	1.6	39
195	Seed germination in parasitic plants: what insights can we expect from strigolactone research?. <i>Journal of Experimental Botany</i> , 2018, 69, 2265-2280.	2.4	39
196	CYP707As are effectors of karrikin and strigolactone signalling pathways in <i>Arabidopsis thaliana</i> and parasitic plants. <i>Plant, Cell and Environment</i> , 2019, 42, 2612-2626.	2.8	39
197	Effect of phospholipid molecular structure on its interaction with whey proteins in aqueous solution. <i>Food Hydrocolloids</i> , 2013, 32, 312-321.	5.6	38
198	The proteome under translational control. <i>Proteomics</i> , 2014, 14, 2647-2662.	1.3	38

#	ARTICLE	IF	CITATIONS
199	Protein processing and other modifications analyzed by diagonal peptide chromatography. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 1801-1810.	1.1	37
200	The substrate specificity profile of human granzyme A. <i>Biological Chemistry</i> , 2010, 391, 983-97.	1.2	37
201	Human and mouse granzyme M display divergent and species-specific substrate specificities. <i>Biochemical Journal</i> , 2011, 437, 431-442.	1.7	37
202	A novel strategy for the comprehensive analysis of the biomolecular composition of isolated plasma membranes. <i>Molecular Systems Biology</i> , 2011, 7, 541.	3.2	37
203	Degradomics Reveals That Cleavage Specificity Profiles of Caspase-2 and Effector Caspases Are Alike. <i>Journal of Biological Chemistry</i> , 2012, 287, 33983-33995.	1.6	37
204	Robust sequential biophysical fractionation of blood plasma to study variations in the biomolecular landscape of systemically circulating extracellular vesicles across clinical conditions. <i>Journal of Extracellular Vesicles</i> , 2021, 10, e12122.	5.5	37
205	Abolition of stress-induced protein synthesis sensitizes leukemia cells to anthracycline-induced death. <i>Blood</i> , 2008, 111, 2866-2877.	0.6	35
206	Structural Investigation of B-Raf Paradox Breaker and Inducer Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 1818-1831.	2.9	35
207	Glutaredoxin GRXS17 Associates with the Cytosolic Iron-Sulfur Cluster Assembly Pathway. <i>Plant Physiology</i> , 2016, 172, pp.00261.2016.	2.3	35
208	The CEP5 Peptide Promotes Abiotic Stress Tolerance, As Revealed by Quantitative Proteomics, and Attenuates the AUX/IAA Equilibrium in Arabidopsis. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1248-1262.	2.5	35
209	Investigation of Rifampicin Resistance Mechanisms in <i>Brucella abortus</i> Using MS-Driven Comparative Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 2374-2385.	1.8	34
210	High entomotoxicity and mechanism of the fungal GalNAc/Gal-specific <i>Rhizoctonia solani</i> lectin in pest insects. <i>Journal of Insect Physiology</i> , 2013, 59, 295-305.	0.9	34
211	MSqRob Takes the Missing Hurdle: Uniting Intensity- and Count-Based Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 6278-6287.	3.2	34
212	N-Terminal Proteoforms in Human Disease. <i>Trends in Biochemical Sciences</i> , 2020, 45, 308-320.	3.7	34
213	Glycosylation Signatures in <i>Drosophila</i> : Fishing with Lectins. <i>Journal of Proteome Research</i> , 2010, 9, 3235-3242.	1.8	33
214	<i>Arabidopsis thaliana</i> RNase H2 Deficiency Counteracts the Needs for the WEE1 Checkpoint Kinase but Triggers Genome Instability. <i>Plant Cell</i> , 2014, 26, 3680-3692.	3.1	33
215	NBPF1, a tumor suppressor candidate in neuroblastoma, exerts growth inhibitory effects by inducing a G1 cell cycle arrest. <i>BMC Cancer</i> , 2015, 15, 391.	1.1	33
216	The Whats, the Wheres and the Hows of strigolactone action in the roots. <i>Planta</i> , 2016, 243, 1327-1337.	1.6	33

#	ARTICLE	IF	CITATIONS
217	Integrator restrains paraspeckles assembly by promoting isoform switching of the lncRNA <i>NEAT1</i> . <i>Science Advances</i> , 2020, 6, eaaz9072.	4.7	33
218	A catalogue of putative HIV-1 protease host cell substrates. <i>Biological Chemistry</i> , 2012, 393, 915-931.	1.2	32
219	A New Functional, Chemical Proteomics Technology To Identify Purine Nucleotide Binding Sites in Complex Proteomes. <i>Journal of Proteome Research</i> , 2006, 5, 3438-3445.	1.8	31
220	Contemporary positional proteomics strategies to study protein processing. <i>Current Opinion in Chemical Biology</i> , 2013, 17, 66-72.	2.8	31
221	Early mannitol-triggered changes in the Arabidopsis leaf (phospho)proteome reveal growth regulators. <i>Journal of Experimental Botany</i> , 2018, 69, 4591-4607.	2.4	31
222	A <i>Phelipanche ramosa</i> KAI2 protein perceives strigolactones and isothiocyanates enzymatically. <i>Plant Communications</i> , 2021, 2, 100166.	3.6	31
223	The proteome of the human neuroblastoma cell line SH-SY5Y: An enlarged proteome. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 983-985.	1.1	30
224	Analysis of the transthyretin-like (TTL) gene family in <i>Ostertagia ostertagi</i> – Comparison with other stronglyid nematodes and <i>Caenorhabditis elegans</i> . <i>International Journal for Parasitology</i> , 2008, 38, 1545-1556.	1.3	30
225	Substrate Specificities of the Granzyme Trypsases A and K. <i>Journal of Proteome Research</i> , 2014, 13, 6067-6077.	1.8	30
226	Taximin, a conserved plant-specific peptide is involved in the modulation of plant-specialized metabolism. <i>Plant Biotechnology Journal</i> , 2014, 12, 971-983.	4.1	30
227	Temperature-induced changes in the wheat phosphoproteome reveal temperature-regulated interconversion of phosphoforms. <i>Journal of Experimental Botany</i> , 2018, 69, 4609-4624.	2.4	30
228	The membrane-localized protein kinase MAP4K4/TOT3 regulates thermomorphogenesis. <i>Nature Communications</i> , 2021, 12, 2842.	5.8	30
229	Importance of extracellular vesicle secretion at the blood-cerebrospinal fluid interface in the pathogenesis of Alzheimer's disease. <i>Acta Neuropathologica Communications</i> , 2021, 9, 143.	2.4	30
230	UBP12 and UBP13 negatively regulate the activity of the ubiquitin-dependent peptidases DA1, DAR1 and DAR2. <i>ELife</i> , 2020, 9, .	2.8	30
231	Four Stage Liquid Chromatographic Selection of Methionyl Peptides for Peptide-Centric Proteome Analysis: A The Proteome of Human Multipotent Adult Progenitor Cells. <i>Journal of Proteome Research</i> , 2006, 5, 1415-1428.	1.8	29
232	Natural substrates of plant proteases: how can protease degradomics extend our knowledge?. <i>Physiologia Plantarum</i> , 2012, 145, 28-40.	2.6	29
233	Early Targets of miR-34a in Neuroblastoma. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2114-2131.	2.5	29
234	Implementation and application of a versatile clustering tool for tandem mass spectrometry data. <i>Proteomics</i> , 2007, 7, 3245-3258.	1.3	28

#	ARTICLE	IF	CITATIONS
235	The actin propulsive machinery: The proteome of <i>Listeria monocytogenes</i> tails. <i>Biochemical and Biophysical Research Communications</i> , 2008, 375, 194-199.	1.0	28
236	Probing the Efficiency of Proteolytic Events by Positional Proteomics. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S10.	2.5	28
237	A phylogenetic approach to study the origin and evolution of the CRINKLY4 family. <i>Frontiers in Plant Science</i> , 2015, 6, 880.	1.7	28
238	The Response of the Root Proteome to the Synthetic Strigolactone GR24 in <i>Arabidopsis</i> . <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2744-2755.	2.5	28
239	The autophagy receptor SQSTM1/p62 mediates anti-inflammatory actions of the selective NR3C1/glucocorticoid receptor modulator compound A (CpdA) in macrophages. <i>Autophagy</i> , 2018, 14, 2049-2064.	4.3	28
240	Dehydrin ERD14 activates glutathione transferase Phi9 in <i>Arabidopsis thaliana</i> under osmotic stress. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129506.	1.1	28
241	Bacterial Genetic Engineering by Means of Recombineering for Reverse Genetics. <i>Frontiers in Microbiology</i> , 2020, 11, 548410.	1.5	28
242	SCX charge state selective separation of tryptic peptides combined with 2D-RP-HPLC allows for detailed proteome mapping. <i>Journal of Proteomics</i> , 2013, 91, 164-171.	1.2	27
243	Identification of Serpinb6b as a Species-specific Mouse Granzyme A Inhibitor Suggests Functional Divergence between Human and Mouse Granzyme A. <i>Journal of Biological Chemistry</i> , 2014, 289, 9408-9417.	1.6	27
244	<i>Salmonella</i> Typhi, Paratyphi A, Enteritidis and Typhimurium core proteomes reveal differentially expressed proteins linked to the cell surface and pathogenicity. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007416.	1.3	27
245	Mechanisms of Congenital Heart Disease Caused by NAA15 Haploinsufficiency. <i>Circulation Research</i> , 2021, 128, 1156-1169.	2.0	27
246	Simple Peptide Quantification Approach for MS-Based Proteomics Quality Control. <i>ACS Omega</i> , 2020, 5, 6754-6762.	1.6	26
247	A comparison of the HUPO Brain Proteome Project pilot with other proteomics studies. <i>Proteomics</i> , 2006, 6, 5076-5086.	1.3	25
248	Assessing a novel microfluidic interface for shotgun proteome analyses. <i>Journal of Separation Science</i> , 2007, 30, 1468-1476.	1.3	25
249	Structure of granzyme C reveals an unusual mechanism of protease autoinhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5587-5592.	3.3	25
250	The Apaf-1-binding protein Aven is cleaved by Cathepsin D to unleash its anti-apoptotic potential. <i>Cell Death and Differentiation</i> , 2012, 19, 1435-1445.	5.0	25
251	Protein N-terminal Acetyltransferases Act as N-terminal Propionyltransferases In Vitro and In Vivo. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 42-54.	2.5	25
252	C-terminomics Screen for Natural Substrates of Cytosolic Carboxypeptidase 1 Reveals Processing of Acidic Protein C termini. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 177-190.	2.5	25

#	ARTICLE	IF	CITATIONS
253	Xilmass: A New Approach toward the Identification of Cross-Linked Peptides. <i>Analytical Chemistry</i> , 2016, 88, 9949-9957.	3.2	25
254	N-terminal Acetylation Levels Are Maintained During Acetyl-CoA Deficiency in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2309-2323.	2.5	25
255	Improved Glucocorticoid Receptor Ligands: Fantastic Beasts, but How to Find Them?. <i>Frontiers in Endocrinology</i> , 2020, 11, 559673.	1.5	25
256	Compound A, a Selective Glucocorticoid Receptor Modulator, Enhances Heat Shock Protein Hsp70 Gene Promoter Activation. <i>PLoS ONE</i> , 2013, 8, e69115.	1.1	25
257	Applications of diagonal chromatography for proteome-wide characterization of protein modifications and activity-based analyses. <i>FEBS Journal</i> , 2007, 274, 6277-6289.	2.2	24
258	Interaction of Î±-Catulin with Dystrobrevin Contributes to Integrity of Dystrophin Complex in Muscle. <i>Journal of Biological Chemistry</i> , 2012, 287, 21717-21728.	1.6	24
259	Proteogenomics in Aid of Host-Pathogen Interaction Studies: A Bacterial Perspective. <i>Proteomes</i> , 2017, 5, 26.	1.7	24
260	Pollens destroy respiratory epithelial cell anchors and drive alphaherpesvirus infection. <i>Scientific Reports</i> , 2019, 9, 4787.	1.6	24
261	Selection of egg peptide biomarkers in processed food products by high resolution mass spectrometry. <i>Journal of Chromatography A</i> , 2019, 1584, 115-125.	1.8	24
262	Novel techniques for identification and characterization of proteins loaded on gels in femtomole amounts. <i>The Protein Journal</i> , 1997, 16, 335-342.	1.1	23
263	Gender-enriched transcription of activation associated secreted proteins in <i>Ostertagia ostertagi</i> . <i>International Journal for Parasitology</i> , 2008, 38, 455-465.	1.3	23
264	Analysis of proteins in <i>Chlamydia trachomatis</i> L2 outer membrane complex, COMC. <i>FEMS Immunology and Medical Microbiology</i> , 2009, 55, 187-195.	2.7	23
265	Quantitative Proteome Profiling of <i>C. burnetii</i> under Tetracycline Stress Conditions. <i>PLoS ONE</i> , 2012, 7, e33599.	1.1	23
266	Deregulation of focal adhesion formation and cytoskeletal tension due to loss of A-type lamins. <i>Cell Adhesion and Migration</i> , 2017, 11, 447-463.	1.1	23
267	A comparison of MS2-based label-free quantitative proteomic techniques with regards to accuracy and precision. <i>Proteomics</i> , 2011, 11, 1110-1113.	1.3	22
268	GalNAc/Gal-Binding <i>Rhizoctonia solani</i> Agglutinin Has Antiproliferative Activity in <i>Drosophila melanogaster</i> S2 Cells via MAPK and JAK/STAT Signaling. <i>PLoS ONE</i> , 2012, 7, e33680.	1.1	22
269	Improving the Identification Rate of Endogenous Peptides Using Electron Transfer Dissociation and Collision-Induced Dissociation. <i>Journal of Proteome Research</i> , 2013, 12, 5410-5421.	1.8	22
270	Identification of Immune-Responsive Gene 1 (IRG1) as a Target of A20. <i>Journal of Proteome Research</i> , 2018, 17, 2182-2191.	1.8	22

#	ARTICLE	IF	CITATIONS
271	Selection of universal peptide biomarkers for the detection of the allergen hazelnut in food through a comprehensive, high resolution mass spectrometric (HRMS) based approach. <i>Food Chemistry</i> , 2020, 309, 125679.	4.2	22
272	A New Approach for Mapping Sialylated N-Glycosites in Serum Proteomes. <i>Journal of Proteome Research</i> , 2007, 6, 4304-4312.	1.8	21
273	RIBAR and xRIBAR: Methods for Reproducible Relative MS/MS-based Label-Free Protein Quantification. <i>Journal of Proteome Research</i> , 2011, 10, 3183-3189.	1.8	21
274	Development of an enzyme-linked immunosorbent assay for detection of cellular and in vivo LRRK2 S935 phosphorylation. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2013, 76, 49-58.	1.4	21
275	Organellar Omics: A Reviving Strategy to Untangle the Biomolecular Complexity of the Cell. <i>Proteomics</i> , 2018, 18, 1700113.	1.3	21
276	Cell_motility: a cross-platform, open source application for the study of cell motion paths. <i>BMC Bioinformatics</i> , 2006, 7, 289.	1.2	20
277	m-Calpain activation in vitro does not require autolysis or subunit dissociation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 864-872.	1.1	20
278	The growing story of (ARABIDOPSIS) CRINKLY 4. <i>Journal of Experimental Botany</i> , 2016, 67, 4835-4847.	2.4	20
279	Isolation of protein complexes from the model legume <i>Medicago truncatula</i> by tandem affinity purification in hairy root cultures. <i>Plant Journal</i> , 2016, 88, 476-489.	2.8	20
280	SFINX: Straightforward Filtering Index for Affinity Purification Mass Spectrometry Data Analysis. <i>Journal of Proteome Research</i> , 2016, 15, 332-338.	1.8	20
281	Gold nanodome SERS platform for label-free detection of protease activity. <i>Faraday Discussions</i> , 2017, 205, 345-361.	1.6	20
282	Disulfide bond formation protects <i>Arabidopsis thaliana</i> glutathione transferase tau 23 from oxidative damage. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 775-789.	1.1	20
283	Comparison of Free-Space and Waveguide-Based SERS Platforms. <i>Nanomaterials</i> , 2019, 9, 1401.	1.9	20
284	Plant proteases and programmed cell death. <i>Journal of Experimental Botany</i> , 2019, 70, 1991-1995.	2.4	20
285	Granzyme M targets topoisomerase II alpha to trigger cell cycle arrest and caspase-dependent apoptosis. <i>Cell Death and Differentiation</i> , 2014, 21, 416-426.	5.0	19
286	GS ^{yellow} , a Multifaceted Tag for Functional Protein Analysis in Monocot and Dicot Plants. <i>Plant Physiology</i> , 2018, 177, 447-464.	2.3	19
287	Mass spectrometry and the cellular surfaceome. <i>Mass Spectrometry Reviews</i> , 2022, 41, 804-841.	2.8	19
288	Identification of Potentially Involved Proteins in Levofloxacin Resistance Mechanisms in <i>Coxiella burnetii</i> . <i>Journal of Proteome Research</i> , 2011, 10, 756-762.	1.8	18

#	ARTICLE	IF	CITATIONS
289	Combining quantitative proteomics data processing workflows for greater sensitivity. <i>Nature Methods</i> , 2011, 8, 481-483.	9.0	18
290	High-resolution mass spectrometry-based selection of peanut peptide biomarkers considering food processing and market type variation. <i>Food Chemistry</i> , 2020, 304, 125428.	4.2	18
291	Molecular analysis of astacin-like metalloproteases of <i>Ostertagia ostertagi</i> . <i>Parasitology</i> , 2005, 130, 89-98.	0.7	17
292	An aspartyl protease inhibitor of <i>Ostertagia ostertagi</i> : Molecular cloning, analysis of stage and tissue specific expression and vaccine trial. <i>Molecular and Biochemical Parasitology</i> , 2005, 141, 81-88.	0.5	17
293	Disentanglement of protease substrate repertoires. <i>Biological Chemistry</i> , 2008, 389, 371-381.	1.2	17
294	HyperISGylation of Old World Monkey ISG15 in Human Cells. <i>PLoS ONE</i> , 2008, 3, e2427.	1.1	17
295	The Online Protein Processing Resource (TOPPR): a database and analysis platform for protein processing events. <i>Nucleic Acids Research</i> , 2013, 41, D333-D337.	6.5	17
296	FRS7 and FRS12 recruit NINJA to regulate expression of glucosinolate biosynthesis genes. <i>New Phytologist</i> , 2020, 227, 1124-1137.	3.5	17
297	Identification by two-dimensional electrophoresis of a new adhesin expressed by a low-passaged strain of <i>Mycoplasma bovis</i> . <i>Research in Microbiology</i> , 2005, 156, 713-718.	1.0	16
298	Combination of COFRADIC and high temperature " extended column length conventional liquid chromatography: A very efficient way to tackle complex protein samples, such as serum. <i>Journal of Separation Science</i> , 2007, 30, 658-668.	1.3	16
299	The Arabidopsis Iron-Sulfur Protein GRXS17 is a Target of the Ubiquitin E3 Ligases RGLG3 and RGLG4. <i>Plant and Cell Physiology</i> , 2016, 57, 1801-1813.	1.5	16
300	Proteome Profiling of Wheat Shoots from Different Cultivars. <i>Frontiers in Plant Science</i> , 2017, 8, 332.	1.7	16
301	A Novel Receptor-mediated Regulation Mechanism of Type I Inositol Polyphosphate 5-Phosphatase by Calcium/Calmodulin-dependent Protein Kinase II Phosphorylation. <i>Journal of Biological Chemistry</i> , 2001, 276, 38738-38747.	1.6	15
302	Evaluation of Encoded Layer-by-Layer Coated Microparticles As Protease Sensors. <i>Advanced Functional Materials</i> , 2008, 18, 1624-1631.	7.8	15
303	Hybrid N-glycans on the host protective activation-associated secreted proteins of <i>Ostertagia ostertagi</i> and their importance in immunogenicity. <i>Molecular and Biochemical Parasitology</i> , 2008, 161, 67-71.	0.5	15
304	Analysis of the translationally controlled tumour protein in the nematodes <i>Ostertagia ostertagi</i> and <i>Caenorhabditis elegans</i> suggests a pivotal role in egg production. <i>International Journal for Parasitology</i> , 2009, 39, 1205-1213.	1.3	15
305	Study of Protein Expression in Peri-Infarct Tissue after Cerebral Ischemia. <i>Scientific Reports</i> , 2015, 5, 12030.	1.6	15
306	An extra dimension in protein tagging by quantifying universal proteotypic peptides using targeted proteomics. <i>Scientific Reports</i> , 2016, 6, 27220.	1.6	15

#	ARTICLE	IF	CITATIONS
307	Resolution of protein structure by mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2016, 35, 653-665.	2.8	15
308	Analyzing trapped protein complexes by Virotrap and SFINX. <i>Nature Protocols</i> , 2017, 12, 881-898.	5.5	15
309	Use of Hybrid Data-Dependent and -Independent Acquisition Spectral Libraries Empowers Dual-Proteome Profiling. <i>Journal of Proteome Research</i> , 2021, 20, 1165-1177.	1.8	15
310	Proteome-wide cellular thermal shift assay reveals unexpected cross-talk between brassinosteroid and auxin signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2118220119.	3.3	15
311	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.	0.4	14
312	A stringent approach to improve the quality of nitrotyrosine peptide identifications. <i>Proteomics</i> , 2011, 11, 1094-1098.	1.3	14
313	Study of the Whole Cell Lysate of Two <i>Coxiella burnetii</i> Strains Using N-Terminomics. <i>Journal of Proteome Research</i> , 2012, 11, 3150-3159.	1.8	14
314	Conservation of the Extended Substrate Specificity Profiles Among Homologous Granzymes Across Species. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2921-2934.	2.5	14
315	Proteomic approaches to identify substrates of the three Deg/HtrA proteases of the cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Biochemical Journal</i> , 2015, 468, 373-384.	1.7	14
316	Comparative study of concatemer efficiency as an isotope-labelled internal standard for allergen quantification. <i>Food Chemistry</i> , 2020, 332, 127413.	4.2	14
317	The Final Maturation State of β -actin Involves N-terminal Acetylation by NAA80, not N-terminal Arginylation by ATE1. <i>Journal of Molecular Biology</i> , 2022, 434, 167397.	2.0	14
318	A new generation of AD biomarkers: 2019 to 2021. <i>Ageing Research Reviews</i> , 2022, 79, 101654.	5.0	14
319	Multiple isoforms of the tumor suppressor myopodin are simultaneously transcribed in cancer cells. <i>Biochemical and Biophysical Research Communications</i> , 2008, 370, 269-273.	1.0	13
320	The Tandem PDZ Protein Syntenin Interacts with the Aminoacyl tRNA Synthetase Complex in a Lysyl-tRNA Synthetase-Dependent Manner. <i>Journal of Proteome Research</i> , 2008, 7, 4962-4973.	1.8	13
321	Asn ₃ , a Reliable, Robust, and Universal Lock Mass for Improved Accuracy in LC-MS and LC-MS/MS. <i>Analytical Chemistry</i> , 2013, 85, 11054-11060.	3.2	13
322	In-Gel N-Acetylation for the Quantification of the Degree of Protein In Vivo N-Terminal Acetylation. <i>Methods in Molecular Biology</i> , 2013, 981, 115-126.	0.4	13
323	Plant hormone signalling through the eye of the mass spectrometer. <i>Proteomics</i> , 2015, 15, 1113-1126.	1.3	13
324	A Well-Controlled BioID Design for Endogenous Bait Proteins. <i>Journal of Proteome Research</i> , 2019, 18, 95-106.	1.8	13

#	ARTICLE	IF	CITATIONS
325	Quantitative Tandem Affinity Purification, an Effective Tool to Investigate Protein Complex Composition in Plant Hormone Signaling: Strigolactones in the Spotlight. <i>Frontiers in Plant Science</i> , 2018, 9, 528.	1.7	13
326	An AKT2-specific nanobody that targets the hydrophobic motif induces cell cycle arrest, autophagy and loss of focal adhesions in MDA-MB-231 cells. <i>Biomedicine and Pharmacotherapy</i> , 2021, 133, 111055.	2.5	13
327	Proteomic and metabolomic responses to connexin43 silencing in primary hepatocyte cultures. <i>Archives of Toxicology</i> , 2013, 87, 883-894.	1.9	12
328	Expanding the Interactome of TES by Exploiting TES Modules with Different Subcellular Localizations. <i>Journal of Proteome Research</i> , 2017, 16, 2054-2071.	1.8	12
329	RIPK4 activity in keratinocytes is controlled by the SCF ^{β2} -TrCP ubiquitin ligase to maintain cortical actin organization. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 2827-2841.	2.4	12
330	The C-terminus of CIS defines its interaction pattern. <i>Biochemical Journal</i> , 2007, 401, 257-267.	1.7	11
331	Protease Substrate Profiling by N-Terminal COFRADIC. <i>Methods in Molecular Biology</i> , 2017, 1574, 51-76.	0.4	11
332	Extracellular peptide Kratos restricts cell death during vascular development and stress in Arabidopsis. <i>Journal of Experimental Botany</i> , 2019, 70, 2199-2210.	2.4	11
333	Protein amino-termini and how to identify them. <i>Expert Review of Proteomics</i> , 2020, 17, 581-594.	1.3	11
334	Unraveling the MAX2 Protein Network in Arabidopsis thaliana: Identification of the Protein Phosphatase PAPP5 as a Novel MAX2 Interactor. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100040.	2.5	11
335	Prune-1 drives polarization of tumor-associated macrophages (TAMs) within the lung metastatic niche in triple-negative breast cancer. <i>iScience</i> , 2021, 24, 101938.	1.9	11
336	Triazolinedione protein modification: from an overlooked off-target effect to a tryptophan-based bioconjugation strategy. <i>Chemical Science</i> , 2022, 13, 5390-5397.	3.7	11
337	Limited Evidence for Protein Products of Noncoding Transcripts in the HEK293T Cellular Cytosol. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100264.	2.5	11
338	Targeting of Aminopeptidase I to the Yeast Vacuole Is Mediated by Ssa1p, a Cytosolic Member of the 70-kDa Stress Protein Family. <i>Journal of Biological Chemistry</i> , 2000, 275, 34054-34059.	1.6	10
339	COFRADIC ² : the Hubble telescope of proteomics. <i>Drug Discovery Today: TARGETS</i> , 2004, 3, 16-22.	0.5	10
340	Proteome profiling of the green sulfur bacterium <i>Chlorobaculum tepidum</i> by N-terminal proteomics. <i>Proteomics</i> , 2012, 12, 63-67.	1.3	10
341	Selective Glucocorticoid Receptor Properties of GSK866 Analogs with Cysteine Reactive Warheads. <i>Frontiers in Immunology</i> , 2017, 8, 1324.	2.2	10
342	Evolutionarily conserved and species-specific glycoproteins in the N-glycoproteomes of diverse insect species. <i>Insect Biochemistry and Molecular Biology</i> , 2018, 100, 22-29.	1.2	10

#	ARTICLE	IF	CITATIONS
343	N-glycosylation Site Analysis Reveals Sex-related Differences in Protein N-glycosylation in the Rice Brown Planthopper (<i>Nilaparvata lugens</i>). <i>Molecular and Cellular Proteomics</i> , 2020, 19, 529-539.	2.5	10
344	Identification and characterization of a novel specific secreted protein family for selected members of the subfamily Ostertagiinae (Nematoda). <i>Parasitology</i> , 2008, 135, 63-70.	0.7	9
345	Phosphoproteomics-based peptide ligand-receptor kinase pairing. Commentary on: "A peptide hormone and its receptor protein kinase regulate plant cell expansion". <i>Frontiers in Plant Science</i> , 2015, 6, 224.	1.7	9
346	HIV-1 Vpr N-terminal tagging affects alternative splicing of the viral genome. <i>Scientific Reports</i> , 2016, 6, 34573.	1.6	9
347	Construction and analysis of a human testis/sperm-enriched interaction network: Unraveling the PPP1CC2 interactome. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 375-385.	1.1	9
348	Quantitative proteomics and systems analysis of cultured H9C2 cardiomyoblasts during differentiation over time supports a "function follows form" model of differentiation. <i>Molecular Omics</i> , 2018, 14, 181-196.	1.4	9
349	Reverse-Phase Diagonal Chromatography for Phosphoproteome Research. <i>Methods in Molecular Biology</i> , 2009, 527, 219-227.	0.4	9
350	SAMBA controls cell division rate during maize development. <i>Plant Physiology</i> , 2022, 188, 411-424.	2.3	9
351	A SMALL HEAT SHOCK PROTEIN OF OSTERTAGIA OSTERTAGI: STAGE-SPECIFIC EXPRESSION, HEAT INDUCIBILITY, AND PROTECTION TRIAL. <i>Journal of Parasitology</i> , 2006, 92, 1244-1250.	0.3	8
352	Unraveling Persistent Host Cell Infection with <i>Coxiella burnetii</i> by Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2011, 10, 4241-4251.	1.8	8
353	Holistic View on the Extended Substrate Specificities of Orthologous Granzymes. <i>Journal of Proteome Research</i> , 2014, 13, 1785-1793.	1.8	8
354	Intelligent Mixing of Proteomes for Elimination of False Positives in Affinity Purification-Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 3929-3937.	1.8	8
355	New Strategies in High Sensitivity Characterization of Proteins Separated from 1-D or 2-D Gels. , 1995, , 15-26.		8
356	Preparation of <i>Arabidopsis thaliana</i> Seedling Proteomes for Identifying Metacaspase Substrates by N-terminal COFRADIC. <i>Methods in Molecular Biology</i> , 2014, 1133, 255-261.	0.4	8
357	Waveguide-based surface-enhanced Raman spectroscopy detection of protease activity using non-natural aromatic amino acids. <i>Biomedical Optics Express</i> , 2020, 11, 4800.	1.5	8
358	Who gets cut during cell death?. <i>Current Opinion in Cell Biology</i> , 2010, 22, 859-864.	2.6	7
359	The chlorosome of <i>Chlorobaculum tepidum</i> : Size, mass and protein composition revealed by electron microscopy, dynamic light scattering and mass spectrometry-driven proteomics. <i>Proteomics</i> , 2011, 11, 2867-2880.	1.3	7
360	A reproducibility-based evaluation procedure for quantifying the differences between MS/MS peak intensity normalization methods. <i>Proteomics</i> , 2011, 11, 1172-1180.	1.3	7

#	ARTICLE	IF	CITATIONS
361	Activation of ADF/cofilin by phosphorylation-regulated Slingshot phosphatase is required for the meiotic spindle assembly in <i>Xenopus laevis</i> oocytes. <i>Molecular Biology of the Cell</i> , 2013, 24, 1933-1946.	0.9	7
362	Unraveling the specificities of the different human methionine sulfoxide reductases. <i>Proteomics</i> , 2014, 14, 1990-1998.	1.3	7
363	Limited Proteolysis Combined with Stable Isotope Labeling Reveals Conformational Changes in Protein (Pseudo)kinases upon Binding Small Molecules. <i>Journal of Proteome Research</i> , 2015, 14, 4179-4193.	1.8	7
364	Proteomics in the genome engineering era. <i>Proteomics</i> , 2016, 16, 177-187.	1.3	7
365	Transferring an optimized TAP-toolbox for the isolation of protein complexes to a portfolio of rice tissues. <i>Plant Molecular Biology</i> , 2016, 91, 341-354.	2.0	7
366	Challenges in the Structural-Functional Characterization of Multidomain, Partially Disordered Proteins CBP and p300: Preparing Native Proteins and Developing Nanobody Tools. <i>Methods in Enzymology</i> , 2018, 611, 607-675.	0.4	7
367	Peanut Stunt Virus and Its Satellite RNA Trigger Changes in Phosphorylation in <i>N. benthamiana</i> Infected Plants at the Early Stage of the Infection. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3223.	1.8	7
368	Caught green-handed: methods for in vivo detection and visualization of protease activity. <i>Journal of Experimental Botany</i> , 2019, 70, 2125-2141.	2.4	7
369	Protein Processing Characterized by a Gel-Free Proteomics Approach. <i>Methods in Molecular Biology</i> , 2008, 484, 245-262.	0.4	7
370	Novel assays monitoring direct glucocorticoid receptor protein activity exhibit high predictive power for ligand activity on endogenous gene targets. <i>Biomedicine and Pharmacotherapy</i> , 2022, 152, 113218.	2.5	7
371	Mass Spectrometry-Driven Proteomics: An Introduction. <i>Methods in Molecular Biology</i> , 2011, 753, 1-27.	0.4	6
372	Design and visualization of second-generation cyanoisindole-based fluorescent strigolactone analogs. <i>Plant Journal</i> , 2019, 98, 165-180.	2.8	6
373	Binding of <i>Oryzata</i> lectin induces an immune response in insect cells. <i>Insect Science</i> , 2021, , .	1.5	6
374	Time-dependent expression and processing of a hypothetical protein of possible importance for regulation of the <i>Chlamydia pneumoniae</i> developmental cycle. <i>Electrophoresis</i> , 2001, 22, 1697-1704.	1.3	5
375	Integrated Proteomic Analysis Reveals a Substantial Enrichment of Protein Trafficking Processes in Hippocampus Tissue after Hypoxic Stress. <i>Journal of Proteome Research</i> , 2010, 9, 204-215.	1.8	5
376	How many spots with missing values can be tolerated in quantitative two-dimensional gel electrophoresis when applying univariate statistics?. <i>Journal of Proteomics</i> , 2012, 75, 1792-1802.	1.2	5
377	HPLC-Based Quantification of In Vitro N-Terminal Acetylation. <i>Methods in Molecular Biology</i> , 2013, 981, 95-102.	0.4	5
378	Importance of extended protease substrate recognition motifs in steering BNIP-2 cleavage by human and mouse granzymes B. <i>BMC Biochemistry</i> , 2014, 15, 21.	4.4	5

#	ARTICLE	IF	CITATIONS
379	Development and characterization of protein kinase B/AKT isoform-specific nanobodies. PLoS ONE, 2020, 15, e0240554.	1.1	5
380	Mass spectrometry-based clinical proteomics – a revival. Expert Review of Proteomics, 2021, 18, 411-414.	1.3	5
381	Transcriptional Analysis in the Arabidopsis Roots Reveals New Regulators that Link <i>rac</i> -GR24 Treatment with Changes in Flavonol Accumulation, Root Hair Elongation and Lateral Root Density. Plant and Cell Physiology, 2022, 63, 104-119.	1.5	5
382	How has urinary proteomics contributed to the discovery of early biomarkers of acute kidney injury?. Expert Review of Proteomics, 2014, 11, 415-424.	1.3	4
383	Identification of Carboxypeptidase Substrates by C-Terminal COFRADIC. Methods in Molecular Biology, 2017, 1574, 115-133.	0.4	4
384	The lectin Oryzata induces phosphatase-mediated and carbohydrate-independent aggregation of insect cells. Journal of Insect Physiology, 2021, 131, 104241.	0.9	4
385	Techniques for sample preparation including methods for concentrating peptide samples. , 2000, 88, 29-42.		4
386	Selecting Processing Robust Markers Using High-Resolution Mass Spectrometry for the Detection of Milk in Food Products. Journal of AOAC INTERNATIONAL, 2022, 105, 463-475.	0.7	4
387	Proteolytic cleavage of the <i>Chlamydia pneumoniae</i> major outer membrane protein in the absence of Pmp10. Proteomics, 2007, 7, 4477-4487.	1.3	3
388	Membrane proteome of the green sulfur bacterium Chlorobium tepidum (syn. Chlorobaculum tepidum) analyzed by gel-based and gel-free methods. Photosynthesis Research, 2010, 104, 153-162.	1.6	3
389	The neural cell adhesion molecules L1 and CHL1 are cleaved by BACE1 protease in vivo.. Journal of Biological Chemistry, 2012, 287, 33719.	1.6	2
390	PepShell: Visualization of Conformational Proteomics Data. Journal of Proteome Research, 2015, 14, 1987-1990.	1.8	2
391	Proteome Analysis of Arabidopsis Roots. Methods in Molecular Biology, 2018, 1761, 263-274.	0.4	2
392	Chemical Genetics Approach Identifies Abnormal Inflorescence Meristem 1 as a Putative Target of a Novel Sulfonamide That Protects Catalase2-Deficient Arabidopsis against Photorespiratory Stress. Cells, 2020, 9, 2026.	1.8	2
393	Protein identification methods in proteomics. Electrophoresis, 2000, 21, 1145-1154.	1.3	2
394	Proteome analysis of the Chlamydia pneumoniae elementary body. , 2001, 22, 1204.		2
395	Sample preparation procedures for ultrasensitive protein identification by PSD-MALDI-TOF mass spectrometry. The Protein Journal, 1998, 17, 560.	1.1	2
396	Development and Validation of a Quantitative Method for Multiple Allergen Detection in Food Using Concatemer-Based Isotope Dilution Mass Spectrometry. Journal of AOAC INTERNATIONAL, 2022, 105, 1585-1595.	0.7	2

#	ARTICLE	IF	CITATIONS
397	Front Cover: Organellar Omics – A Reviving Strategy to Untangle the Biomolecular Complexity of the Cell. <i>Proteomics</i> , 2018, 18, 1870041.	1.3	1
398	Characterization of the β -secretase subunit interactome in <i>Arabidopsis thaliana</i> . <i>Acta Physiologiae Plantarum</i> , 2019, 41, 1.	1.0	1
399	Comparative proteome analysis of <i>Chlamydia trachomatis</i> serovar A, D and L2. , 2002, 2, 164.		1
400	Nongel-Based Proteomics Selective Reversed-Phase Chromatographic Isolation of Methionine-Containing Peptides from Complex Peptide Mixtures. , 2006, , 451-455.		1
401	Abstract 5506: SOX11 acts as part of the MYCN-WEE1 regulatory protein complex implicated in neuroblastoma. , 2017, , .		1
402	Platelet Proteomics and its Applications to Study Platelet-Related Disorders. , 2017, , 157-170.		1
403	The Use of Proteomics to Identify and Characterize Cell Death Proteins. , 2005, , 403-434.		0
404	Mapping protein N-Glycosylation by COFRADIC. <i>Springer Protocols</i> , 2009, , 1395-1402.	0.1	0
405	Vpr content of HIV-1 virions determines infection of resting peripheral blood CD4+ lymphocytes. <i>Retrovirology</i> , 2013, 10, .	0.9	0
406	OMICS views on protein N-terminal biology. <i>Proteomics</i> , 2015, 15, 2383-2384.	1.3	0
407	Diagonal chromatography to study plant protein modifications. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 945-951.	1.1	0
408	Abstract 5057: Activation of stroma-derived matrix metalloproteinases (MMPs) in a model of gastric cancer.. , 2013, , .		0
409	Towards SERS-based multiplexed monitoring of protease activity using non-natural aromatic amino acids. <i>EPJ Web of Conferences</i> , 2020, 238, 04001.	0.1	0
410	Waveguide-based Detection of Protease Activity using Surface-Enhanced Raman Spectroscopy. , 2020, , .		0
411	A Strong Cation Exchange Chromatography Protocol for Examining N-Terminal Proteoforms. <i>Methods in Molecular Biology</i> , 2022, 2477, 293-309.	0.4	0