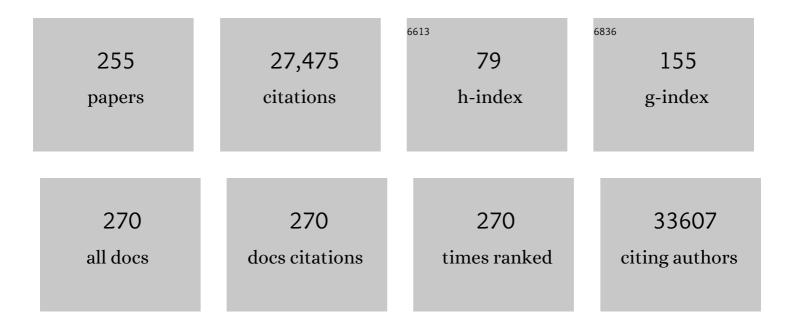
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Evaluation of Multidimensional Chromatography Coupled with Tandem Mass Spectrometry (LC/LCâ°`MS/MS) for Large-Scale Protein Analysis:  The Yeast Proteome. Journal of Proteome Research, 2003, 2, 43-50.	3.7	1,557
2	A proteomics approach to understanding protein ubiquitination. Nature Biotechnology, 2003, 21, 921-926.	17.5	1,465
3	Neurotoxicity induces cleavage of p35 to p25 by calpain. Nature, 2000, 405, 360-364.	27.8	985
4	Quantitative Proteomics Reveals the Function of Unconventional Ubiquitin Chains in Proteasomal Degradation. Cell, 2009, 137, 133-145.	28.9	948
5	Molecular characterization of LC3-associated phagocytosis reveals distinct roles for Rubicon, NOX2Âand autophagy proteins. Nature Cell Biology, 2015, 17, 893-906.	10.3	702
6	Transcription elongation factor P-TEFb is required for HIV-1 Tat transactivation in vitro. Genes and Development, 1997, 11, 2622-2632.	5.9	642
7	Lysine Propionylation and Butyrylation Are Novel Post-translational Modifications in Histones. Molecular and Cellular Proteomics, 2007, 6, 812-819.	3.8	639
8	Proteomics: the move to mixtures. Journal of Mass Spectrometry, 2001, 36, 1083-1091.	1.6	586
9	C9orf72 Dipeptide Repeats Impair the Assembly, Dynamics, and Function of Membrane-Less Organelles. Cell, 2016, 167, 774-788.e17.	28.9	577
10	Control of RNA Polymerase II Elongation Potential by a Novel Carboxyl-terminal Domain Kinase. Journal of Biological Chemistry, 1996, 271, 27176-27183.	3.4	559
11	P-TEFb kinase is required for HIV Tat transcriptional activation in vivo and in vitro. Genes and Development, 1997, 11, 2633-2644.	5.9	494
12	Identification of multiple cyclin subunits of humanÂP-TEFb. Genes and Development, 1998, 12, 755-762.	5.9	463
13	NUDEL Is a Novel Cdk5 Substrate that Associates with LIS1 and Cytoplasmic Dynein. Neuron, 2000, 28, 697-711.	8.1	447
14	Relative and Absolute Quantification of Postsynaptic Density Proteome Isolated from Rat Forebrain and Cerebellum. Molecular and Cellular Proteomics, 2006, 5, 1158-1170.	3.8	440
15	Semiquantitative Proteomic Analysis of Rat Forebrain Postsynaptic Density Fractions by Mass Spectrometry. Journal of Biological Chemistry, 2004, 279, 21003-21011.	3.4	417
16	Identification of Neuronal RNA Targets of TDP-43-containing Ribonucleoprotein Complexes. Journal of Biological Chemistry, 2011, 286, 1204-1215.	3.4	366
17	MicroRNA miR-137 Regulates Neuronal Maturation by Targeting Ubiquitin Ligase Mind Bomb-1. Stem Cells, 2010, 28, 1060-1070.	3.2	349
18	Deep Multilayer Brain Proteomics Identifies Molecular Networks in Alzheimer's Disease Progression. Neuron, 2020, 105, 975-991.e7.	8.1	287

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19	U1 small nuclear ribonucleoprotein complex and RNA splicing alterations in Alzheimer's disease. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16562-16567.	7.1	268
20	Proteomic Characterization of Postmortem Amyloid Plaques Isolated by Laser Capture Microdissection. Journal of Biological Chemistry, 2004, 279, 37061-37068.	3.4	267
21	Integrative Proteomics and Phosphoproteomics Profiling Reveals Dynamic Signaling Networks and Bioenergetics Pathways Underlying T Cell Activation. Immunity, 2017, 46, 488-503.	14.3	265
22	Cdk5-Mediated Inhibition of the Protective Effects of Transcription Factor MEF2 in Neurotoxicity-Induced Apoptosis. Neuron, 2003, 38, 33-46.	8.1	264
23	Regulation of Estrogen Receptor α by the SET7 Lysine Methyltransferase. Molecular Cell, 2008, 30, 336-347.	9.7	259
24	Structure and Regulation of the CDK5-p25nck5a Complex. Molecular Cell, 2001, 8, 657-669.	9.7	255
25	Autophosphorylated CaMKIIα Acts as a Scaffold to Recruit Proteasomes to Dendritic Spines. Cell, 2010, 140, 567-578.	28.9	249
26	The Cotranslational Function of Ribosome-Associated Hsp70 in Eukaryotic Protein Homeostasis. Cell, 2013, 152, 196-209.	28.9	240
27	Tat Modifies the Activity of CDK9 To Phosphorylate Serine 5 of the RNA Polymerase II Carboxyl-Terminal Domain during Human Immunodeficiency Virus Type 1 Transcription. Molecular and Cellular Biology, 2000, 20, 5077-5086.	2.3	234
28	The Deubiquitinating Enzyme Ataxin-3, a Polyglutamine Disease Protein, Edits Lys63 Linkages in Mixed Linkage Ubiquitin Chains. Journal of Biological Chemistry, 2008, 283, 26436-26443.	3.4	226
29	Genetic inactivation of p62 leads to accumulation of hyperphosphorylated tau and neurodegeneration. Journal of Neurochemistry, 2008, 106, 107-120.	3.9	222
30	C3PO, an Endoribonuclease That Promotes RNAi by Facilitating RISC Activation. Science, 2009, 325, 750-753.	12.6	220
31	Prolyl 4-hydroxylation regulates Argonaute 2 stability. Nature, 2008, 455, 421-424.	27.8	210
32	Human LSD2/KDM1b/AOF1 Regulates Gene Transcription by Modulating Intragenic H3K4me2 Methylation. Molecular Cell, 2010, 39, 222-233.	9.7	209
33	Enhanced photocatalytic ozonation degradation of organic pollutants by ZnO modified TiO2 nanocomposites. Applied Catalysis B: Environmental, 2018, 221, 223-234.	20.2	209
34	Automation of Nanoscale Microcapillary Liquid Chromatographyâ^'Tandem Mass Spectrometry with a Vented Column. Analytical Chemistry, 2002, 74, 3076-3083.	6.5	206
35	Large-scale deep multi-layer analysis of Alzheimer's disease brain reveals strong proteomic disease-related changes not observed at the RNA level. Nature Neuroscience, 2022, 25, 213-225.	14.8	202
36	Quantitative phosphoproteomic analysis of the molecular substrates of sleep need. Nature, 2018, 558, 435-439.	27.8	195

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37	Cell type-restricted activity of hnRNPM promotes breast cancer metastasis via regulating alternative splicing. Genes and Development, 2014, 28, 1191-1203.	5.9	193
38	Joint mouse–human phenome-wide association to test gene function and disease risk. Nature Communications, 2016, 7, 10464.	12.8	190
39	Cyclin K Functions as a CDK9 Regulatory Subunit and Participates in RNA Polymerase II Transcription. Journal of Biological Chemistry, 1999, 274, 34527-34530.	3.4	188
40	Analysis of the Large Inactive P-TEFb Complex Indicates That It Contains One 7SK Molecule, a Dimer of HEXIM1 or HEXIM2, and Two P-TEFb Molecules Containing Cdk9 Phosphorylated at Threonine 186. Journal of Biological Chemistry, 2005, 280, 28819-28826.	3.4	181
41	Systematical Optimization of Reverse-Phase Chromatography for Shotgun Proteomics. Journal of Proteome Research, 2009, 8, 3944-3950.	3.7	163
42	A novel transferrin/TfR2-mediated mitochondrial iron transport system is disrupted in Parkinson's disease. Neurobiology of Disease, 2009, 34, 417-431.	4.4	162
43	Identification of a Cyclin Subunit Required for the Function ofDrosophila P-TEFb. Journal of Biological Chemistry, 1998, 273, 13855-13860.	3.4	156
44	Essential Role of Sequestosome 1/p62 in Regulating Accumulation of Lys63-ubiquitinated Proteins. Journal of Biological Chemistry, 2008, 283, 6783-6789.	3.4	155
45	Hippo/Mst signalling couples metabolic state and immune function of CD8α+ dendritic cells. Nature, 2018, 558, 141-145.	27.8	152
46	Ube2w and Ataxin-3 Coordinately Regulate the Ubiquitin Ligase CHIP. Molecular Cell, 2011, 43, 599-612.	9.7	151
47	Polyubiquitin Linkage Profiles in Three Models of Proteolytic Stress Suggest the Etiology of Alzheimer Disease. Journal of Biological Chemistry, 2011, 286, 10457-10465.	3.4	151
48	The Ability of Positive Transcription Elongation Factor b To Transactivate Human Immunodeficiency Virus Transcription Depends on a Functional Kinase Domain, Cyclin T1, and Tat. Journal of Virology, 1998, 72, 7154-7159.	3.4	150
49	The Noncanonical Role of ULK/ATG1 in ER-to-Golgi Trafficking Is Essential for Cellular Homeostasis. Molecular Cell, 2016, 62, 491-506.	9.7	148
50	Efficacy of Retinoids in IKZF1-Mutated BCR-ABL1 Acute Lymphoblastic Leukemia. Cancer Cell, 2015, 28, 343-356.	16.8	145
51	Proteomic identification of novel proteins associated with Lewy bodies. Frontiers in Bioscience - Landmark, 2008, Volume, 3850.	3.0	134
52	Upregulation of cyclin T1/CDK9 complexes during T cell activation. Oncogene, 1998, 17, 3093-3102.	5.9	128
53	Synaptic Protein Ubiquitination in Rat Brain Revealed by Antibody-based Ubiquitome Analysis. Journal of Proteome Research, 2012, 11, 4722-4732.	3.7	128
54	Partial loss of psychiatric risk gene Mir137 in mice causes repetitive behavior and impairs sociability and learning via increased Pde10a. Nature Neuroscience, 2018, 21, 1689-1703.	14.8	127

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55	Site-specific ubiquitination exposes a linear motif to promote interferon-α receptor endocytosis. Journal of Cell Biology, 2007, 179, 935-950.	5.2	124
56	ULK1 and ULK2 Regulate Stress Granule Disassembly Through Phosphorylation and Activation of VCP/p97. Molecular Cell, 2019, 74, 742-757.e8.	9.7	123
57	Loss of LR11/SORLA Enhances Early Pathology in a Mouse Model of Amyloidosis: Evidence for a Proximal Role in Alzheimer's Disease. Journal of Neuroscience, 2008, 28, 12877-12886.	3.6	121
58	ALS-FTLD-linked mutations of SQSTM1/p62 disrupt selective autophagy and NFE2L2/NRF2 anti-oxidative stress pathway. Autophagy, 2020, 16, 917-931.	9.1	118
59	The Lysine 48 and Lysine 63 Ubiquitin Conjugates Are Processed Differently by the 26 S Proteasome. Journal of Biological Chemistry, 2009, 284, 35485-35494.	3.4	117
60	JUMP: A Tag-based Database Search Tool for Peptide Identification with High Sensitivity and Accuracy. Molecular and Cellular Proteomics, 2014, 13, 3663-3673.	3.8	117
61	Neuroprotective Actions of PIKE-L by Inhibition of SET Proteolytic Degradation by Asparagine Endopeptidase. Molecular Cell, 2008, 29, 665-678.	9.7	116
62	Nucleophosmin/B23, a Nuclear PI(3,4,5)P3 Receptor, Mediates the Antiapoptotic Actions of NGF by Inhibiting CAD. Molecular Cell, 2005, 18, 435-445.	9.7	114
63	Efficient Internalization of MHC I Requires Lysineâ€11 and Lysineâ€63 Mixed Linkage Polyubiquitin Chains. Traffic, 2010, 11, 210-220.	2.7	111
64	Nuclear Akt associates with PKC-phosphorylated Ebp1, preventing DNA fragmentation by inhibition of caspase-activated DNase. EMBO Journal, 2006, 25, 2083-2095.	7.8	108
65	Mutant LRRK2 mediates peripheral and central immune responses leading to neurodegeneration in vivo. Brain, 2018, 141, 1753-1769.	7.6	106
66	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. Cancer Cell, 2018, 34, 411-426.e19.	16.8	106
67	Integrated analysis of ultra-deep proteomes in cortex, cerebrospinal fluid and serum reveals a mitochondrial signature in Alzheimer's disease. Molecular Neurodegeneration, 2020, 15, 43.	10.8	104
68	Characterization of Polyubiquitin Chain Structure by Middle-down Mass Spectrometry. Analytical Chemistry, 2008, 80, 3438-3444.	6.5	99
69	Ligand-induced monoubiquitination of BIK1 regulates plant immunity. Nature, 2020, 581, 199-203.	27.8	99
70	Structural analysis of the full-length human LRRK2. Cell, 2021, 184, 3519-3527.e10.	28.9	98
71	Coaggregation of RNA-Binding Proteins in a Model of TDP-43 Proteinopathy with Selective RGG Motif Methylation and a Role for RRM1 Ubiquitination. PLoS ONE, 2012, 7, e38658.	2.5	98
72	Proteomic landscape of Alzheimer's Disease: novel insights into pathogenesis and biomarker discovery. Molecular Neurodegeneration, 2021, 16, 55.	10.8	95

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73	Deep undepleted human serum proteome profiling toward biomarker discovery for Alzheimer's disease. Clinical Proteomics, 2019, 16, 16.	2.1	93
74	Multiplex SILAC Analysis of a Cellular TDP-43 Proteinopathy Model Reveals Protein Inclusions Associated with SUMOylation and Diverse Polyubiquitin Chains. Molecular and Cellular Proteomics, 2010, 9, 705-718.	3.8	92
75	Extensive Peptide Fractionation and <i>y</i> <sub>1</sub> Ion-Based Interference Detection Method for Enabling Accurate Quantification by Isobaric Labeling and Mass Spectrometry. Analytical Chemistry, 2017, 89, 2956-2963.	6.5	91
76	Structural Insights into the Functions of TBK1 in Innate Antimicrobial Immunity. Structure, 2013, 21, 1137-1148.	3.3	90
77	The U4/U6 Recycling Factor SART3 Has Histone Chaperone Activity and Associates with USP15 to Regulate H2B Deubiquitination. Journal of Biological Chemistry, 2014, 289, 8916-8930.	3.4	90
78	Deep Profiling of Proteome and Phosphoproteome by Isobaric Labeling, Extensive Liquid Chromatography, and Mass Spectrometry. Methods in Enzymology, 2017, 585, 377-395.	1.0	90
79	USP19 Deubiquitinating Enzyme Supports Cell Proliferation by Stabilizing KPC1, a Ubiquitin Ligase for p27 <sup>Kip1</sup> . Molecular and Cellular Biology, 2009, 29, 547-558.	2.3	89
80	Galectin-3 Is a Candidate Biomarker for Amyotrophic Lateral Sclerosis: Discovery by a Proteomics Approach. Journal of Proteome Research, 2010, 9, 5133-5141.	3.7	88
81	Phosphoproteomic Analysis of Human Brain by Calcium Phosphate Precipitation and Mass Spectrometry. Journal of Proteome Research, 2008, 7, 2845-2851.	3.7	87
82	Protein kinase C inhibits autophagy and phosphorylates LC3. Biochemical and Biophysical Research Communications, 2010, 395, 471-476.	2.1	87
83	Combinatorial expression of GPCR isoforms affects signalling and drug responses. Nature, 2020, 587, 650-656.	27.8	87
84	Ubiquitination is essential for recovery of cellular activities after heat shock. Science, 2021, 372, eabc3593.	12.6	86
85	Molecular determinants of polyubiquitin linkage selection by an HECT ubiquitin ligase. EMBO Journal, 2006, 25, 1710-1719.	7.8	84
86	Proteomics of gliomas: Initial biomarker discovery and evolution of technology. Neuro-Oncology, 2011, 13, 926-942.	1.2	84
87	Hippo Kinases Mst1 and Mst2 Sense and Amplify IL-2R-STAT5 Signaling in Regulatory T Cells to Establish Stable Regulatory Activity. Immunity, 2018, 49, 899-914.e6.	14.3	84
88	Interactions between Tat and TAR and Human Immunodeficiency Virus Replication Are Facilitated by Human Cyclin T1 but Not Cyclins T2a or T2b. Virology, 1999, 255, 182-189.	2.4	80
89	Blocking an N-terminal acetylation–dependent protein interaction inhibits an E3 ligase. Nature Chemical Biology, 2017, 13, 850-857.	8.0	80
90	Cooperative control of multiple heterogeneous agents with unknown high-frequency-gain signs. Systems and Control Letters, 2014, 68, 51-56.	2.3	79

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91	Polyubiquitination of Prolactin Receptor Stimulates Its Internalization, Postinternalization Sorting, and Degradation via the Lysosomal Pathway. Molecular and Cellular Biology, 2008, 28, 5275-5287.	2.3	78
92	A Novel Strategy to Isolate Ubiquitin Conjugates Reveals Wide Role for Ubiquitination during Neural Development. Molecular and Cellular Proteomics, 2011, 10, M110.002188.	3.8	77
93	The neoepitope landscape in pediatric cancers. Genome Medicine, 2017, 9, 78.	8.2	77
94	Control of Early B Cell Development by the RNA N6-Methyladenosine Methylation. Cell Reports, 2020, 31, 107819.	6.4	77
95	Proteomics Analysis Reveals Novel Components in the Detergent-Insoluble Subproteome in Alzheimer's Disease. Journal of Proteome Research, 2009, 8, 5069-5079.	3.7	76
96	JUMPg: An Integrative Proteogenomics Pipeline Identifying Unannotated Proteins in Human Brain and Cancer Cells. Journal of Proteome Research, 2016, 15, 2309-2320.	3.7	76
97	Amino Acids License Kinase mTORC1 Activity and Treg Cell Function via Small G Proteins Rag and Rheb. Immunity, 2019, 51, 1012-1027.e7.	14.3	76
98	CDK2 inhibitors as candidate therapeutics for cisplatin- and noise-induced hearing loss. Journal of Experimental Medicine, 2018, 215, 1187-1203.	8.5	75
99	The C.Âelegans Taste Receptor Homolog LITE-1 Is a Photoreceptor. Cell, 2016, 167, 1252-1263.e10.	28.9	73
100	PHD3-dependent hydroxylation of HCLK2 promotes the DNA damage response. Journal of Clinical Investigation, 2012, 122, 2827-2836.	8.2	73
101	Dissecting the ubiquitin pathway by mass spectrometry. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 1940-1947.	2.3	72
102	ELMOD2 Is an Arl2 GTPase-activating Protein That Also Acts on Arfs. Journal of Biological Chemistry, 2007, 282, 17568-17580.	3.4	72
103	Phosphoproteomic Analysis Reveals Site-Specific Changes in GFAP and NDRG2 Phosphorylation in Frontotemporal Lobar Degeneration. Journal of Proteome Research, 2010, 9, 6368-6379.	3.7	71
104	Autoregulation of the 26S proteasome by in situ ubiquitination. Molecular Biology of the Cell, 2014, 25, 1824-1835.	2.1	71
105	Systematic Optimization of Long Gradient Chromatography Mass Spectrometry for Deep Analysis of Brain Proteome. Journal of Proteome Research, 2015, 14, 829-838.	3.7	71
106	Huntingtin-associated protein 1 interacts with Ahi1 to regulate cerebellar and brainstem development in mice. Journal of Clinical Investigation, 2008, 118, 2785-2795.	8.2	71
107	Network-based systems pharmacology reveals heterogeneity in LCK and BCL2 signaling and therapeutic sensitivity of T-cell acute lymphoblastic leukemia. Nature Cancer, 2021, 2, 284-299.	13.2	70
108	Neuronal Morphogenesis Is Regulated by the Interplay between Cyclin-Dependent Kinase 5 and the Ubiquitin Ligase Mind Bomb 1. Journal of Neuroscience, 2007, 27, 9503-9512.	3.6	68

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109	Cerebrospinal fluid tau fragment correlates with tau PET: a candidate biomarker for tangle pathology. Brain, 2020, 143, 650-660.	7.6	68
110	27-Plex Tandem Mass Tag Mass Spectrometry for Profiling Brain Proteome in Alzheimer's Disease. Analytical Chemistry, 2020, 92, 7162-7170.	6.5	68
111	A Nano Ultra-Performance Liquid Chromatography–High Resolution Mass Spectrometry Approach for Global Metabolomic Profiling and Case Study on Drug-Resistant Multiple Myeloma. Analytical Chemistry, 2014, 86, 3667-3675.	6.5	67
112	Identification and Validation of Eukaryotic Aspartate and Glutamate Methylation in Proteins. Journal of Proteome Research, 2008, 7, 1001-1006.	3.7	65
113	Systematic Approach for Validating the Ubiquitinated Proteome. Analytical Chemistry, 2008, 80, 4161-4169.	6.5	65
114	Binding of PLD2-Generated Phosphatidic Acid to KIF5B Promotes MT1-MMP Surface Trafficking and Lung Metastasis of Mouse Breast Cancer Cells. Developmental Cell, 2017, 43, 186-197.e7.	7.0	63
115	Sjögren Syndrome Antigen B (SSB)/La Promotes Global MicroRNA Expression by Binding MicroRNA Precursors through Stem-Loop Recognition. Journal of Biological Chemistry, 2013, 288, 723-736.	3.4	62
116	Human BRE1 Is an E3 Ubiquitin Ligase for Ebp1 Tumor Suppressor. Molecular Biology of the Cell, 2009, 20, 757-768.	2.1	61
117	Structural basis of SETD6-mediated regulation of the NF-kB network via methyl-lysine signaling. Nucleic Acids Research, 2011, 39, 6380-6389.	14.5	61
118	Quantitative Analysis of the Detergent-Insoluble Brain Proteome in Frontotemporal Lobar Degeneration Using SILAC Internal Standards. Journal of Proteome Research, 2012, 11, 2721-2738.	3.7	61
119	Novel specialized cell state and spatial compartments within the germinal center. Nature Immunology, 2020, 21, 660-670.	14.5	60
120	Altered ubiquitin causes perturbed calcium homeostasis, hyperactivation of calpain, dysregulated differentiation, and cataract. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1071-1076.	7.1	57
121	Nuclear Accumulation of Stress Response mRNAs Contributes to the Neurodegeneration Caused by Fragile X Premutation rCGG Repeats. PLoS Genetics, 2011, 7, e1002102.	3.5	56
122	A Key Role for the Ubiquitin Ligase UBR4 in Myofiber Hypertrophy in Drosophila and Mice. Cell Reports, 2019, 28, 1268-1281.e6.	6.4	56
123	Identification of a Functional Non-coding Variant in the GABAA Receptor α2 Subunit of the C57BL/6J Mouse Reference Genome: Major Implications for Neuroscience Research. Frontiers in Genetics, 2019, 10, 188.	2.3	56
124	Characterizing Ubiquitination Sites by Peptide-based Immunoaffinity Enrichment. Molecular and Cellular Proteomics, 2012, 11, 1529-1540.	3.8	55
125	Targeting human Mas-related G protein-coupled receptor X1 to inhibit persistent pain. Proceedings of the United States of America, 2017, 114, E1996-E2005.	7.1	53
126	Asparaginyl endopeptidase cleaves TDPâ€43 in brain. Proteomics, 2012, 12, 2455-2463.	2.2	52

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127	A Cancer-Specific Ubiquitin Ligase Drives mRNA Alternative Polyadenylation by Ubiquitinating the mRNA 3′ End Processing Complex. Molecular Cell, 2020, 77, 1206-1221.e7.	9.7	52
128	Identification of Potent, Selective, and Orally Bioavailable Small-Molecule GSPT1/2 Degraders from a Focused Library of Cereblon Modulators. Journal of Medicinal Chemistry, 2021, 64, 7296-7311.	6.4	51
129	Rho Kinase II Phosphorylation of the Lipoprotein Receptor LR11/SORLA Alters Amyloid-β Production. Journal of Biological Chemistry, 2011, 286, 6117-6127.	3.4	50
130	Cooperative control of high-order nonlinear systems with unknown control directions. Systems and Control Letters, 2018, 113, 101-108.	2.3	50
131	Akt Phosphorylates NQO1 and Triggers its Degradation, Abolishing Its Antioxidative Activities in Parkinson's Disease. Journal of Neuroscience, 2019, 39, 7291-7305.	3.6	50
132	SOX4 interacts with plakoglobin in a Wnt3a-dependent manner in prostate cancer cells. BMC Cell Biology, 2011, 12, 50.	3.0	47
133	Ubiquitin-specific Protease 9x Deubiquitinates and Stabilizes the Spinal Muscular Atrophy Protein-Survival Motor Neuron. Journal of Biological Chemistry, 2012, 287, 43741-43752.	3.4	47
134	The F-box Protein FBXO44 Mediates BRCA1 Ubiquitination and Degradation. Journal of Biological Chemistry, 2012, 287, 41014-41022.	3.4	45
135	LKB1 orchestrates dendritic cell metabolic quiescence and anti-tumor immunity. Cell Research, 2019, 29, 391-405.	12.0	45
136	Multiple Weak Linear Motifs Enhance Recruitment and Processivity in SPOP-Mediated Substrate Ubiquitination. Journal of Molecular Biology, 2016, 428, 1256-1271.	4.2	44
137	Enhanced Purification of Ubiquitinated Proteins by Engineered Tandem Hybrid Ubiquitin-binding Domains (ThUBDs). Molecular and Cellular Proteomics, 2016, 15, 1381-1396.	3.8	44
138	Varicella-Zoster Virus Fc Receptor Component gl Is Phosphorylated on Its Endodomain by a Cyclin-Dependent Kinase. Journal of Virology, 1999, 73, 1320-1330.	3.4	43
139	Proteomic analysis of postsynaptic density in Alzheimer's Disease. Clinica Chimica Acta, 2013, 420, 62-68.	1.1	42
140	Distributed adaptive controller for the output-synchronization of networked systems in semi-strict feedback form. Journal of the Franklin Institute, 2014, 351, 412-428.	3.4	42
141	Refined phosphopeptide enrichment by phosphate additive and the analysis of human brain phosphoproteome. Proteomics, 2015, 15, 500-507.	2.2	42
142	Targeting Histone Demethylases in MYC-Driven Neuroblastomas with Ciclopirox. Cancer Research, 2017, 77, 4626-4638.	0.9	42
143	Deep multiomics profiling of brain tumors identifies signaling networks downstream of cancer driver genes. Nature Communications, 2019, 10, 3718.	12.8	42
144	Protein Fold Classification with Backbone Torsional Characters Using Multi- Class Linear Discriminant Analysis. Journal of Proteomics and Bioinformatics, 2013, 06, 196-209.	0.4	42

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145	Quantitative Protein Analysis by Mass Spectrometry. Methods in Molecular Biology, 2015, 1278, 281-305.	0.9	40
146	Evaluation of proteomic strategies for analyzing ubiquitinated proteins. BMB Reports, 2008, 41, 177-183.	2.4	40
147	Regulation of behavioral circadian rhythms and clock protein PER1 by the deubiquitinating enzyme USP2. Biology Open, 2012, 1, 789-801.	1.2	38
148	BDNF inhibits neurodegenerative disease–associated asparaginyl endopeptidase activity via phosphorylation by AKT. JCI Insight, 2018, 3, .	5.0	37
149	Sequential Elution Interactome Analysis of the Mind Bomb 1 Ubiquitin Ligase Reveals a Novel Role in Dendritic Spine Outgrowth. Molecular and Cellular Proteomics, 2015, 14, 1898-1910.	3.8	36
150	PHD2/3-dependent hydroxylation tunes cardiac response to Î <sup>2</sup> -adrenergic stress via phospholamban. Journal of Clinical Investigation, 2015, 125, 2759-2771.	8.2	36
151	CRISPR screens unveil signal hubs for nutrient licensing of T cell immunity. Nature, 2021, 600, 308-313.	27.8	36
152	Identification and Characterization of Neuronal Mitogen-activated Protein Kinase Substrates Using a Specific Phosphomotif Antibody. Molecular and Cellular Proteomics, 2009, 8, 681-695.	3.8	35
153	Discrete roles and bifurcation of PTEN signaling and mTORC1-mediated anabolic metabolism underlie IL-7–driven B lymphopoiesis. Science Advances, 2018, 4, eaar5701.	10.3	35
154	Stable Isotope Labeling with Amino Acids in <i>Drosophila</i> for Quantifying Proteins and Modifications. Journal of Proteome Research, 2012, 11, 4403-4412.	3.7	34
155	Reducing histone acetylation rescues cognitive deficits in a mouse model of Fragile X syndrome. Nature Communications, 2018, 9, 2494.	12.8	34
156	Target-Decoy-Based False Discovery Rate Estimation for Large-Scale Metabolite Identification. Journal of Proteome Research, 2018, 17, 2328-2334.	3.7	33
157	Kinase network dysregulation in a human induced pluripotent stem cell model of DISC1 schizophrenia. Molecular Omics, 2019, 15, 173-188.	2.8	33
158	Regulation of gene expression by miR-144/451 during mouse erythropoiesis. Blood, 2019, 133, 2518-2528.	1.4	33
159	Differentiation of human pluripotent stem cells into neurons or cortical organoids requires transcriptional co-regulation by UTX and 53BP1. Nature Neuroscience, 2019, 22, 362-373.	14.8	33
160	Systems immunology: Integrating multi-omics data to infer regulatory networks and hidden drivers of immunity. Current Opinion in Systems Biology, 2019, 15, 19-29.	2.6	32
161	Integrated genomic and proteomic analyses identify stimulus-dependent molecular changes associated with distinct modes of skeletal muscle atrophy. Cell Reports, 2021, 37, 109971.	6.4	32
162	Identification and characterization of phosphorylation sites within the pregnane X receptor protein. Biochemical Pharmacology, 2014, 87, 360-370.	4.4	30

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163	Epidithiodiketopiperazines Inhibit Protein Degradation by Targeting Proteasome Deubiquitinase Rpn11. Cell Chemical Biology, 2018, 25, 1350-1358.e9.	5.2	30
164	Antagonistic control of myofiber size and muscle protein quality control by the ubiquitin ligase UBR4 during aging. Nature Communications, 2021, 12, 1418.	12.8	30
165	Acute depletion of CTCF rewires genome-wide chromatin accessibility. Genome Biology, 2021, 22, 244.	8.8	29
166	Merger of Laser Capture Microdissection and Mass Spectrometry: A Window into the Amyloid Plaque Proteome. Methods in Enzymology, 2006, 412, 77-93.	1.0	28
167	Integrated Approaches for Analyzing U1-70K Cleavage in Alzheimer's Disease. Journal of Proteome Research, 2014, 13, 4526-4534.	3.7	28
168	Regulation of <scp>MAGE</scp> â€A3/6 by the <scp>CRL</scp> 4― <scp>DCAF</scp> 12 ubiquitin ligase and nutrient availability. EMBO Reports, 2019, 20, e47352.	4.5	26
169	Deletion of <i>Abi3</i> gene locus exacerbates neuropathological features of Alzheimer's disease in a mouse model of Al² amyloidosis. Science Advances, 2021, 7, eabe3954.	10.3	26
170	The METTL5-TRMT112 N6-methyladenosine methyltransferase complex regulates mRNA translation via 18S rRNA methylation. Journal of Biological Chemistry, 2022, 298, 101590.	3.4	26
171	Multimodal Imaging of Amyloid Plaques: Fusion of the Single-Probe Mass Spectrometry Image and Fluorescence Microscopy Image. Analytical Chemistry, 2019, 91, 12882-12889.	6.5	25
172	Desumoylation of the Endoplasmic Reticulum Membrane VAP Family Protein Scs2 by Ulp1 and SUMO Regulation of the Inositol Synthesis Pathway. Molecular and Cellular Biology, 2012, 32, 64-75.	2.3	24
173	Upregulation of the CaV 1.1-ryanodine receptor complex in a rat model of critical illness myopathy. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2011, 300, R1384-R1391.	1.8	23
174	A Conserved Protein with AN1 Zinc Finger and Ubiquitin-like Domains Modulates Cdc48 (p97) Function in the Ubiquitin-Proteasome Pathway. Journal of Biological Chemistry, 2013, 288, 33682-33696.	3.4	23
175	Deep Profiling of the Aggregated Proteome in Alzheimer's Disease: From Pathology to Disease Mechanisms. Proteomes, 2018, 6, 46.	3.5	23
176	A brain proteomic signature of incipient Alzheimer's disease in young <i>APOE</i> ε4 carriers identifies novel drug targets. Science Advances, 2021, 7, eabi8178.	10.3	23
177	SUMO Pathway Modulation of Regulatory Protein Binding at the Ribosomal DNA Locus in <i>Saccharomyces cerevisiae</i> . Genetics, 2016, 202, 1377-1394.	2.9	22
178	Clinical proteomics in neurodegenerative diseases. Proteomics - Clinical Applications, 2007, 1, 1342-1350.	1.6	21
179	Diverse polyubiquitin chains accumulate following 26S proteasomal dysfunction in mammalian neurones. Neuroscience Letters, 2011, 491, 44-47.	2.1	21
180	A Degenerate Cohort of Yeast Membrane Trafficking DUBs Mediates Cell Polarity and Survival*. Molecular and Cellular Proteomics, 2015, 14, 3132-3141.	3.8	21

#	Article	IF	CITATIONS
181	Spectral Library Search Improves Assignment of TMT Labeled MS/MS Spectra. Journal of Proteome Research, 2018, 17, 3325-3331.	3.7	21
182	Enhanced Photocatalytic Ozonation of Phenol by Ag/ZnO Nanocomposites. Catalysts, 2019, 9, 1006.	3.5	21
183	Deep Profiling of Microgram-Scale Proteome by Tandem Mass Tag Mass Spectrometry. Journal of Proteome Research, 2021, 20, 337-345.	3.7	21
184	A Proteomic Strategy for Quantifying Polyubiquitin Chain Topologies. Israel Journal of Chemistry, 2006, 46, 171-182.	2.3	20
185	Ubiquitin Chain Elongation Enzyme Ufd2 Regulates a Subset of Doa10 Substrates. Journal of Biological Chemistry, 2010, 285, 10265-10272.	3.4	20
186	Quantitative proteomics to decipher ubiquitin signaling. Amino Acids, 2012, 43, 1049-1060.	2.7	20
187	Deubiquitinase USP9X Maintains Centriolar Satellite Integrity by Stabilizing Pericentriolar Material 1 Protein. Journal of Cell Science, 2019, 132, .	2.0	20
188	Circadian gene variants and the skeletal muscle circadian clock contribute to the evolutionary divergence in longevity across <i>Drosophila</i> populations. Genome Research, 2019, 29, 1262-1276.	5.5	20
189	Proteomic Analysis of Ubiquitin Conjugates in Yeast. Methods in Enzymology, 2005, 399, 367-381.	1.0	19
190	Proteomic Analysis of Hippocampal Dentate Granule Cells in Frontotemporal Lobar Degeneration: Application of Laser Capture Technology. Frontiers in Neurology, 2011, 2, 24.	2.4	18
191	Mutant and Wild-Type Isocitrate Dehydrogenase 1 Share Enhancing Mechanisms Involving Distinct Tyrosine Kinase Cascades in Cancer. Cancer Discovery, 2019, 9, 756-777.	9.4	18
192	Aberrant septin 11 is associated with sporadic frontotemporal lobar degeneration. Molecular Neurodegeneration, 2011, 6, 82.	10.8	17
193	Deep Single-Cell-Type Proteome Profiling of Mouse Brain by Nonsurgical AAV-Mediated Proximity Labeling. Analytical Chemistry, 2022, 94, 5325-5334.	6.5	17
194	Targeting KDM4 for treating PAX3-FOXO1–driven alveolar rhabdomyosarcoma. Science Translational Medicine, 2022, 14, .	12.4	16
195	An In Vitro Transcription System that Recapitulates Equine Infectious Anemia Virus Tat-Mediated Inhibition of Human Immunodeficiency Virus Type 1 Tat Activity Demonstrates a Role for Positive Transcription Elongation Factor b and Associated Proteins in the Mechanism of Tat Activation. Virology, 2000, 274, 356-366.	2.4	15
196	Enhanced Purification of Ubiquitinated Proteins by Engineered Tandem Hybrid Ubiquitin-binding Domains (ThUBDs). Molecular and Cellular Proteomics, 2016, 15, 1381-1396.	3.8	15
197	Isotope Labeling-Assisted Evaluation of Hydrophilic and Hydrophobic Liquid Chromatograph–Mass Spectrometry for Metabolomics Profiling. Analytical Chemistry, 2018, 90, 8538-8545.	6.5	15
198	Proteomic Alterations and Novel Markers of Neurotoxic Reactive Astrocytes in Human Induced Pluripotent Stem Cell Models. Frontiers in Molecular Neuroscience, 2022, 15, 870085.	2.9	15

#	Article	IF	CITATIONS
199	29â€Plex tandem mass tag mass spectrometry enabling accurate quantification by interference correction. Proteomics, 2022, 22, .	2.2	15
200	Altered sodium channel-protein associations in critical illness myopathy. Skeletal Muscle, 2012, 2, 17.	4.2	14
201	Molecular basis of crosstalk in nuclear receptors: heterodimerization between PXR and CAR and the implication in gene regulation. Nucleic Acids Research, 2022, 50, 3254-3275.	14.5	14
202	Tau modification by the norepinephrine metabolite DOPEGAL stimulates its pathology and propagation. Nature Structural and Molecular Biology, 2022, 29, 292-305.	8.2	14
203	Ca2+-mediated mitochondrial inner membrane permeabilization induces cell death independently of Bax and Bak. Cell Death and Differentiation, 2022, 29, 1318-1334.	11.2	14
204	Phosphatidic acid generated by PLD2 promotes the plasma membrane recruitment of IQGAP1 and neointima formation. FASEB Journal, 2019, 33, 6713-6725.	0.5	12
205	SJPYT-195: A Designed Nuclear Receptor Degrader That Functions as a Molecular Glue Degrader of GSPT1. ACS Medicinal Chemistry Letters, 2022, 13, 1311-1320.	2.8	12
206	An age-downregulated ribosomal RpS28 protein variant regulates the muscle proteome. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	11
207	Deciphering Tissue-Specific Ubiquitylation by Mass Spectrometry. Methods in Molecular Biology, 2012, 832, 65-80.	0.9	11
208	Combining selinexor with alisertib to target the p53 pathway in neuroblastoma. Neoplasia, 2022, 26, 100776.	5.3	11
209	Deep Proteome Profiling by Isobaric Labeling, Extensive Liquid Chromatography, Mass Spectrometry, and Software-assisted Quantification. Journal of Visualized Experiments, 2017, , .	0.3	10
210	An ABC Transporter Drives Medulloblastoma Pathogenesis by Regulating Sonic Hedgehog Signaling. Cancer Research, 2020, 80, 1524-1537.	0.9	10
211	High-Throughput Profiling of Proteome and Posttranslational Modifications by 16-Plex TMT Labeling and Mass Spectrometry. Methods in Molecular Biology, 2021, 2228, 205-224.	0.9	10
212	Integrative network analysis reveals USP7 haploinsufficiency inhibits E-protein activity in pediatric T-lineage acute lymphoblastic leukemia (T-ALL). Scientific Reports, 2021, 11, 5154.	3.3	10
213	Global Profiling of Lysine Accessibility to Evaluate Protein Structure Changes in Alzheimer's Disease. Journal of the American Society for Mass Spectrometry, 2021, 32, 936-945.	2.8	10
214	JUMPn: A Streamlined Application for Protein Co-Expression Clustering and Network Analysis in Proteomics. Journal of Visualized Experiments, 2021, , .	0.3	9
215	Analysis of Ubiquitinated Proteome by Quantitative Mass Spectrometry. Methods in Molecular Biology, 2012, 893, 417-429.	0.9	8
216	Toxicoproteomic Profiling of hPXR Transgenic Mice Treated with Rifampicin and Isoniazid. Cells, 2020, 9, 1654.	4.1	8

#	Article	IF	CITATIONS
217	JUMPm: A Tool for Large-Scale Identification of Metabolites in Untargeted Metabolomics. Metabolites, 2020, 10, 190.	2.9	8
218	JUMPt: Comprehensive Protein Turnover Modeling of In Vivo Pulse SILAC Data by Ordinary Differential Equations. Analytical Chemistry, 2021, 93, 13495-13504.	6.5	8
219	TET2 stabilization by 14-3-3 binding to the phosphorylated Serine 99 is deregulated by mutations in cancer. Cell Research, 2019, 29, 248-250.	12.0	7
220	High-throughput and Deep-proteome Profiling by 16-plex Tandem Mass Tag Labeling Coupled with Two-dimensional Chromatography and Mass Spectrometry. Journal of Visualized Experiments, 2020, , .	0.3	7
221	Proteomic Profiling of Cerebrospinal Fluid by 16-Plex TMT-Based Mass Spectrometry. Methods in Molecular Biology, 2022, 2420, 21-37.	0.9	7
222	Global Proteomic Profiling of Pediatric AML: A Pilot Study. Cancers, 2021, 13, 3161.	3.7	6
223	Consensus control of networked nonlinear systems. , 2012, , .		5
224	Quantitative Phosphoproteomic Analysis of Brain Tissues. Methods in Molecular Biology, 2017, 1598, 199-211.	0.9	4
225	Clobal Ubiquitination Analysis by SILAC in Mammalian Cells. Methods in Molecular Biology, 2014, 1188, 149-160.	0.9	4
226	At the crossroads of ubiquitin signaling and mass spectrometry. Expert Review of Proteomics, 2010, 7, 643-645.	3.0	3
227	Deep multilayer brain proteomics identifies molecular networks and Netrinâ€1 accumulation in Alzheimer's disease progression. Alzheimer's and Dementia, 2020, 16, e037231.	0.8	3
228	Decentralized Control of Multiple Strict-Feedback Systems With Unknown Control Directions. IEEE Access, 2022, 10, 59228-59235.	4.2	3
229	Cenetic architecture of protein expression and its regulation in the mouse brain. BMC Genomics, 2021, 22, 875.	2.8	3
230	SMAP is a pipeline for sample matching in proteogenomics. Nature Communications, 2022, 13, 744.	12.8	3
231	Distributed control of multi-agents system via static feedback controllers under directed networks. Transactions of the Institute of Measurement and Control, 2021, 43, 464-472.	1.7	2
232	Development of Proteolytic Targeting Chimeras to Target Lck in T-Cell Acute Lymphoblastic Leukemia. Blood, 2021, 138, 867-867.	1.4	2
233	Specificity of Ubiquitin-Binding Proteins: Recognition of Different Faces of Ubiquitin. Israel Journal of Chemistry, 2006, 46, 159-169.	2.3	1
234	Proteome Analysis of the Ubiquitin Pathway. , 0, , 443-453.		1

Proteome Analysis of the Ubiquitin Pathway. , 0, , 443-453. 234

#	Article	IF	CITATIONS
235	Distributed Control of Multiple Supercapacitors via Static Feedback. Mathematical Problems in Engineering, 2019, 2019, 1-8.	1.1	1
236	Metabolic switching in pluripotent stem cells reorganizes energy metabolism and subcellular organelles. Experimental Cell Research, 2019, 379, 55-64.	2.6	1
237	Decentralized Control for the Multiple Agents in Strict Feedback Form. IEEE Access, 2020, 8, 194850-194857.	4.2	1
238	Quantifying Proteome and Protein Modifications in Activated T Cells by Multiplexed Isobaric Labeling Mass Spectrometry. Methods in Molecular Biology, 2021, 2285, 297-317.	0.9	1
239	Abstract 1543: Mining cancer-specific isoforms as CAR T-cell therapy targets for pediatric solid and brain tumors. , 2021, , .		1
240	Analysis of Brain Phosphoproteome Using Titanium Dioxide Enrichment and High-Resolution LC-MS/MS. Neuromethods, 2017, , 141-159.	0.3	1
241	Multi-Omic Based Antigen Discovery for the Immunotherapy of Pediatric Acute T Cell Lymphoblastic Leukemia. Blood, 2020, 136, 17-18.	1.4	1
242	Logic-Based Switching Mechanism for Multiple Parametric-Strict-Feedback Systems With Unknown Control Directions. IEEE Access, 2022, 10, 40027-40035.	4.2	1
243	Largeâ€scale deep multiâ€layer analysis of Alzheimer's disease brain reveals strong proteomic diseaseâ€related changes not observed at the RNA level. Alzheimer's and Dementia, 2021, 17, e055041.	0.8	1
244	Output synchronization of multiple FOSMIB power systems. , 2017, , .		0
245	Decentralized Control of Networked Systems with Unknown Control Directions and Uncertainties. , 2020, , .		0
246	Decentralized Control of Multiple Agents with Unknown Control Directions. , 2021, , .		0
247	Abstract 3912: Comprehensive Characterization of SOX4 Protein Complexes in Prostate Cancer Cells. , 2010, , .		0
248	Expression of K6Wâ€ubiquitin in the lens perturbs calcium homeostasis and results in calpain hyperactivation and differentiation abnormality. FASEB Journal, 2013, 27, 785.7.	0.5	0
249	Abstract B05: MicroRNA-206 drives rhabdomyosarcoma differentiation through downregulation of PAX7. Cancer Research, 2016, 76, B05-B05.	0.9	0
250	A Promiscuous Biotin Ligase as a Global Strategy to Interrogate the Protein Interactome of Human ABCC4. FASEB Journal, 2018, 32, 695.18.	0.5	0
251	Abstract PR08: Overexpression and mutations of CXorf67 in "infant-type―posterior fossa type-A ependymomas. , 2018, , .		0
252	Abstract IA12: Modeling and targeting CREBBP mutations in relapsed acute lymphoblastic leukemia. , 2018, , .		0

#	Article	IF	CITATIONS
253	Abstract 3652: USP7 heterozygous loss-of-function affects T-cell differentiation in pediatric T-ALL. , 2019, , .		0
254	Output Synchronization for Networked Strict-feedback Systems in the Presence of Uncertainties. , 2021, , .		0
255	Dynamic Changes in ABCC4 Proteinâ€Protein Interactions during PKA Signaling: Role of the ABCC4 PDZ Motif. FASEB Journal, 2022, 36, .	0.5	0