Matthias Mann

List of Publications by Year
in descending order

829 papers	259,066 citations	4 226 h-index	12 475 g-index
908 all docs	908 docs citations	908 times ranked	167819 citing authors

#	Article	IF	Citations
1	MaxQuant enables high peptide identification rates, individualized p.p.b.-range mass accuracies and proteome-wide protein quantification. Nature Biotechnology, 2008, 26, 1367-1372.	9.4	12,966
2	Mass Spectrometric Sequencing of Proteins from Silver-Stained Polyacrylamide Gels. Analytical Chemistry, 1996, 68, 850-858.	3.2	8,535
3	Electrospray ionization for mass spectrometry of large biomolecules. Science, 1989, 246, 64-71.	6.0	6,875
4	Universal sample preparation method for proteome analysis. Nature Methods, 2009, 6, 359-362.	9.0	6,678
5	Mass spectrometry-based proteomics. Nature, 2003, 422, 198-207.	13.7	6,282
6	The Perseus computational platform for comprehensive analysis of (prote)omics data. Nature Methods, 2016, 13, 731-740.	9.0	6,181
7	Andromeda: A Peptide Search Engine Integrated into the MaxQuant Environment. Journal of Proteome Research, 2011, 10, 1794-1805.	1.8	4,935
8	Stable Isotope Labeling by Amino Acids in Cell Culture, SILAC, as a Simple and Accurate Approach to Expression Proteomics. Molecular and Cellular Proteomics, 2002, 1, 376-386.	2.5	4,931
9	In-gel digestion for mass spectrometric characterization of proteins and proteomes. Nature Protocols, 2006, 1, 2856-2860.	5.5	4,265
10	Accurate Proteome-wide Label-free Quantification by Delayed Normalization and Maximal Peptide Ratio Extraction, Termed MaxLFQ. Molecular and Cellular Proteomics, 2014, 13, 2513-2526.	2.5	4,178
11	Lysine Acetylation Targets Protein Complexes and Co-Regulates Major Cellular Functions. Science, 2009, 325, 834-840.	6.0	3,883
12	Protocol for micro-purification, enrichment, pre-fractionation and storage of peptides for proteomics using StageTips. Nature Protocols, 2007, 2, 1896-1906.	5.5	3,693
13	Systematic identification of protein complexes in Saccharomyces cerevisiae by mass spectrometry. Nature, 2002, 415, 180-183.	13.7	3,445
14	Global, In Vivo, and Site-Specific Phosphorylation Dynamics in Signaling Networks. Cell, 2006, 127, 635-648.	13.5	3,201
15	FLICE, A Novel FADD-Homologous ICE/CED-3â€"like Protease, Is Recruited to the CD95 (Fas/APO-1) Death-Inducing Signaling Complex. Cell, 1996, 85, 817-827.	13.5	2,944
16	A generic protein purification method for protein complex characterization and proteome exploration. Nature Biotechnology, 1999, 17, 1030-1032.	9.4	2,543
17	Stop and Go Extraction Tips for Matrix-Assisted Laser Desorption/Ionization, Nanoelectrospray, and LC/MS Sample Pretreatment in Proteomics. Analytical Chemistry, 2003, 75, 663-670.	3.2	2,337
18	Proteomics to study genes and genomes. Nature, 2000, 405, 837-846.	13.7	2,173

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19	IKK-1 and IKK-2: Cytokine-Activated IB Kinases Essential for NF-B Activation. Science, 1997, 278, 860-866.	6.0	1,995
20	Analytical Properties of the Nanoelectrospray Ion Source. Analytical Chemistry, 1996, 68, 1-8.	3.2	1,828
21	Exponentially Modified Protein Abundance Index (emPAI) for Estimation of Absolute Protein Amount in Proteomics by the Number of Sequenced Peptides per Protein. Molecular and Cellular Proteomics, 2005, 4, 1265-1272.	2.5	1,817
22	Proteomic analysis of post-translational modifications. Nature Biotechnology, 2003, 21, 255-261.	9.4	1,809
23	Femtomole sequencing of proteins from polyacrylamide gels by nano-electrospray mass spectrometry. Nature, 1996, 379, 466-469.	13.7	1,723
24	Mass-spectrometric exploration of proteome structure and function. Nature, 2016, 537, 347-355.	13.7	1,573
25	Error-Tolerant Identification of Peptides in Sequence Databases by Peptide Sequence Tags. Analytical Chemistry, 1994, 66, 4390-4399.	3.2	1,521
26	Electrospray ionization-principles and practice. Mass Spectrometry Reviews, 1990, 9, 37-70.	2.8	1,511
27	Minimal, encapsulated proteomic-sample processing applied to copy-number estimation in eukaryotic cells. Nature Methods, 2014, 11, 319-324.	9.0	1,447
28	Mass spectrometryâ€"based proteomics turns quantitative. Nature Chemical Biology, 2005, 1, 252-262.	3.9	1,426
29	Linking genome and proteome by mass spectrometry: Large-scale identification of yeast proteins from two dimensional gels. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 14440-14445.	3.3	1,415
30	Parts per Million Mass Accuracy on an Orbitrap Mass Spectrometer via Lock Mass Injection into a C-trap. Molecular and Cellular Proteomics, 2005, 4, 2010-2021.	2.5	1,395
31	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. Science Signaling, 2010, 3, ra3.	1.6	1,319
32	Proteomic characterization of the human centrosome by protein correlation profiling. Nature, 2003, 426, 570-574.	13.7	1,204
33	Reverse Transcriptase Motifs in the Catalytic Subunit of Telomerase. Science, 1997, 276, 561-567.	6.0	1,172
34	The growing landscape of lysine acetylation links metabolism and cell signalling. Nature Reviews Molecular Cell Biology, 2014, 15, 536-550.	16.1	1,153
35	A Human Interactome in Three Quantitative Dimensions Organized by Stoichiometries and Abundances. Cell, 2015, 163, 712-723.	13.5	1,132
36	L-Arginine Modulates T Cell Metabolism and Enhances Survival and Anti-tumor Activity. Cell, 2016, 167, 829-842.e13.	13.5	1,077

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37	FLICE is activated by association with the CD95 death-inducing signaling complex (DISC). EMBO Journal, 1997, 16, 2794-2804.	3.5	1,073
38	Nucleolar proteome dynamics. Nature, 2005, 433, 77-83.	13.7	1,061
39	Analysis of Proteins and Proteomes by Mass Spectrometry. Annual Review of Biochemistry, 2001, 70, 437-473.	5.0	1,044
40	Glucosylation of Rho proteins by Clostridium difficile toxin B. Nature, 1995, 375, 500-503.	13.7	1,030
41	Directed Proteomic Analysis of the Human Nucleolus. Current Biology, 2002, 12, 1-11.	1.8	962
42	Trypsin Cleaves Exclusively C-terminal to Arginine and Lysine Residues. Molecular and Cellular Proteomics, 2004, 3, 608-614.	2.5	957
43	The abc's (and xyz's) of peptide sequencing. Nature Reviews Molecular Cell Biology, 2004, 5, 699-711.	16.1	948
44	miRNPs: a novel class of ribonucleoproteins containing numerous microRNAs. Genes and Development, 2002, 16, 720-728.	2.7	926
45	From genomics to proteomics. Nature, 2003, 422, 193-197.	13.7	886
46	Deep proteome and transcriptome mapping of a human cancer cell line. Molecular Systems Biology, 2011, 7, 548.	3.2	878
47	Analysis of protein phosphorylation using mass spectrometry: deciphering the phosphoproteome. Trends in Biotechnology, 2002, 20, 261-268.	4.9	877
48	Functional and quantitative proteomics using SILAC. Nature Reviews Molecular Cell Biology, 2006, 7, 952-958.	16.1	865
49	The Exosome: A Conserved Eukaryotic RNA Processing Complex Containing Multiple 3â€²â†’5â€² Exoribonucleases. Cell, 1997, 91, 457-466.	13.5	859
50	Circular non-coding RNA ANRIL modulates ribosomal RNA maturation and atherosclerosis in humans. Nature Communications, 2016, 7, 12429.	5.8	859
51	Higher-energy C-trap dissociation for peptide modification analysis. Nature Methods, 2007, 4, 709-712.	9.0	844
52	Ultradeep Human Phosphoproteome Reveals a Distinct Regulatory Nature of Tyr and Ser/Thr-Based Signaling. Cell Reports, 2014, 8, 1583-1594.	2.9	839
53	Specificity in Toll-like receptor signalling through distinct effector functions of TRAF3 and TRAF6. Nature, 2006, 439, 204-207.	13.7	836
54	Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast. Nature, 2008, 455, 1251-1254.	13.7	835

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55	Use of mass spectrometric molecular weight information to identify proteins in sequence databases. Biological Mass Spectrometry, 1993, 22, 338-345.	0.5	832
56	Electrospray and Taylor-Cone theory, Dole's beam of macromolecules at last?. International Journal of Mass Spectrometry and Ion Processes, 1994, 136, 167-180.	1.9	828
57	A practical recipe for stable isotope labeling by amino acids in cell culture (SILAC). Nature Protocols, 2006, 1, 2650-2660.	5.5	816
58	Integrated Analysis of Protein Composition, Tissue Diversity, and Gene Regulation in Mouse Mitochondria. Cell, 2003, 115, 629-640.	13.5	815
59	Large-Scale Proteomic Analysis of the Human Spliceosome. Genome Research, 2002, 12, 1231-1245.	2.4	808
60	AU Binding Proteins Recruit the Exosome to Degrade ARE-Containing mRNAs. Cell, 2001, 107, 451-464.	13.5	803
61	Precision Mapping of an In Vivo N-Glycoproteome Reveals Rigid Topological and Sequence Constraints. Cell, 2010, 141, 897-907.	13.5	789
62	Unbiased quantitative proteomics of lipid rafts reveals high specificity for signaling factors. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5813-5818.	3.3	783
63	Selective Anchoring of TFIID to Nucleosomes by Trimethylation of Histone H3 Lysine 4. Cell, 2007, 131, 58-69.	13.5	769
64	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. Nature Protocols, 2009, 4, 698-705.	5.5	769
65	Phosphoproteomics reveals that Parkinson's disease kinase LRRK2 regulates a subset of Rab GTPases. ELife, 2016, 5, .	2.8	766
66	Mechanism of regulation of WAVE1-induced actin nucleation by Rac1 and Nck. Nature, 2002, 418, 790-793.	13.7	758
67	A Proteome-wide, Quantitative Survey of In Vivo Ubiquitylation Sites Reveals Widespread Regulatory Roles. Molecular and Cellular Proteomics, 2011, 10, M111.013284.	2.5	754
68	Quantitative Interaction Proteomics and Genome-wide Profiling of Epigenetic Histone Marks and Their Readers. Cell, 2010, 142, 967-980.	13.5	710
69	Quantitative Phosphoproteomics Applied to the Yeast Pheromone Signaling Pathway. Molecular and Cellular Proteomics, 2005, 4, 310-327.	2.5	708
70	A proteomics strategy to elucidate functional protein-protein interactions applied to EGF signaling. Nature Biotechnology, 2003, 21, 315-318.	9.4	702
71	Mass Spectrometry-based Proteomics Using Q Exactive, a High-performance Benchtop Quadrupole Orbitrap Mass Spectrometer. Molecular and Cellular Proteomics, 2011, 10, M111.011015.	2.5	701
72	Comparative Proteomic Analysis of Eleven Common Cell Lines Reveals Ubiquitous but Varying Expression of Most Proteins. Molecular and Cellular Proteomics, 2012, 11, M111.014050.	2.5	701

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73	The minimum information about a proteomics experiment (MIAPE). Nature Biotechnology, 2007, 25, 887-893.	9.4	694
74	Temporal analysis of phosphotyrosine-dependent signaling networks by quantitative proteomics. Nature Biotechnology, 2004, 22, 1139-1145.	9.4	680
75	Improved Resolution and Very High Sensitivity in MALDI TOF of Matrix Surfaces Made by Fast Evaporation. Analytical Chemistry, 1994, 66, 3281-3287.	3.2	679
76	Cell typeâ€“ and brain regionâ€“resolved mouse brain proteome. Nature Neuroscience, 2015, 18, 1819-1831.	7.1	672
77	Identification of the receptor component of the IÎºBÎ±â€“ubiquitin ligase. Nature, 1998, 396, 590-594.	13.7	650
78	SILAC Mouse for Quantitative Proteomics Uncovers Kindlin-3 as an Essential Factor for Red Blood Cell Function. Cell, 2008, 134, 353-364.	13.5	631
79	Quantitative, High-Resolution Proteomics for Data-Driven Systems Biology. Annual Review of Biochemistry, 2011, 80, 273-299.	5.0	630
80	Axin-mediated CKI phosphorylation of beta -catenin at Ser 45: a molecular switch for the Wnt pathway. Genes and Development, 2002, 16, 1066-1076.	2.7	621
81	Direct identification of clinically relevant neoepitopes presented on native human melanoma tissue by mass spectrometry. Nature Communications, 2016, 7, 13404.	5.8	613
82	Online Parallel Accumulationâ€“Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. Molecular and Cellular Proteomics, 2018, 17, 2534-2545.	2.5	602
83	The human urinary proteome contains more than 1500 proteins, including a large proportion of membrane proteins. Genome Biology, 2006, 7, R80.	13.9	598
84	Revisiting biomarker discovery by plasmaÂproteomics. Molecular Systems Biology, 2017, 13, 942.	3.2	597
85	Analysis of the Plasmodium falciparum proteome by high-accuracy mass spectrometry. Nature, 2002, 419, 537-542.	13.7	596
86	More than 100,000 Detectable Peptide Species Elute in Single Shotgun Proteomics Runs but the Majority is Inaccessible to Data-Dependent LCâˆ'MS/MS. Journal of Proteome Research, 2011, 10, 1785-1793.	1.8	595
87	Phosphorylation and Inactivation of BAD by Mitochondria-Anchored Protein Kinase A. Molecular Cell, 1999, 3, 413-422.	4.5	593
88	Proteome-wide Analysis of Chaperonin-Dependent Protein Folding in Escherichia coli. Cell, 2005, 122, 209-220.	13.5	590
89	Interpreting mass spectra of multiply charged ions. Analytical Chemistry, 1989, 61, 1702-1708.	3.2	587
90	Activity of DNA ligase IV stimulated by complex formation with XRCC4 protein in mammalian cells. Nature, 1997, 388, 492-495.	13.7	586

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91	An ESP1/PDS1 Complex Regulates Loss of Sister Chromatid Cohesion at the Metaphase to Anaphase Transition in Yeast. Cell, 1998, 93, 1067-1076.	13.5	564
92	Cell-cycle-regulated association of RAD50/MRE11/NBS1 with TRF2 and human telomeres. Nature Genetics, 2000, 25, 347-352.	9.4	560
93	A Novel Rab5 GDP/GTP Exchange Factor Complexed to Rabaptin-5 Links Nucleotide Exchange to Effector Recruitment and Function. Cell, 1997, 90, 1149-1159.	13.5	552
94	Plasma Proteome Profiling to Assess Human Health and Disease. Cell Systems, 2016, 2, 185-195.	2.9	549
95	Kinase-Selective Enrichment Enables Quantitative Phosphoproteomics of the Kinome across the Cell Cycle. Molecular Cell, 2008, 31, 438-448.	4.5	548
96	Decoding Human Cytomegalovirus. Science, 2012, 338, 1088-1093.	6.0	546
97	Quantitative Proteomics Reveals Subset-Specific Viral Recognition in Dendritic Cells. Immunity, 2010, 32, 279-289.	6.6	544
98	1D and 2D annotation enrichment: a statistical method integrating quantitative proteomics with complementary high-throughput data. BMC Bioinformatics, 2012, 13, S12.	1.2	542
99	A Mammalian Organelle Map by Protein Correlation Profiling. Cell, 2006, 125, 187-199.	13.5	538
100	Glnâ€‰63 of Rho is deamidated by Escherichia coli cytotoxic necrotizing factor-1. Nature, 1997, 387, 725-729.	13.7	534
101	Decoding signalling networks by mass spectrometry-based proteomics. Nature Reviews Molecular Cell Biology, 2010, 11, 427-439.	16.1	534
102	Mechanism of Divergent Growth Factor Effects in Mesenchymal Stem Cell Differentiation. Science, 2005, 308, 1472-1477.	6.0	531
103	A â€œProteomic Rulerâ€•for Protein Copy Number and Concentration Estimation without Spike-in Standards. Molecular and Cellular Proteomics, 2014, 13, 3497-3506.	2.5	530
104	Identification of a gene causing human cytochrome c oxidase deficiency by integrative genomics. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 605-610.	3.3	526
105	Nucleosome-Interacting Proteins Regulated by DNA and Histone Methylation. Cell, 2010, 143, 470-484.	13.5	524
106	Metabolic priming by a secreted fungal effector. Nature, 2011, 478, 395-398.	13.7	509
107	Combination of FASP and StageTip-Based Fractionation Allows In-Depth Analysis of the Hippocampal Membrane Proteome. Journal of Proteome Research, 2009, 8, 5674-5678.	1.8	507
108	Status of Large-scale Analysis of Post-translational Modifications by Mass Spectrometry. Molecular and Cellular Proteomics, 2013, 12, 3444-3452.	2.5	491

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109	Trans-complex formation by proteolipid channels in the terminal phase of membrane fusion. Nature, 2001, 409, 581-588.	13.7	487
110	p70S6 kinase signals cell survival as well as growth, inactivating the pro-apoptotic molecule BAD. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 9666-9670.	3.3	487
111	Chromatin-remodelling factor CHRAC contains the ATPases ISWI and topoisomerase II. Nature, 1997, 388, 598-602.	13.7	484
112	Super-SILAC mix for quantitative proteomics of human tumor tissue. Nature Methods, 2010, 7, 383-385.	9.0	480
113	Widespread Proteome Remodeling and Aggregation in Aging C.Âelegans. Cell, 2015, 161, 919-932.	13.5	478
114	Multilevel proteomics reveals host perturbations by SARS-CoV-2 and SARS-CoV. Nature, 2021, 594, 246-252.	13.7	475
115	Mass spectrometry and EST-database searching allows characterization of the multi-protein spliceosome complex. Nature Genetics, 1998, 20, 46-50.	9.4	470
116	Phosphotyrosine interactome of the ErbBâ€receptor kinase family. Molecular Systems Biology, 2005, 1, 2005.0008.	3.2	468
117	mRNA Silencing in Erythroid Differentiation: hnRNP K and hnRNP E1 Regulate 15-Lipoxygenase Translation from the 3â€² End. Cell, 1997, 89, 597-606.	13.5	467
118	Mass spectrometry in high-throughput proteomics: ready for the big time. Nature Methods, 2010, 7, 681-685.	9.0	465
119	Paraspeckles. Current Biology, 2002, 12, 13-25.	1.8	455
120	The Enterotoxin from Clostridium difficile (ToxA) Monoglucosylates the Rho Proteins. Journal of Biological Chemistry, 1995, 270, 13932-13936.	1.6	450
121	Mass Spectrometry of Human Leukocyte Antigen Class I Peptidomes Reveals Strong Effects of Protein Abundance and Turnover on Antigen Presentation. Molecular and Cellular Proteomics, 2015, 14, 658-673.	2.5	445
122	Properties of13C-Substituted Arginine in Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC). Journal of Proteome Research, 2003, 2, 173-181.	1.8	439
123	Protein abundance profiling of the Escherichia coli cytosol. BMC Genomics, 2008, 9, 102.	1.2	432
124	Identifying and quantifying in vivo methylation sites by heavy methyl SILAC. Nature Methods, 2004, 1, 119-126.	9.0	427
125	Quantitative proteomics combined with BAC TransgeneOmics reveals in vivo protein interactions. Journal of Cell Biology, 2010, 189, 739-754.	2.3	427
126	Rapid â€˜de novoâ€™ peptide sequencing by a combination of nanoelectrospray, isotopic labeling and a quadrupole/time-of-flight mass spectrometer. , 1997, 11, 1015-1024.		426

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127	Comparative Proteomic Phenotyping of Cell Lines and Primary Cells to Assess Preservation of Cell Type-specific Functions. Molecular and Cellular Proteomics, 2009, 8, 443-450.	2.5	426
128	System-Wide Changes to SUMO Modifications in Response to Heat Shock. Science Signaling, 2009, 2, ra24.	1.6	415
129	Analysis of receptor signaling pathways by mass spectrometry: Identification of Vav-2 as a substrate of the epidermal and platelet-derived growth factor receptors. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 179-184.	3.3	410
130	Is Proteomics the New Genomics?. Cell, 2007, 130, 395-398.	13.5	410
131	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. Genome Biology, 2007, 8, R250.	13.9	410
132	Phosphatidylcholine Synthesis for Lipid Droplet Expansion Is Mediated by Localized Activation of CTP:Phosphocholine Cytidylyltransferase. Cell Metabolism, 2011, 14, 504-515.	7.2	408
133	Uncovering global SUMOylation signaling networks in a site-specific manner. Nature Structural and Molecular Biology, 2014, 21, 927-936.	3.6	408
134	High-throughput phosphoproteomics reveals in vivo insulin signaling dynamics. Nature Biotechnology, 2015, 33, 990-995.	9.4	408
135	An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics. Nature Communications, 2019, 10, 963.	5.8	408
136	Mitotic Regulation of the APC Activator Proteins CDC20 and CDH1. Molecular Biology of the Cell, 2000, 11, 1555-1569.	0.9	405
137	The yeast exosome and human PM-Scl are related complexes of 3' right-arrow 5' exonucleases. Genes and Development, 1999, 13, 2148-2158.	2.7	402
138	Protein Phosphorylation: A Major Switch Mechanism for Metabolic Regulation. Trends in Endocrinology and Metabolism, 2015, 26, 676-687.	3.1	402
139	Pervasive functional translation of noncanonical human open reading frames. Science, 2020, 367, 1140-1146.	6.0	400
140	Mass spectrometric-based approaches in quantitative proteomics. Methods, 2003, 29, 124-130.	1.9	398
141	A Dual Pressure Linear Ion Trap Orbitrap Instrument with Very High Sequencing Speed. Molecular and Cellular Proteomics, 2009, 8, 2759-2769.	2.5	398
142	The mitochondrial contact site complex, a determinant of mitochondrial architecture. EMBO Journal, 2011, 30, 4356-4370.	3.5	395
143	System-Wide Temporal Characterization of the Proteome and Phosphoproteome of Human Embryonic Stem Cell Differentiation. Science Signaling, 2011, 4, rs3.	1.6	389
144	In-depth analysis of the membrane and cytosolic proteome of red blood cells. Blood, 2006, 108, 791-801.	0.6	388

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145	Precision proteomics: The case for high resolution and high mass accuracy. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18132-18138.	3.3	388
146	The Mex67p-mediated nuclear mRNA export pathway is conserved from yeast to human. EMBO Journal, 1999, 18, 2593-2609.	3.5	387
147	diaPASEF: parallel accumulationâ€"serial fragmentation combined with data-independent acquisition. Nature Methods, 2020, 17, 1229-1236.	9.0	387
148	Î²1- and Î±v-class integrins cooperate to regulate myosinÂII during rigidity sensing of fibronectin-based microenvironments. Nature Cell Biology, 2013, 15, 625-636.	4.6	386
149	Phosphoproteome Analysis of E. coli Reveals Evolutionary Conservation of Bacterial Ser/Thr/Tyr Phosphorylation. Molecular and Cellular Proteomics, 2008, 7, 299-307.	2.5	385
150	Global and Site-Specific Quantitative Phosphoproteomics: Principles and Applications. Annual Review of Pharmacology and Toxicology, 2009, 49, 199-221.	4.2	382
151	Identification of Proteins in the Postsynaptic Density Fraction by Mass Spectrometry. Journal of Neuroscience, 2000, 20, 4069-4080.	1.7	380
152	Global analysis of genome, transcriptome and proteome reveals the response to aneuploidy in human cells. Molecular Systems Biology, 2012, 8, 608.	3.2	379
153	PHOSIDA 2011: the posttranslational modification database. Nucleic Acids Research, 2011, 39, D253-D260.	6.5	366
154	The Methylosome, a 20S Complex Containing JBP1 and pICln, Produces Dimethylarginine-Modified Sm Proteins. Molecular and Cellular Biology, 2001, 21, 8289-8300.	1.1	365
155	The Serine/Threonine/Tyrosine Phosphoproteome of the Model Bacterium Bacillus subtilis. Molecular and Cellular Proteomics, 2007, 6, 697-707.	2.5	359
156	In-Vivo Quantitative Proteomics Reveals a Key Contribution of Post-Transcriptional Mechanisms to the Circadian Regulation of Liver Metabolism. PLoS Genetics, 2014, 10, e1004047.	1.5	358
157	Chromatin-Remodeling Components of the BAF Complex Facilitate Reprogramming. Cell, 2010, 141, 943-955.	13.5	357
158	Jmjd6 Catalyses Lysyl-Hydroxylation of U2AF65, a Protein Associated with RNA Splicing. Science, 2009, 325, 90-93.	6.0	356
159	A Mass Spectrometry-based Proteomic Approach for Identification of Serine/Threonine-phosphorylated Proteins by Enrichment with Phospho-specific Antibodies. Molecular and Cellular Proteomics, 2002, 1, 517-527.	2.5	353
160	Proteomic Analysis of the Arabidopsis Nucleolus Suggests Novel Nucleolar Functions. Molecular Biology of the Cell, 2005, 16, 260-269.	0.9	352
161	System-wide Perturbation Analysis with Nearly Complete Coverage of the Yeast Proteome by Single-shot Ultra HPLC Runs on a Bench Top Orbitrap. Molecular and Cellular Proteomics, 2012, 11, M111.013722.	2.5	350
162	ERCC1/XPF Removes the 3â€² Overhang from Uncapped Telomeres and Represses Formation of Telomeric DNA-Containing Double Minute Chromosomes. Molecular Cell, 2003, 12, 1489-1498.	4.5	349

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163	Mass spectrometryâ€"based proteomics in cell biology. Journal of Cell Biology, 2010, 190, 491-500.	2.3	348
164	Requirement of ATM-Dependent Monoubiquitylation of Histone H2B for Timely Repair of DNA Double-Strand Breaks. Molecular Cell, 2011, 41, 529-542.	4.5	347
165	Identification of 491 proteins in the tear fluid proteome reveals a large number of proteases and protease inhibitors. Genome Biology, 2006, 7, R72.	13.9	344
166	Systematic proteomic analysis of LRRK2-mediated Rab GTPase phosphorylation establishes a connection to ciliogenesis. ELife, 2017, 6, .	2.8	344
167	Pre-mRNA splicing and mRNA export linked by direct interactions between UAP56 and Aly. Nature, 2001, 413, 644-647.	13.7	339
168	Proteome Analysis of Separated Male and Female Gametocytes Reveals Novel Sex-Specific Plasmodium Biology. Cell, 2005, 121, 675-687.	13.5	336
169	Cytoplasmic protein aggregates interfere with nucleocytoplasmic transport of protein and RNA. Science, 2016, 351, 173-176.	6.0	336
170	A Systematic Mammalian Genetic Interaction Map Reveals Pathways Underlying Ricin Susceptibility. Cell, 2013, 152, 909-922.	13.5	332
171	Proteomics reveals NNMT as a master metabolic regulator of cancer-associated fibroblasts. Nature, 2019, 569, 723-728.	13.7	330
172	The Coming Age of Complete, Accurate, and Ubiquitous Proteomes. Molecular Cell, 2013, 49, 583-590.	4.5	329
173	Microcolumns with self-assembled particle frits for proteomics. Journal of Chromatography A, 2002, 979, 233-239.	1.8	327
174	Robust Salmonella metabolism limits possibilities for new antimicrobials. Nature, 2006, 440, 303-307.	13.7	327
175	Defining the transcriptome and proteome in three functionally different human cell lines. Molecular Systems Biology, 2010, 6, 450.	3.2	324
176	TNF receptor 1 genetic risk mirrors outcome of anti-TNF therapy in multiple sclerosis. Nature, 2012, 488, 508-511.	13.7	323
177	Arginine methylation at histone H3R2 controls deposition of H3K4 trimethylation. Nature, 2007, 449, 928-932.	13.7	322
178	Large-scale and high-confidence proteomic analysis of human seminal plasma. Genome Biology, 2006, 7, R40.	13.9	321
179	IÎºB Kinase (IKK)-Associated Protein 1, a Common Component of the Heterogeneous IKK Complex. Molecular and Cellular Biology, 1999, 19, 1526-1538.	1.1	320
180	In mouse brain profilin I and profilin II associate with regulators of the endocytic pathway and actin assembly. EMBO Journal, 1998, 17, 967-976.	3.5	317

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181	Mass Spectrometric Analysis of the Anaphase-Promoting Complex from Yeast: Identification of a Subunit Related to Cullins. Science, 1998, 279, 1216-1219.	6.0	317
182	Analysis of the Saccharomyces Spindle Pole by Matrix-assisted Laser Desorption/Ionization (MALDI) Mass Spectrometry. Journal of Cell Biology, 1998, 141, 967-977.	2.3	317
183	Improved peptide identification in proteomics by two consecutive stages of mass spectrometric fragmentation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13417-13422.	3.3	317
184	A genome-wide resource for the analysis of protein localisation in Drosophila. ELife, 2016, 5, e12068.	2.8	315
185	Analysis of Nucleolar Protein Dynamics Reveals the Nuclear Degradation of Ribosomal Proteins. Current Biology, 2007, 17, 749-760.	1.8	314
186	Nucleolin and YB-1 are required for JNK-mediated interleukin-2 mRNA stabilization during T-cell activation. Genes and Development, 2000, 14, 1236-1248.	2.7	314
187	Deep and Highly Sensitive Proteome Coverage by LC-MS/MS Without Prefractionation. Molecular and Cellular Proteomics, 2011, 10, M110.003699.	2.5	311
188	Delayed Extraction Improves Specificity in Database Searches by Matrix-assisted Laser Desorption/Ionization Peptide Maps. Rapid Communications in Mass Spectrometry, 1996, 10, 1371-1378.	0.7	307
189	Detection of Tyrosine Phosphorylated Peptides by Precursor Ion Scanning Quadrupole TOF Mass Spectrometry in Positive Ion Mode. Analytical Chemistry, 2001, 73, 1440-1448.	3.2	306
190	Ultra High Resolution Linear Ion Trap Orbitrap Mass Spectrometer (Orbitrap Elite) Facilitates Top Down LC MS/MS and Versatile Peptide Fragmentation Modes. Molecular and Cellular Proteomics, 2012, 11, O111.013698.	2.5	303
191	BoxCar acquisition method enables single-shot proteomics at a depth of 10,000 proteins in 100 minutes. Nature Methods, 2018, 15, 440-448.	9.0	303
192	C9orf72 FTLD/ALS-associated Gly-Ala dipeptide repeat proteins cause neuronal toxicity and Unc119 sequestration. Acta Neuropathologica, 2014, 128, 485-503.	3.9	300
193	Proteomic Investigations Reveal a Role for RNA Processing Factor THRAP3 in the DNA Damage Response. Molecular Cell, 2012, 46, 212-225.	4.5	298
194	Phosphorylation Is a Central Mechanism for Circadian Control of Metabolism and Physiology. Cell Metabolism, 2017, 25, 118-127.	7.2	297
195	Social network architecture of human immune cells unveiled by quantitative proteomics. Nature Immunology, 2017, 18, 583-593.	7.0	296
196	Spindle Checkpoint Protein Xmad1 Recruits Xmad2 to Unattached Kinetochores. Journal of Cell Biology, 1998, 143, 283-295.	2.3	295
197	Modular Stop and Go Extraction Tips with Stacked Disks for Parallel and Multidimensional Peptide Fractionation in Proteomics. Journal of Proteome Research, 2006, 5, 988-994.	1.8	294
198	Parent Ion Scans of Unseparated Peptide Mixtures. Analytical Chemistry, 1996, 68, 527-533.	3.2	287

#	Article	IF	Citations
199	The Q Exactive HF, a Benchtop Mass Spectrometer with a Pre-filter, High-performance Quadrupole and an Ultra-high-field Orbitrap Analyzer. Molecular and Cellular Proteomics, 2014, 13, 3698-3708.	2.5	285
200	High Recovery FASP Applied to the Proteomic Analysis of Microdissected Formalin Fixed Paraffin Embedded Cancer Tissues Retrieves Known Colon Cancer Markers. Journal of Proteome Research, 2011, 10, 3040-3049.	1.8	281
201	Parallel Accumulationâ€"Serial Fragmentation (PASEF): Multiplying Sequencing Speed and Sensitivity by Synchronized Scans in a Trapped Ion Mobility Device. Journal of Proteome Research, 2015, 14, 5378-5387.	1.8	281
202	Regulation of ubiquitin-binding proteins by monoubiquitination. Nature Cell Biology, 2006, 8, 163-169.	4.6	279
203	Mislocalized Activation of Oncogenic RTKs Switches Downstream Signaling Outcomes. Molecular Cell, 2009, 36, 326-339.	4.5	278
204	Consecutive Proteolytic Digestion in an Enzyme Reactor Increases Depth of Proteomic and Phosphoproteomic Analysis. Analytical Chemistry, 2012, 84, 2631-2637.	3.2	278
205	Distinct and Overlapping Sets of SUMO-1 and SUMO-2 Target Proteins Revealed by Quantitative Proteomics. Molecular and Cellular Proteomics, 2006, 5, 2298-2310.	2.5	274
206	Inflammatory signaling in human tuberculosis granulomas is spatially organized. Nature Medicine, 2016, 22, 531-538.	15.2	273
207	RGM is a repulsive guidance molecule for retinal axons. Nature, 2002, 419, 392-395.	13.7	272
208	Regulation of G2/M events by Cdc25A through phosphorylation-dependent modulation of its stability. EMBO Journal, 2002, 21, 5911-5920.	3.5	272
209	A Novel LC System Embeds Analytes in Pre-formed Gradients for Rapid, Ultra-robust Proteomics. Molecular and Cellular Proteomics, 2018, 17, 2284-2296.	2.5	270
210	Iodoacetamide-induced artifact mimics ubiquitination in mass spectrometry. Nature Methods, 2008, 5, 459-460.	9.0	268
211	Use of stable isotope labeling by amino acids in cell culture as a spike-in standard in quantitative proteomics. Nature Protocols, 2011, 6, 147-157.	5.5	265
212	A Novel Proteomic Screen for Peptide-Protein Interactions. Journal of Biological Chemistry, 2004, 279, 10756-10764.	1.6	262
213	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) and Proteome Quantitation of Mouse Embryonic Stem Cells to a Depth of 5,111 Proteins. Molecular and Cellular Proteomics, 2008, 7, 672-683.	2.5	261
214	Ultraâ€high sensitivity mass spectrometry quantifies singleâ€cell proteome changes upon perturbation. Molecular Systems Biology, 2022, 18, e10798.	3.2	261
215	Nucleolin and YB-1 are required for JNK-mediated interleukin-2 mRNA stabilization during T-cell activation. Genes and Development, 2000, 14, 1236-48.	2.7	259
216	Large-scale Proteomics Analysis of the Human Kinome. Molecular and Cellular Proteomics, 2009, 8, 1751-1764.	2.5	257

#	Article	IF	Citations
217	Mapping of Phosphorylation Sites of Gel-Isolated Proteins by Nanoelectrospray Tandem Mass Spectrometry:Â Potentials and Limitations. Analytical Chemistry, 1999, 71, 235-242.	3.2	256
218	Proteomic maps of breast cancer subtypes. Nature Communications, 2016, 7, 10259.	5.8	256
219	Site-Specific Identification of SUMO-2 Targets in Cells Reveals an Inverted SUMOylation Motif and a Hydrophobic Cluster SUMOylation Motif. Molecular Cell, 2010, 39, 641-652.	4.5	255
220	Identification of the Components of Simple Protein Mixtures by High-Accuracy Peptide Mass Mapping and Database Searching. Analytical Chemistry, 1997, 69, 4741-4750.	3.2	253
221	Brain Phosphoproteome Obtained by a FASP-Based Method Reveals Plasma Membrane Protein Topology. Journal of Proteome Research, 2010, 9, 3280-3289.	1.8	253
222	Gemin3. Journal of Cell Biology, 1999, 147, 1181-1194.	2.3	251
223	In Vivo Identification of Human Small Ubiquitin-like Modifier Polymerization Sites by High Accuracy Mass Spectrometry and an in Vitro to in Vivo Strategy. Molecular and Cellular Proteomics, 2008, 7, 132-144.	2.5	251
224	Quantitative Proteomic Comparison of Rat Mitochondria from Muscle, Heart, and Liver. Molecular and Cellular Proteomics, 2006, 5, 608-619.	2.5	250
225	Dissection of the insulin signaling pathway via quantitative phosphoproteomics. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2451-2456.	3.3	250
226	Visualization of LCâ€MS/MS proteomics data in MaxQuant. Proteomics, 2015, 15, 1453-1456.	1.3	248
227	Status of complete proteome analysis by mass spectrometry: SILAC labeled yeast as a model system. Genome Biology, 2006, 7, R50.	13.9	244
228	Repo-Man recruits PP1Î³ to chromatin and is essential for cell viability. Journal of Cell Biology, 2006, 172, 679-692.	2.3	240
229	The complex containing actin-related proteins Arp2 and Arp3 is required for the motility and integrity of yeast actin patches. Current Biology, 1997, 7, 519-529.	1.8	239
230	Protein interaction screening by quantitative immunoprecipitation combined with knockdown (QUICK). Nature Methods, 2006, 3, 981-983.	9.0	239
231	Mapping N-Glycosylation Sites across Seven Evolutionarily Distant Species Reveals a Divergent Substrate Proteome Despite a Common Core Machinery. Molecular Cell, 2012, 46, 542-548.	4.5	238
232	High-throughput and high-sensitivity phosphoproteomics with the EasyPhos platform. Nature Protocols, 2018, 13, 1897-1916.	5.5	238
233	Polymerization of Purified Yeast Septins: Evidence That Organized Filament Arrays May Not Be Required for Septin Function. Journal of Cell Biology, 1998, 143, 737-749.	2.3	237
234	RNA and RNA Binding Proteins Participate in Early Stages of Cell Spreading through Spreading Initiation Centers. Cell, 2004, 117, 649-662.	13.5	237

#	Article	IF	Citations
235	MSQuant, an Open Source Platform for Mass Spectrometry-Based Quantitative Proteomics. Journal of Proteome Research, 2010, 9, 393-403.	1.8	237
236	Acetylation site specificities of lysine deacetylase inhibitors in human cells. Nature Biotechnology, 2015, 33, 415-423.	9.4	237
237	Systems-wide Proteomic Analysis in Mammalian Cells Reveals Conserved, Functional Protein Turnover. Journal of Proteome Research, 2011, 10, 5275-5284.	1.8	235
238	Deep Proteomics of Mouse Skeletal Muscle Enables Quantitation of Protein Isoforms, Metabolic Pathways, and Transcription Factors*. Molecular and Cellular Proteomics, 2015, 14, 841-853.	2.5	234
239	Accurate Protein Complex Retrieval by Affinity Enrichment Mass Spectrometry (AE-MS) Rather than Affinity Purification Mass Spectrometry (AP-MS). Molecular and Cellular Proteomics, 2015, 14, 120-135.	2.5	231
240	Functional classification of memory CD8+ T cells by CX3CR1 expression. Nature Communications, 2015, 6, 8306.	5.8	231
241	Of protons or proteins. Zeitschrift FÃ¼r Physik D-Atoms Molecules and Clusters, 1988, 10, 361-368.	1.0	227
242	A Proteomic Approach for Identification of Secreted Proteins during the Differentiation of 3T3-L1 Preadipocytes to Adipocytes. Molecular and Cellular Proteomics, 2002, 1, 213-222.	2.5	227
243	SH2 Signaling in a Lower Eukaryote: A STAT Protein That Regulates Stalk Cell Differentiation in Dictyostelium. Cell, 1997, 89, 909-916.	13.5	221
244	Extensive quantitative remodeling of the proteome between normal colon tissue and adenocarcinoma. Molecular Systems Biology, 2012, 8, 611.	3.2	221
245	Sequence tag identification of intact proteins by matching tanden mass spectral data against sequence data bases.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 8264-8267.	3.3	219
246	Gemin4. Journal of Cell Biology, 2000, 148, 1177-1186.	2.3	219
247	Proteome, Phosphoproteome, and N-Glycoproteome Are Quantitatively Preserved in Formalin-Fixed Paraffin-Embedded Tissue and Analyzable by High-Resolution Mass Spectrometry. Journal of Proteome Research, 2010, 9, 3688-3700.	1.8	219
248	Electrospray: Its potential and limitations as an ionization method for biomolecules. Organic Mass Spectrometry, 1990, 25, 575-587.	1.3	217
249	eIF4A3 is a novel component of the exon junction complex. Rna, 2004, 10, 200-209.	1.6	215
250	Quantitative Analysis of the Intra- and Inter-Individual Variability of the Normal Urinary Proteome. Journal of Proteome Research, 2011, 10, 637-645.	1.8	215
251	A novel complex of membrane proteins required for formation of a spherical nucleus. EMBO Journal, 1998, 17, 6449-6464.	3.5	213
252	A Functional Interaction between the Survival Motor Neuron Complex and RNA Polymerase II. Journal of Cell Biology, 2001, 152, 75-86.	2.3	213

#	Article	IF	Citations
253	Proteomics on an Orbitrap Benchtop Mass Spectrometer Using All-ion Fragmentation. Molecular and Cellular Proteomics, 2010, 9, 2252-2261.	2.5	213
254	Single Muscle Fiber Proteomics Reveals Fiber-Type-Specific Features of Human Muscle Aging. Cell Reports, 2017, 19, 2396-2409.	2.9	213
255	Region and cell-type resolved quantitative proteomic map of the human heart. Nature Communications, 2017, 8, 1469.	5.8	213
256	Electrospray mass spectrometry for protein characterization. Trends in Biochemical Sciences, 1995, 20, 219-224.	3.7	212
257	A strategy for identifying gel-separated proteins in sequence databases by MS alone. Biochemical Society Transactions, 1996, 24, 893-896.	1.6	212
258	Sample Preparation Methods for Mass Spectrometric Peptide Mapping Directly from 2-DE Gels. , 1999, 112, 513-530.		211
259	Timeâ€•and compartmentâ€•resolved proteome profiling of the extracellular niche in lung injury and repair. Molecular Systems Biology, 2015, 11, 819.	3.2	211
260	Activation of the ATR kinase by the RPA-binding protein ETAA1. Nature Cell Biology, 2016, 18, 1196-1207.	4.6	208
261	The yeast protein Arc1p binds to tRNA and functions as a cofactor for the methionyl- and glutamyl-tRNA synthetases.. EMBO Journal, 1996, 15, 5437-5448.	3.5	207
262	Maturation and Intranuclear Transport of Pre-Ribosomes Requires Noc Proteins. Cell, 2001, 105, 499-509.	13.5	206
263	Mass Spectrometric Mapping of Linker Histone H1 Variants Reveals Multiple Acetylations, Methylations, and Phosphorylation as Well as Differences between Cell Culture and Tissue. Molecular and Cellular Proteomics, 2007, 6, 72-87.	2.5	205
264	Proteome Differences between Brown and White Fat Mitochondria Reveal Specialized Metabolic Functions. Cell Metabolism, 2009, 10, 324-335.	7.2	205
265	Initial Quantitative Proteomic Map of 28 Mouse Tissues Using the SILAC Mouse. Molecular and Cellular Proteomics, 2013, 12, 1709-1722.	2.5	204
266	A Generic Strategy To Analyze the Spatial Organization of Multi-Protein Complexes by Cross-Linking and Mass Spectrometry. Analytical Chemistry, 2000, 72, 267-275.	3.2	202
267	Absolute SILAC for Accurate Quantitation of Proteins in Complex Mixtures Down to the Attomole Level. Journal of Proteome Research, 2008, 7, 1118-1130.	1.8	200
268	ER-60, a chaperone with thiol-dependent reductase activity involved in MHC class I assembly. EMBO Journal, 1998, 17, 2186-2195.	3.5	199
269	A Novel WD Repeat Protein Component of the Methylosome Binds Sm Proteins. Journal of Biological Chemistry, 2002, 277, 8243-8247.	1.6	199
270	Quantitative proteomic analysis of single pancreatic islets. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18902-18907.	3.3	199

#	Article	IF	Citations
271	A Proteomic Study of SUMO-2 Target Proteins. Journal of Biological Chemistry, 2004, 279, 33791-33798.	1.6	197
272	Cbf5p, a potential pseudouridine synthase, and Nhp2p, a putative RNA-binding protein, are present together with Gar1p in all H BOX/ACA-motif snoRNPs and constitute a common bipartite structure. Rna, 1998, 4, 1549-1568.	1.6	195
273	Global Effects of Kinase Inhibitors on Signaling Networks Revealed by Quantitative Phosphoproteomics. Molecular and Cellular Proteomics, 2009, 8, 2796-2808.	2.5	194
274	Identification of the proteins of the yeast U1 small nuclear ribonucleoprotein complex by mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 385-390.	3.3	191
275	Ubc9 Sumoylation Regulates SUMO Target Discrimination. Molecular Cell, 2008, 31, 371-382.	4.5	191
276	Proteomic Profiling of Plasmodium Sporozoite Maturation Identifies New Proteins Essential for Parasite Development and Infectivity. PLoS Pathogens, 2008, 4, e1000195.	2.1	191
277	The NOT proteins are part of the CCR4 transcriptional complex and affect gene expression both positively and negatively. EMBO Journal, 1998, 17, 1096-1106.	3.5	190
278	Circadian control of oscillations in mitochondrial rate-limiting enzymes and nutrient utilization by PERIOD proteins. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1673-82.	3.3	190
279	Stable Isotope Labeling of Arabidopsis thaliana Cells and Quantitative Proteomics by Mass Spectrometry. Molecular and Cellular Proteomics, 2005, 4, 1697-1709.	2.5	189
280	Stable Isotope Labeling by Amino Acids in Cell Culture for Quantitative Proteomics. Methods in Molecular Biology, 2007, 359, 37-52.	0.4	189
281	Proteomics reveals the effects of sustained weight loss on the human plasma proteome. Molecular Systems Biology, 2016, 12, 901.	3.2	188
282	Copy Number Analysis of the Murine Platelet Proteome Spanning the Complete Abundance Range. Molecular and Cellular Proteomics, 2014, 13, 3435-3445.	2.5	187
283	Differential Expression Profiling of Membrane Proteins by Quantitative Proteomics in a Human Mesenchymal Stem Cell Line Undergoing Osteoblast Differentiation. Stem Cells, 2005, 23, 1367-1377.	1.4	185
284	Organellar proteomics: turning inventories into insights. EMBO Reports, 2006, 7, 874-879.	2.0	185
285	Functional analysis of the human CDC5L complex and identification of its components by mass spectrometry. EMBO Journal, 2000, 19, 6569-6581.	3.5	183
286	Proteomics reveals dynamic assembly of repair complexes during bypass of DNA cross-links. Science, 2015, 348, 1253671.	6.0	183
287	Soluble Oligomers of PolyQ-Expanded Huntingtin Target a Multiplicity of Key Cellular Factors. Molecular Cell, 2016, 63, 951-964.	4.5	181
288	Sleep-wake cycles drive daily dynamics of synaptic phosphorylation. Science, 2019, 366, .	6.0	181

#	Article	IF	Citations
289	Top-down Protein Sequencing and MS3 on a Hybrid Linear Quadrupole Ion Trap-Orbitrap Mass Spectrometer. Molecular and Cellular Proteomics, 2006, 5, 949-958.	2.5	179
290	Noncovalent interaction between Ubc9 and SUMO promotes SUMO chain formation. EMBO Journal, 2007, 26, 2797-2807.	3.5	177
291	Protein Kinase CK2 Is Coassembled with Small Conductance Ca2+-Activated K+ Channels and Regulates Channel Gating. Neuron, 2004, 43, 847-858.	3.8	176
292	Plasma proteome profiling discovers novel proteins associated with nonâ€alcoholic fatty liver disease. Molecular Systems Biology, 2019, 15, e8793.	3.2	176
293	Tyrosine Phosphorylation Mapping of the Epidermal Growth Factor Receptor Signaling Pathway. Journal of Biological Chemistry, 2002, 277, 1031-1039.	1.6	175
294	PROTEOMICS. Annual Review of Genomics and Human Genetics, 2004, 5, 267-293.	2.5	175
295	Host Cell Interactome of Tyrosine-Phosphorylated Bacterial Proteins. Cell Host and Microbe, 2009, 5, 397-403.	5.1	175
296	Mtr10p functions as a nuclear import receptor for the mRNA-binding protein Npl3p. EMBO Journal, 1998, 17, 2196-2207.	3.5	174
297	What does it mean to identify a protein in proteomics?. Trends in Biochemical Sciences, 2002, 27, 74-78.	3.7	174
298	Direct Proteomic Quantification of the Secretome of Activated Immune Cells. Science, 2013, 340, 475-478.	6.0	174
299	OpenCell: Endogenous tagging for the cartography of human cellular organization. Science, 2022, 375, eabi6983.	6.0	174
300	The RING-H2 finger protein APC11 and the E2 enzyme UBC4 are sufficient to ubiquitinate substrates of the anaphase-promoting complex. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 8973-8978.	3.3	173
301	p53 down-regulates SARS coronavirus replication and is targeted by the SARS-unique domain and PL ‹sup›pro‹/sup› via E3 ubiquitin ligase RCHY1. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5192-201.	3.3	172
302	Integrative proteomic profiling of ovarian cancer cell lines reveals precursor cell associated proteins and functional status. Nature Communications, 2016, 7, 12645.	5.8	171
303	Plasma Proteome Profiling to detect and avoid sampleâ€related biases in biomarker studies. EMBO Molecular Medicine, 2019, 11, e10427.	3.3	171
304	The chicken egg yolk plasma and granule proteomes. Proteomics, 2008, 8, 178-191.	1.3	170
305	A Map of General and Specialized Chromatin Readers in Mouse Tissues Generated by Label-free Interaction Proteomics. Molecular Cell, 2013, 49, 368-378.	4.5	170
306	Ultra-deep and quantitative saliva proteome reveals dynamics of the oral microbiome. Genome Medicine, 2016, 8, 44.	3.6	170

#	Article	IF	Citations
307	Loss-less Nano-fractionator for High Sensitivity, High Coverage Proteomics. Molecular and Cellular Proteomics, 2017, 16, 694-705.	2.5	169
308	The forebrain synaptic transcriptome is organized by clocks but its proteome is driven by sleep. Science, 2019, 366, .	6.0	169
309	Integral and Associated Lysosomal Membrane Proteins. Traffic, 2007, 8, 1676-1686.	1.3	166
310	Comparison of ultrafiltration units for proteomic and N-glycoproteomic analysis by the filter-aided sample preparation method. Analytical Biochemistry, 2011, 410, 307-309.	1.1	166
311	Histone Variant H2A.Z.2 Mediates Proliferation and Drug Sensitivity of Malignant Melanoma. Molecular Cell, 2015, 59, 75-88.	4.5	166
312	A large synthetic peptide and phosphopeptide reference library for mass spectrometryâ€“based proteomics. Nature Biotechnology, 2013, 31, 557-564.	9.4	164
313	High susceptibility to fatty liver disease in two-pore channel 2-deficient mice. Nature Communications, 2014, 5, 4699.	5.8	164
314	Single muscle fiber proteomics reveals unexpected mitochondrial specialization. EMBO Reports, 2015, 16, 387-395.	2.0	163
315	Integrated Analysis of the Cerebrospinal Fluid Peptidome and Proteome. Journal of Proteome Research, 2008, 7, 386-399.	1.8	162
316	Deep Visual Proteomics defines single-cell identity and heterogeneity. Nature Biotechnology, 2022, 40, 1231-1240.	9.4	160
317	Detection of Arginine Dimethylated Peptides by Parallel Precursor Ion Scanning Mass Spectrometry in Positive Ion Mode. Analytical Chemistry, 2003, 75, 3107-3114.	3.2	158
318	Proteome profiling in cerebrospinal fluid reveals novel biomarkers of Alzheimer's disease. Molecular Systems Biology, 2020, 16, e9356.	3.2	157
319	High confidence determination of specific proteinâ€“protein interactions using quantitative mass spectrometry. Current Opinion in Biotechnology, 2008, 19, 331-337.	3.3	156
320	Human Proteinpedia enables sharing of human protein data. Nature Biotechnology, 2008, 26, 164-167.	9.4	155
321	Super-SILAC Allows Classification of Diffuse Large B-cell Lymphoma Subtypes by Their Protein Expression Profiles. Molecular and Cellular Proteomics, 2012, 11, 77-89.	2.5	155
322	Identification by mass spectrometry and functional analysis of novel proteins of the yeast [U4/U6middle dotU5] tri-snRNP. EMBO Journal, 1999, 18, 4535-4548.	3.5	154
323	18O-Labeling of N-Glycosylation Sites To Improve the Identification of Gel-Separated Glycoproteins Using Peptide Mass Mapping and Database Searching. Analytical Chemistry, 1999, 71, 1431-1440.	3.2	154
324	Peptide separation with immobilized pI strips is an attractive alternative to inâ€gel protein digestion for proteome analysis. Proteomics, 2008, 8, 4862-4872.	1.3	154

#	Article	IF	Citations
325	Integrin-Linked Kinase Controls Microtubule Dynamics Required for Plasma Membrane Targeting of Caveolae. Developmental Cell, 2010, 19, 574-588.	3.1	154
326	Functional Repurposing Revealed by Comparing S.Âpombe and S.Âcerevisiae Genetic Interactions. Cell, 2012, 149, 1339-1352.	13.5	154
327	A proteomic fingerprint of dissolved organic carbon and of soil particles. Oecologia, 2005, 142, 335-343.	0.9	153
328	Comparative Proteomic Analysis Identifies a Role for SUMO in Protein Quality Control. Science Signaling, 2011, 4, rs4.	1.6	153
329	Control of the Terminal Step of Intracellular Membrane Fusion by Protein Phosphatase 1 . Science, 1999, 285, 1084-1087.	6.0	152
330	N Îµ -Formylation of lysine is a widespread post-translational modification of nuclear proteins occurring at residues involved in regulation of chromatin function. Nucleic Acids Research, 2008, 36, 570-577.	6.5	152
331	The Impact II, a Very High-Resolution Quadrupole Time-of-Flight Instrument (QTOF) for Deep Shotgun Proteomics *. Molecular and Cellular Proteomics, 2015, 14, 2014-2029.	2.5	150
332	Identification of proteins in polyacrylamide gels by mass spectrometric peptide mapping combined with database search. Biological Mass Spectrometry, 1994, 23, 249-261.	0.5	149
333	Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. Journal of Proteome Research, 2010, 9, 6786-6794.	1.8	149
334	Regulation of Translesion Synthesis DNA Polymerase Î· by Monoubiquitination. Molecular Cell, 2010, 37, 396-407.	4.5	148
335	Nup93, a Vertebrate Homologue of Yeast Nic96p, Forms a Complex with a Novel 205-kDa Protein and Is Required for Correct Nuclear Pore Assembly. Molecular Biology of the Cell, 1997, 8, 2017-2038.	0.9	147
336	Proteomic Mapping of Brain Plasma Membrane Proteins. Molecular and Cellular Proteomics, 2005, 4, 402-408.	2.5	147
337	Bioinformatics analysis of mass spectrometryâ€based proteomics data sets. FEBS Letters, 2009, 583, 1703-1712.	1.3	147
338	Analysis of High Accuracy, Quantitative Proteomics Data in the MaxQB Database. Molecular and Cellular Proteomics, 2012, 11, M111.014068.	2.5	147
339	The Ser/Thr/Tyr phosphoproteome of Lactococcus lactis IL1403 reveals multiply phosphorylated proteins. Proteomics, 2008, 8, 3486-3493.	1.3	145
340	Limited Environmental Serine and Glycine Confer Brain Metastasis Sensitivity to PHGDH Inhibition. Cancer Discovery, 2020, 10, 1352-1373.	7.7	145
341	Rrp47p Is an Exosome-Associated Protein Required for the 3â€² Processing of Stable RNAs. Molecular and Cellular Biology, 2003, 23, 6982-6992.	1.1	144
342	On the Proper Use of Mass Accuracy in Proteomics. Molecular and Cellular Proteomics, 2007, 6, 377-381.	2.5	144

#	Article	IF	Citations
343	A SILAC-based DNA protein interaction screen that identifies candidate binding proteins to functional DNA elements. Genome Research, 2009, 19, 284-293.	2.4	144
344	The Ubiquitin-Proteasome System Is a Key Component of the SUMO-2/3 Cycle. Molecular and Cellular Proteomics, 2008, 7, 2107-2122.	2.5	143
345	Cell-Type-Resolved Quantitative Proteomics of Murine Liver. Cell Metabolism, 2014, 20, 1076-1087.	7.2	143
346	The phosphoproteome of tollâ€like receptorâ€activated macrophages. Molecular Systems Biology, 2010, 6, 371.	3.2	142
347	Quadrupole time-of-flight versus triple-quadrupole mass spectrometry for the determination of phosphopeptides by precursor ion scanning. Journal of Mass Spectrometry, 2001, 36, 782-790.	0.7	141
348	Large-scale phosphosite quantification in tissues by a spike-in SILAC method. Nature Methods, 2011, 8, 655-658.	9.0	141
349	A Protein Epitope Signature Tag (PrEST) Library Allows SILAC-based Absolute Quantification and Multiplexed Determination of Protein Copy Numbers in Cell Lines. Molecular and Cellular Proteomics, 2012, 11, O111.009613.	2.5	141
350	Lysine acetylome profiling uncovers novel histone deacetylase substrate proteins in Arabidopsis. Molecular Systems Biology, 2017, 13, 949.	3.2	141
351	Improved mass accuracy in matrix-assisted laser desorption/ionization time-of-flight mass spectrometry of peptides. Journal of the American Society for Mass Spectrometry, 1994, 5, 955-958.	1.2	140
352	A high confidence, manually validated human blood plasma protein reference set. BMC Medical Genomics, 2008, 1, 41.	0.7	140
353	Gemin5, a Novel WD Repeat Protein Component of the SMN Complex That Binds Sm Proteins. Journal of Biological Chemistry, 2002, 277, 5631-5636.	1.6	139
354	A protein-interaction network of interferon-stimulated genes extends the innate immune system landscape. Nature Immunology, 2019, 20, 493-502.	7.0	139
355	Software Lock Mass by Two-Dimensional Minimization of Peptide Mass Errors. Journal of the American Society for Mass Spectrometry, 2011, 22, 1373-1380.	1.2	138
356	Protein Correlation Profiles Identify Lipid Droplet Proteins with High Confidence. Molecular and Cellular Proteomics, 2013, 12, 1115-1126.	2.5	138
357	Trapped ion mobility spectrometry and PASEF enable in-depth lipidomics from minimal sample amounts. Nature Communications, 2020, 11, 331.	5.8	138
358	Novel Murine Dendritic Cell Lines: A Powerful Auxiliary Tool for Dendritic Cell Research. Frontiers in Immunology, 2012, 3, 331.	2.2	137
359	Evidence of Extrapancreatic Glucagon Secretion in Man. Diabetes, 2016, 65, 585-597.	0.3	136
360	Replication-Coupled DNA-Protein Crosslink Repair by SPRTN and the Proteasome in Xenopus Egg Extracts. Molecular Cell, 2019, 73, 574-588.e7.	4.5	135

#	Article	IF	Citations
361	A Urokinase Receptor-associated Protein with Specific Collagen Binding Properties. Journal of Biological Chemistry, 2000, 275, 1993-2002.	1.6	134
362	Solid Tumor Proteome and Phosphoproteome Analysis by High Resolution Mass Spectrometry. Journal of Proteome Research, 2008, 7, 5314-5326.	1.8	132
363	Highâ€accuracy identification and bioinformatic analysis of in vivo protein phosphorylation sites in yeast. Proteomics, 2009, 9, 4642-4652.	1.3	132
364	Organellar Proteomics and Phospho-Proteomics Reveal Subcellular Reorganization in Diet-Induced Hepatic Steatosis. Developmental Cell, 2018, 47, 205-221.e7.	3.1	132
365	Proteomic workflow for analysis of archival formalinâ€fixed and paraffinâ€embedded clinical samples to a depth of 10â€‰000 proteins. Proteomics - Clinical Applications, 2013, 7, 225-233.	0.8	131
366	C9ORF72 interaction with cofilin modulates actin dynamics in motor neurons. Nature Neuroscience, 2016, 19, 1610-1618.	7.1	131
367	Bioinformatic analysis of the nucleolus. Biochemical Journal, 2003, 376, 553-569.	1.7	130
368	A comprehensive biochemical and genetic analysis of the yeast U1 snRNP reveals five novel proteins. Rna, 1998, 4, 374-93.	1.6	130
369	Structural Model of a CRISPR RNA-Silencing Complex Reveals the RNA-Target Cleavage Activity in Cmr4. Molecular Cell, 2014, 56, 43-54.	4.5	129
370	Clostridium novyi Î±-Toxin-catalyzed Incorporation of GlcNAc into Rho Subfamily Proteins. Journal of Biological Chemistry, 1996, 271, 25173-25177.	1.6	128
371	Two-dimensional gel protein database ofSaccharomyces cerevisiae (update 1999). Electrophoresis, 1999, 20, 2280-2298.	1.3	128
372	Purification and characterization of the 1.0 MDa CCR4-NOT complex identifies two novel components of the complex 1 1Edited by D. Draper. Journal of Molecular Biology, 2001, 314, 683-694.	2.0	128
373	The Phosphotyrosine Interactome of the Insulin Receptor Family and Its Substrates IRS-1 and IRS-2. Molecular and Cellular Proteomics, 2009, 8, 519-534.	2.5	128
374	The proteome landscape of the kingdoms of life. Nature, 2020, 582, 592-596.	13.7	128
375	Peptide sequencing by mass spectrometry for homology searches and cloning of genes. The Protein Journal, 1997, 16, 481-490.	1.1	127
376	Nup116p and Nup100p are interchangeable through a conserved motif which constitutes a docking site for the mRNA transport factor Gle2p. EMBO Journal, 1998, 17, 1107-1119.	3.5	127
377	Accurate Quantification of More Than 4000 Mouse Tissue Proteins Reveals Minimal Proteome Changes During Aging. Molecular and Cellular Proteomics, 2011, 10, S1-S7.	2.5	127
378	Multi-level Proteomics Identifies CT45 as a Chemosensitivity Mediator and Immunotherapy Target in Ovarian Cancer. Cell, 2018, 175, 159-170.e16.	13.5	127

#	Article	IF	Citations
379	The Vtc proteins in vacuole fusion: coupling NSF activity to V0trans-complex formation. EMBO Journal, 2002, 21, 259-269.	3.5	126
380	Proteomic Changes Resulting from Gene Copy Number Variations in Cancer Cells. PLoS Genetics, 2010, 6, e1001090.	1.5	126
381	Mass spectrometry allows direct identification of proteins in large genomes. Proteomics, 2001, 1, 641-650.	1.3	124
382	Unbiased RNAâ€"protein interaction screen by quantitative proteomics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10626-10631.	3.3	124
383	Proteomic Portrait of Human Breast Cancer Progression Identifies Novel Prognostic Markers. Cancer Research, 2012, 72, 2428-2439.	0.4	124
384	A genome-wide screen for genes affecting eisosomes reveals Nce102 function in sphingolipid signaling. Journal of Cell Biology, 2009, 185, 1227-1242.	2.3	123
385	Development of phospho-specific Rab protein antibodies to monitor in vivo activity of the LRRK2 Parkinson's disease kinase. Biochemical Journal, 2018, 475, 1-22.	1.7	123
386	Bacterial single-stranded DNA-binding proteins are phosphorylated on tyrosine. Nucleic Acids Research, 2006, 34, 1588-1596.	6.5	122
387	The Proteome of Primary Prostate Cancer. European Urology, 2016, 69, 942-952.	0.9	122
388	T Cell Receptor (TCR) Interacting Molecule (TRIM), A Novel Disulfide-linked Dimer Associated with the TCRâ€"CD3â€"Î¶ Complex, Recruits Intracellular Signaling Proteins to the Plasma Membrane. Journal of Experimental Medicine, 1998, 188, 561-575.	4.2	121
389	Purification of Native Survival of Motor Neurons Complexes and Identification of Gemin6 as a Novel Component. Journal of Biological Chemistry, 2002, 277, 7540-7545.	1.6	121
390	BASP1 Is a Transcriptional Cosuppressor for the Wilms' Tumor Suppressor Protein WT1. Molecular and Cellular Biology, 2004, 24, 537-549.	1.1	120
391	In-depth analysis of the chicken egg white proteome using an LTQ Orbitrap Velos. Proteome Science, 2011, 9, 7.	0.7	120
392	Dynamics in protein translation sustaining T cell preparedness. Nature Immunology, 2020, 21, 927-937.	7.0	120
393	Oxidation of peptides during electrospray ionization. Rapid Communications in Mass Spectrometry, 1993, 7, 738-743.	0.7	119
394	p95-APP1 links membrane transport to Rac-mediated reorganization of actin. Nature Cell Biology, 2000, 2, 521-530.	4.6	119
395	Thrombomucin, a Novel Cell Surface Protein that Defines Thrombocytes and Multipotent Hematopoietic Progenitors. Journal of Cell Biology, 1997, 138, 1395-1407.	2.3	118
396	The protein encoded by the proto-oncogene DEK changes the topology of chromatin and reduces the efficiency of DNA replication in a chromatin-specific manner. Genes and Development, 2000, 14, 1308-1312.	2.7	118

#	Article	IF	Citations
397	Metamorphosin A: A Novel Peptide Controlling Development of the Lower Metazoan Hydractinia echinata (Coelenterata, Hydrozoa). Developmental Biology, 1994, 163, 440-446.	0.9	117
398	Insights into the molecular architecture of the 26S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11943-11947.	3.3	116
399	Arginine-rhamnosylation as new strategy to activate translation elongation factor P. Nature Chemical Biology, 2015, 11, 266-270.	3.9	116
400	Developments in matrix-assisted laser desorption/ionization peptide mass spectrometry. Current Opinion in Biotechnology, 1996, 7, 11-19.	3.3	115
401	Actin homolog MreB and RNA polymerase interact and are both required for chromosome segregation in Escherichia coli. Genes and Development, 2006, 20, 113-124.	2.7	115
402	Cloning and characterization of PAK5, a novel member of mammalianp21-activated kinase-II subfamily that is predominantly expressed in brain. Oncogene, 2002, 21, 3939-3948.	2.6	114
403	Use of mass spectrometry-derived data to annotate nucleotide and protein sequence databases. Trends in Biochemical Sciences, 2001, 26, 54-61.	3.7	111
404	Multi-omic Profiling Reveals Dynamics of the Phased Progression of Pluripotency. Cell Systems, 2019, 8, 427-445.e10.	2.9	111
405	Pseudosubstrate regulation of the SCFbeta -TrCP ubiquitin ligase by hnRNP-U. Genes and Development, 2002, 16, 439-451.	2.7	110
406	Quantitative proteomic assessment of very early cellular signaling events. Nature Biotechnology, 2007, 25, 566-568.	9.4	110
407	The SH2 Domain Interaction Landscape. Cell Reports, 2013, 3, 1293-1305.	2.9	110
408	The emerging role of mass spectrometry-based proteomics in drug discovery. Nature Reviews Drug Discovery, 2022, 21, 637-654.	21.5	110
409	Identification and Characterization of Gemin7, a Novel Component of the Survival of Motor Neuron Complex. Journal of Biological Chemistry, 2002, 277, 31957-31962.	1.6	109
410	RAD21 Cooperates with Pluripotency Transcription Factors in the Maintenance of Embryonic Stem Cell Identity. PLoS ONE, 2011, 6, e19470.	1.1	109
411	Proteomics-Based Comparative Mapping of the Secretomes of Human Brown and White Adipocytes Reveals EPDR1 as a Novel Batokine. Cell Metabolism, 2019, 30, 963-975.e7.	7.2	109
412	A streamlined mass spectrometryâ€"based proteomics workflow for largeâ€scale FFPE tissue analysis. Journal of Pathology, 2020, 251, 100-112.	2.1	109
413	Identification of the major membrane and core proteins of vaccinia virus by two-dimensional electrophoresis. Journal of Virology, 1996, 70, 7485-7497.	1.5	109
414	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) Applied to Quantitative Proteomics of Bacillus subtilis. Journal of Proteome Research, 2010, 9, 3638-3646.	1.8	108

#	Article	IF	Citations
415	Quantification of the N-glycosylated Secretome by Super-SILAC During Breast Cancer Progression and in Human Blood Samples. Molecular and Cellular Proteomics, 2013, 12, 158-171.	2.5	108
416	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	13.7	108
417	Functional genomics by mass spectrometry. FEBS Letters, 2000, 480, 25-31.	1.3	107
418	Spatiotemporal Proteomic Profiling of Huntingtonâ€™s Disease Inclusions Reveals Widespread Loss of Protein Function. Cell Reports, 2017, 21, 2291-2303.	2.9	107
419	Insulin-dependent Interactions of Proteins with GLUT4 Revealed through Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC)*. Journal of Proteome Research, 2006, 5, 64-75.	1.8	106
420	Investigation of Protein-tyrosine Phosphatase 1B Function by Quantitative Proteomics. Molecular and Cellular Proteomics, 2008, 7, 1763-1777.	2.5	106
421	Artificial intelligence for proteomics and biomarker discovery. Cell Systems, 2021, 12, 759-770.	2.9	106
422	In vivo brain GPCR signaling elucidated by phosphoproteomics. Science, 2018, 360, .	6.0	105
423	A new derivatization strategy for the analysis of phosphopeptides by precursor ion scanning in positive ion mode. Journal of the American Society for Mass Spectrometry, 2002, 13, 996-1003.	1.2	104
424	Identification of a Novel Immunoreceptor Tyrosine-based Activation Motif-containing Molecule, STAM2, by Mass Spectrometry and Its Involvement in Growth Factor and Cytokine Receptor Signaling Pathways. Journal of Biological Chemistry, 2000, 275, 38633-38639.	1.6	103
425	The protein encoded by the proto-oncogene DEK changes the topology of chromatin and reduces the efficiency of DNA replication in a chromatin-specific manner. Genes and Development, 2000, 14, 1308-12.	2.7	103
426	Phosphoproteins of the chicken eggshell calcified layer. Proteomics, 2007, 7, 106-115.	1.3	102
427	In-depth Analysis of the Adipocyte Proteome by Mass Spectrometry and Bioinformatics. Molecular and Cellular Proteomics, 2007, 6, 1257-1273.	2.5	101
428	The sea urchin (Strongylocentrotus purpuratus) test and spine proteomes. Proteome Science, 2008, 6, 22.	0.7	100
429	The mitochondrial lysine acetylome of Arabidopsis. Mitochondrion, 2014, 19, 252-260.	1.6	100
430	Automation of Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry Using Fuzzy Logic Feedback Control. Analytical Chemistry, 1997, 69, 1706-1714.	3.2	98
431	Identifying proteins and post-translational modifications by mass spectrometry. Current Opinion in Structural Biology, 1998, 8, 393-400.	2.6	98
432	De Novo Peptide Sequencing by Nanoelectrospray Tandem Mass Spectrometry Using Triple Quadrupole and Quadrupole/Time-of-Flight Instruments. , 2000, 146, 1-16.		98

#	Article	IF	Citations
433	Phosphorylation of Histone H3 Thr-45 Is Linked to Apoptosis. Journal of Biological Chemistry, 2009, 284, 16575-16583.	1.6	98
434	Reduced CD36-dependent tissue sequestration of Plasmodium-infected erythrocytes is detrimental to malaria parasite growth in vivo. Journal of Experimental Medicine, 2012, 209, 93-107.	4.2	97
435	System-wide identification of wild-type SUMO-2 conjugation sites. Nature Communications, 2015, 6, 7289.	5.8	97
436	Deep Proteome Profiling Reveals Common Prevalence of MZB1-Positive Plasma B Cells in Human Lung and Skin Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2017, 196, 1298-1310.	2.5	97
437	A role of OCRL in clathrin-coated pit dynamics and uncoating revealed by studies of Lowe syndrome cells. ELife, 2014, 3, e02975.	2.8	97
438	A knowledge graph to interpret clinical proteomics data. Nature Biotechnology, 2022, 40, 692-702.	9.4	97
439	Extracting gene function from proteinâ€"protein interactions using Quantitative BAC InteraCtomics (QUBIC). Methods, 2011, 53, 453-459.	1.9	96
440	A Systematic Investigation into the Nature of Tryptic HCD Spectra. Journal of Proteome Research, 2012, 11, 5479-5491.	1.8	96
441	The Arabidopsis Class II Sirtuin Is a Lysine Deacetylase and Interacts with Mitochondrial Energy Metabolism Â Â Â. Plant Physiology, 2014, 164, 1401-1414.	2.3	96
442	Use of Mass Spectrometry to Study Signaling Pathways. Science Signaling, 2000, 2000, pl1-pl1.	1.6	95
443	Interaction between AP-5 and the hereditary spastic paraplegia proteins SPG11 and SPG15. Molecular Biology of the Cell, 2013, 24, 2558-2569.	0.9	95
444	Systems-wide Analysis of a Phosphatase Knock-down by Quantitative Proteomics and Phosphoproteomics. Molecular and Cellular Proteomics, 2009, 8, 1908-1920.	2.5	94
445	H2A.Z.2.2 is an alternatively spliced histone H2A.Z variant that causes severe nucleosome destabilization. Nucleic Acids Research, 2012, 40, 5951-5964.	6.5	94
446	Antisenseâ€mediated exon skipping: a therapeutic strategy for titinâ€based dilated cardiomyopathy. EMBO Molecular Medicine, 2015, 7, 562-576.	3.3	94
447	C/EBPÎ± creates elite cells for iPSC reprogramming by upregulating Klf4 and increasing the levels of Lsd1 andÂBrd4. Nature Cell Biology, 2016, 18, 371-381.	4.6	94
448	Identification of transformation sensitive proteins recorded in human two-dimensional gel protein databases by mass spectrometric peptide mapping alone and in combination with microsequencing. Electrophoresis, 1994, 15, 406-416.	1.3	93
449	Two functionally distinct domains generated by invivo cleavage of Nup145p: a novel biogenesis pathway for nucleoporins. EMBO Journal, 1997, 16, 5086-5097.	3.5	93
450	NOPdb: Nucleolar Proteome Database. Nucleic Acids Research, 2006, 34, D218-D220.	6.5	93

#	Article	IF	Citations
451	Quantitative phosphoproteome analysis of a mouse liver cell line reveals specificity of phosphatase inhibitors. Proteomics, 2008, 8, 4534-4546.	1.3	93
452	Combined Use of RNAi and Quantitative Proteomics to Study Gene Function in Drosophila. Molecular Cell, 2008, 31, 762-772.	4.5	93
453	A plasma-membrane E-MAP reveals links of the eisosome with sphingolipid metabolism and endosomal trafficking. Nature Structural and Molecular Biology, 2010, 17, 901-908.	3.6	93
454	Proteome-Wide Analysis of Disease-Associated SNPs That Show Allele-Specific Transcription Factor Binding. PLoS Genetics, 2012, 8, e1002982.	1.5	92
455	Highâ€resolution serum proteome trajectories in COVIDâ€19 reveal patientâ€specific seroconversion. EMBO Molecular Medicine, 2021, 13, e14167.	3.3	92
456	Quantitative Proteomics Reveals That Hsp90 Inhibition Preferentially Targets Kinases and the DNA Damage Response. Molecular and Cellular Proteomics, 2012, 11, M111.014654.	2.5	91
457	MaxQuant.Live Enables Global Targeting of More Than 25,000 Peptides. Molecular and Cellular Proteomics, 2019, 18, 982a-994.	2.5	91
458	Noninvasive proteomic biomarkers for alcohol-related liver disease. Nature Medicine, 2022, 28, 1277-1287.	15.2	91
459	Tyrosine Phosphoproteomics of Fibroblast Growth Factor Signaling. Journal of Biological Chemistry, 2004, 279, 46438-46447.	1.6	90
460	InÂVivo SILAC-Based Proteomics Reveals Phosphoproteome Changes during Mouse Skin Carcinogenesis. Cell Reports, 2013, 3, 552-566.	2.9	90
461	Quantitative shotgun proteomics: considerations for a high-quality workflow in immunology. Nature Immunology, 2014, 15, 112-117.	7.0	90
462	CRL2^{Lrr1} promotes unloading of the vertebrate replisome from chromatin during replication termination. Genes and Development, 2017, 31, 275-290.	2.7	90
463	Splicing factor YBX1 mediates persistence of JAK2-mutated neoplasms. Nature, 2020, 588, 157-163.	13.7	90
464	mRNA export through an additional cap-binding complex consisting of NCBP1 and NCBP3. Nature Communications, 2015, 6, 8192.	5.8	89
465	Identification of hnRNP P2 as TLS/FUS using electrospray mass spectrometry. Rna, 1995, 1, 724-33.	1.6	89
466	HysTagâ€"A Novel Proteomic Quantification Tool Applied to Differential Display Analysis of Membrane Proteins From Distinct Areas of Mouse Brain. Molecular and Cellular Proteomics, 2004, 3, 82-92.	2.5	88
467	A new class of carriers that transport selective cargo from the trans Golgi network to the cell surface. EMBO Journal, 2012, 31, 3976-3990.	3.5	88
468	EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification. Nature Methods, 2018, 15, 527-530.	9.0	88

#	Article	IF	Citations
469	The Case for Proteomics and Phosphoâ€Proteomics in Personalized Cancer Medicine. Proteomics - Clinical Applications, 2019, 13, e1800113.	0.8	88
470	Urinary proteome profiling for stratifying patients with familial Parkinsonâ€™s disease. EMBO Molecular Medicine, 2021, 13, e13257.	3.3	88
471	Proteomics and C9orf72 neuropathology identify ribosomes as poly-GR/PR interactors driving toxicity. Life Science Alliance, 2018, 1, e201800070.	1.3	88
472	The yeast protein Arc1p binds to tRNA and functions as a cofactor for the methionyl- and glutamyl-tRNA synthetases. EMBO Journal, 1996, 15, 5437-48.	3.5	88
473	Euplotes telomerase contains an La motif protein produced by apparent translational frameshifting. EMBO Journal, 2000, 19, 6230-6239.	3.5	85
474	Functional characterization of Rad18 domains for Rad6, ubiquitin, DNA binding and PCNA modification. Nucleic Acids Research, 2007, 35, 5819-5830.	6.5	85
475	Unbiased spatial proteomics with single-cell resolution in tissues. Molecular Cell, 2022, 82, 2335-2349.	4.5	85
476	Characterization of the DOC1/APC10 Subunit of the Yeast and the Human Anaphase-promoting Complex. Journal of Biological Chemistry, 1999, 274, 14500-14507.	1.6	84
477	Quantitative proteomics?. Nature Biotechnology, 1999, 17, 954-955.	9.4	84
478	A New Variant of the Î³ Subunit of Renal Na,K-ATPase. Journal of Biological Chemistry, 2000, 275, 18441-18446.	1.6	84
479	Ser/Thr/Tyr Protein Phosphorylation in the Archaeon Halobacterium salinarumâ€"A Representative of the Third Domain of Life. PLoS ONE, 2009, 4, e4777.	1.1	84
480	Trapped Ion Mobility Spectrometry and Parallel Accumulationâ€"Serial Fragmentation in Proteomics. Molecular and Cellular Proteomics, 2021, 20, 100138.	2.5	84
481	Analysis of the Mouse Liver Proteome Using Advanced Mass Spectrometry. Journal of Proteome Research, 2007, 6, 2963-2972.	1.8	83
482	Top-down quantitation and characterization of SILAC-labeled proteins. Journal of the American Society for Mass Spectrometry, 2007, 18, 2058-2064.	1.2	83
483	Evolutionary Constraints of Phosphorylation in Eukaryotes, Prokaryotes, and Mitochondria. Molecular and Cellular Proteomics, 2010, 9, 2642-2653.	2.5	83
484	Guidelines for reporting the use of mass spectrometry in proteomics. Nature Biotechnology, 2008, 26, 860-861.	9.4	82
485	Mlp2p, A Component of Nuclear Pore Attached Intranuclear Filaments, Associates with Nic96p. Journal of Biological Chemistry, 2000, 275, 343-350.	1.6	81
486	"De Novo" Sequencing of Peptides Recovered from In-Gel Digested Proteins by Nanoelectrospray Tandem Mass Spectrometry. Molecular Biotechnology, 2002, 20, 107-118.	1.3	81

#	Article	IF	Citations
487	Deep learning the collisional cross sections of the peptide universe from a million experimental values. Nature Communications, 2021, 12, 1185.	5.8	81
488	The chromodomain helicase Chd4 is required for Polycomb-mediated inhibition of astroglial differentiation. EMBO Journal, 2013, 32, 1598-1612.	3.5	80
489	Plasma Proteome Profiling Reveals Dynamics of Inflammatory and Lipid Homeostasis Markers after Roux-En-Y Gastric Bypass Surgery. Cell Systems, 2018, 7, 601-612.e3.	2.9	80
490	In-depth proteomic analysis of a mollusc shell: acid-soluble and acid-insoluble matrix of the limpet Lottia gigantea. Proteome Science, 2012, 10, 28.	0.7	79
491	Deep muscle-proteomic analysis of freeze-dried human muscle biopsies reveals fiber type-specific adaptations to exercise training. Nature Communications, 2021, 12, 304.	5.8	79
492	MaxQuant for In-Depth Analysis of Large SILAC Datasets. Methods in Molecular Biology, 2014, 1188, 351-364.	0.4	79
493	Aspects of the Sequencing of Carbohydrates and Oligonucleotides by Matrix-assisted Laser Desorption/Ionization Post-source Decay. Rapid Communications in Mass Spectrometry, 1996, 10, 100-103.	0.7	78
494	Quantitative proteomics to study mitogen-activated protein kinases. Methods, 2006, 40, 243-250.	1.9	78
495	Molecular basis of PRC1 targeting to Polycomb response elements by PhoRC. Genes and Development, 2016, 30, 1116-1127.	2.7	78
496	Proteins complexed to the P1 adhesin of Mycoplasma pneumoniae. Microbiology (United Kingdom), 2000, 146, 741-747.	0.7	78
497	Detergent-Based but Gel-Free Method Allows Identification of Several Hundred Membrane Proteins in Single LC-MS Runs. Journal of Proteome Research, 2008, 7, 5028-5032.	1.8	77
498	In Vivo Quantitative Proteomics: The SILAC Mouse. Methods in Molecular Biology, 2011, 757, 435-450.	0.4	77
499	N-linked Glycosylation Enrichment for In-depth Cell Surface Proteomics of Diffuse Large B-cell Lymphoma Subtypes. Molecular and Cellular Proteomics, 2014, 13, 240-251.	2.5	77
500	Deep Proteomics of Breast Cancer Cells Reveals that Metformin Rewires Signaling Networks Away from a Pro-growth State. Cell Systems, 2016, 2, 159-171.	2.9	76
501	Multi-omics profiling of living human pancreatic islet donors reveals heterogeneous beta cell trajectories towards type 2 diabetes. Nature Metabolism, 2021, 3, 1017-1031.	5.1	76
502	The AU-rich element mRNA decay-promoting activity of BRF1 is regulated by mitogen-activated protein kinase-activated protein kinase 2. Rna, 2008, 14, 950-959.	1.6	75
503	Comparative Proteomics of Two Life Cycle Stages of Stable Isotope-labeled Trypanosoma brucei Reveals Novel Components of the Parasite's Host Adaptation Machinery. Molecular and Cellular Proteomics, 2013, 12, 172-179.	2.5	75
504	Specificity and Commonality of the Phosphoinositide-Binding Proteome Analyzed by Quantitative Mass Spectrometry. Cell Reports, 2014, 6, 578-591.	2.9	75

#	Article	IF	Citations
505	A systematic RNAi synthetic interaction screen reveals a link between p53 and snoRNP assembly. Nature Cell Biology, 2011, 13, 809-818.	4.6	74
506	HOT1 is a mammalian direct telomere repeat-binding protein contributing to telomerase recruitment. EMBO Journal, 2013, 32, 1681-1701.	3.5	74
507	Absolute Proteome Analysis of Colorectal Mucosa, Adenoma, and Cancer Reveals Drastic Changes in Fatty Acid Metabolism and Plasma Membrane Transporters. Journal of Proteome Research, 2015, 14, 4005-4018.	1.8	74
508	Glucose-regulated and drug-perturbed phosphoproteome reveals molecular mechanisms controlling insulin secretion. Nature Communications, 2016, 7, 13250.	5.8	74
509	Phosphoproteomic approach for agonist-specific signaling in mouse brains: mTOR pathway is involved in Îº opioid aversion. Neuropsychopharmacology, 2019, 44, 939-949.	2.8	74
510	Defective glycosylation and multisystem abnormalities characterize the primary immunodeficiency XMEN disease. Journal of Clinical Investigation, 2019, 130, 507-522.	3.9	74
511	Signaling Initiated by Overexpression of the Fibroblast Growth Factor Receptor-1 Investigated by Mass Spectrometry. Molecular and Cellular Proteomics, 2003, 2, 29-36.	2.5	73
512	Machine Learning-based Classification of Diffuse Large B-cell Lymphoma Patients by Their Protein Expression Profiles. Molecular and Cellular Proteomics, 2015, 14, 2947-2960.	2.5	73
513	A mass spectrometryâ€"friendly database for cSNP identification. Nature Methods, 2007, 4, 465-466.	9.0	72
514	Spatially and cell-type resolved quantitative proteomic atlas of healthy human skin. Nature Communications, 2020, 11, 5587.	5.8	72
515	SHP2-interacting Transmembrane Adaptor Protein (SIT), A Novel Disulfide-linked Dimer Regulating Human T Cell Activation. Journal of Experimental Medicine, 1999, 189, 1181-1194.	4.2	71
516	A Stat6/Pten Axis Links Regulatory T Cells with Adipose Tissue Function. Cell Metabolism, 2017, 26, 475-492.e7.	7.2	71
517	Lysine acetylation in mitochondria: From inventory to function. Mitochondrion, 2017, 33, 58-71.	1.6	71
518	Data-independent acquisition method for ubiquitinome analysis reveals regulation of circadian biology. Nature Communications, 2021, 12, 254.	5.8	71
519	A shortcut to interesting human genes: peptide sequence tags, expressed-sequence tags and computers. Trends in Biochemical Sciences, 1996, 21, 494-495.	3.7	69
520	MAPU: Max-Planck Unified database of organellar, cellular, tissue and body fluid proteomes. Nucleic Acids Research, 2007, 35, D771-D779.	6.5	69
521	In-depth, high-accuracy proteomics of sea urchin tooth organic matrix. Proteome Science, 2008, 6, 33.	0.7	69
522	Quantitative interaction screen of telomeric repeat-containing RNA reveals novel TERRA regulators. Genome Research, 2013, 23, 2149-2157.	2.4	69

#	Article	IF	Citations
523	Molecular and structural architecture of polyQ aggregates in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3446-E3453.	3.3	68
524	The Proteome of Prostate Cancer Bone Metastasis Reveals Heterogeneity with Prognostic Implications. Clinical Cancer Research, 2018, 24, 5433-5444.	3.2	68
525	Proteomics for blood biomarker exploration of severe mental illness: pitfalls of the past and potential for the future. Translational Psychiatry, 2018, 8, 160.	2.4	68
526	A Cell-Autonomous Signature of Dysregulated Protein Phosphorylation Underlies Muscle Insulin Resistance in Type 2 Diabetes. Cell Metabolism, 2020, 32, 844-859.e5.	7.2	68
527	Profiling the Trypanosoma cruzi Phosphoproteome. PLoS ONE, 2011, 6, e25381.	1.1	68
528	Caenorhabditis elegans Has a Phosphoproteome Atypical for Metazoans That Is Enriched in Developmental and Sex Determination Proteins. Journal of Proteome Research, 2009, 8, 4039-4049.	1.8	66
529	Secretome Analysis of Lipid-Induced Insulin Resistance in Skeletal Muscle Cells by a Combined Experimental and Bioinformatics Workflow. Journal of Proteome Research, 2015, 14, 4885-4895.	1.8	66
530	Cell biology and the genome projects a concerted strategy for characterizing multiprotein complexes by using mass spectrometry. Trends in Cell Biology, 1997, 7, 139-142.	3.6	65
531	Computational principles of determining and improving mass precision and accuracy for proteome measurements in an Orbitrap. Journal of the American Society for Mass Spectrometry, 2009, 20, 1477-1485.	1.2	65
532	Proteomic and Genetic Analyses Demonstrate that Plasmodium berghei Blood Stages Export a Large and Diverse Repertoire of Proteins. Molecular and Cellular Proteomics, 2013, 12, 426-448.	2.5	65
533	A Primer on Concepts and Applications of Proteomics in Neuroscience. Neuron, 2017, 96, 558-571.	3.8	65
534	Phosphoproteomics Reveals the GSK3-PDX1 Axis as a Key Pathogenic Signaling Node in Diabetic Islets. Cell Metabolism, 2019, 29, 1422-1432.e3.	7.2	65
535	Protein profile of fiber types in human skeletal muscle: a single-fiber proteomics study. Skeletal Muscle, 2021, 11, 24.	1.9	65
536	Automation of microâ€preparation and enzymatic cleavage of gel electrophoretically separated proteins. FEBS Letters, 1995, 376, 91-94.	1.3	64
537	The HLAâ€"B*2705 peptidome. Arthritis and Rheumatism, 2010, 62, 420-429.	6.7	64
538	C2 Domain-Containing Phosphoprotein CDP138 Regulates GLUT4 Insertion into the Plasma Membrane. Cell Metabolism, 2011, 14, 378-389.	7.2	64
539	Aim24 and MICOS modulate respiratory function, tafazzin-related cardiolipin modification and mitochondrial architecture. ELife, 2014, 3, e01684.	2.8	64
540	The Low Molecular Weight Proteome ofHalobacterium salinarum. Journal of Proteome Research, 2007, 6, 1510-1518.	1.8	63

#	Article	IF	Citations
541	Triple SILAC to Determine Stimulus Specific Interactions in the Wnt Pathway. Journal of Proteome Research, 2012, 11, 982-994.	1.8	63
542	Peptide Sequencing of 2-DE Gel-Isolated Proteins by Nanoelectrospray Tandem Mass Spectrometry. , 1999, 112, 571-588.		62
543	Model for stathmin/OP18 binding to tubulin. EMBO Journal, 2000, 19, 213-222.	3.5	62
544	IKAP: A heuristic framework for inference of kinase activities from Phosphoproteomics data. Bioinformatics, 2016, 32, 424-431.	1.8	62
545	The hemicellulose-degrading enzyme system of the thermophilic bacterium Clostridium stercorarium: comparative characterisation and addition of new hemicellulolytic glycoside hydrolases. Biotechnology for Biofuels, 2018, 11, 229.	6.2	62
546	Inhibition of Adipocyte Differentiation by Resistin-like Molecule Î±. Journal of Biological Chemistry, 2002, 277, 42011-42016.	1.6	61
547	Predicting post-translational lysine acetylation using support vector machines. Bioinformatics, 2010, 26, 1666-1668.	1.8	61
548	Nano electrospray combined with a quadrupole ion trap for the analysis of peptides and protein digests. Journal of the American Society for Mass Spectrometry, 1996, 7, 150-156.	1.2	60
549	SprayQc: A Real-Time LCâ€"MS/MS Quality Monitoring System To Maximize Uptime Using Off the Shelf Components. Journal of Proteome Research, 2012, 11, 3458-3466.	1.8	60
550	Alleles of a Polymorphic ETV6 Binding Site in DCDC2 Confer Risk of Reading and Language Impairment. American Journal of Human Genetics, 2013, 93, 19-28.	2.6	60
551	MiT/ <scp>TFE</scp> factors control <scp>ER</scp> â€phagy via transcriptional regulation of <scp>FAM</scp> 134B. EMBO Journal, 2020, 39, e105696.	3.5	60
552	Similarity between condensed phase and gas phase chemistry: Fragmentation of peptides containing oxidized cysteine residues and its implications for proteomics. Journal of the American Society for Mass Spectrometry, 2001, 12, 228-232.	1.2	59
553	Deep Coverage Mouse Red Blood Cell Proteome. Molecular and Cellular Proteomics, 2008, 7, 1317-1330.	2.5	59
554	Quantitative Proteomics for Epigenetics. ChemBioChem, 2011, 12, 224-234.	1.3	59
555	Expert System for Computer-assisted Annotation of MS/MS Spectra. Molecular and Cellular Proteomics, 2012, 11, 1500-1509.	2.5	59
556	Stabilization of integrin-linked kinase by the Hsp90-CHIP axis impacts cellular force generation, migration and the fibrotic response. EMBO Journal, 2013, 32, 1409-1424.	3.5	59
557	Proteomics to study DNA-bound and chromatin-associated gene regulatory complexes. Human Molecular Genetics, 2016, 25, R106-R114.	1.4	59
558	Parallel accumulation for 100% duty cycle trapped ion mobility-mass spectrometry. International Journal of Mass Spectrometry, 2017, 413, 168-175.	0.7	59

#	Article	IF	Citations
559	Sequence patterns produced by incomplete enzymatic digestion or one-step Edman degradation of peptide mixtures as probes for protein database searches. Electrophoresis, 1996, 17, 938-944.	1.3	58
560	Comparative analysis to guide quality improvements in proteomics. Nature Methods, 2009, 6, 717-719.	9.0	58
561	Red blood cell (RBC) membrane proteomics â€" Part I: Proteomics and RBC physiology. Journal of Proteomics, 2010, 73, 403-420.	1.2	58
562	Comparative Proteomic Profiling of Membrane Proteins in Rat Cerebellum, Spinal Cord, and Sciatic Nerve. Journal of Proteome Research, 2009, 8, 2418-2425.	1.8	57
563	<scp>PP</scp> 2A delays <scp>APC</scp> /Câ€dependent degradation of separaseâ€associated but not free securin. EMBO Journal, 2014, 33, 1134-1147.	3.5	57
564	microRNA-mediated regulation of mTOR complex components facilitates discrimination between activation and anergy in CD4 T cells. Journal of Experimental Medicine, 2014, 211, 2281-2295.	4.2	57
565	FoxK1 and FoxK2 in insulin regulation of cellular and mitochondrial metabolism. Nature Communications, 2019, 10, 1582.	5.8	57
566	A Wiring of the Human Nucleolus. Molecular Cell, 2006, 22, 285-295.	4.5	56
567	Proteomic snapshot of the EGFâ€induced ubiquitin network. Molecular Systems Biology, 2011, 7, 462.	3.2	56
568	Quantitative proteomic analysis reveals concurrent RNAâ€"protein interactions and identifies new RNA-binding proteins in Saccharomyces cerevisiae. Genome Research, 2013, 23, 1028-1038.	2.4	56
569	Efficient mitotic checkpoint signaling depends on integrated activities of Bub1 and the <scp>RZZ</scp> complex. EMBO Journal, 2019, 38, .	3.5	56
570	The Nuclear Export Receptor Xpo1p Forms Distinct Complexes with NES Transport Substrates and the Yeast Ran Binding Protein 1 (Yrb1p). Molecular Biology of the Cell, 2001, 12, 539-549.	0.9	55
571	Advancing Cell Biology Through Proteomics in Space and Time (PROSPECTS). Molecular and Cellular Proteomics, 2012, 11, O112.017731.	2.5	55
572	SILAC-Based Proteomics of Human Primary Endothelial Cell Morphogenesis Unveils Tumor Angiogenic Markers. Molecular and Cellular Proteomics, 2013, 12, 3599-3611.	2.5	55
573	Identification of early neurodegenerative pathways in progressive multiple sclerosis. Nature Neuroscience, 2022, 25, 944-955.	7.1	55
574	Association of Yeast RNA Polymerase I with a Nucleolar Substructure Active in Rrna Synthesis and Processing. Journal of Cell Biology, 2000, 149, 575-590.	2.3	54
575	Experiences and perspectives of MALDI MS and MS/MS in proteomic research. International Journal of Mass Spectrometry, 2003, 226, 223-237.	0.7	54
576	Can Proteomics Retire the Western Blot?. Journal of Proteome Research, 2008, 7, 3065-3065.	1.8	54

#	Article	IF	Citations
577	Phosphorylation Variation during the Cell Cycle Scales with Structural Propensities of Proteins. PLoS Computational Biology, 2013, 9, e1002842.	1.5	54
578	Correlation of acidic and basic carrier ampholyte and immobilized pH gradient two-dimensional gel electrophoresis patterns based on mass spectrometric protein identification. Electrophoresis, 1998, 19, 1024-1035.	1.3	53
579	Molecular Patterning of the Oikoplastic Epithelium of the Larvacean Tunicate Oikopleura dioica. Journal of Biological Chemistry, 2001, 276, 20624-20632.	1.6	53
580	Cloning of MASK, a Novel Member of the Mammalian Germinal Center Kinase III Subfamily, with Apoptosis-inducing Properties. Journal of Biological Chemistry, 2002, 277, 5929-5939.	1.6	53
581	A domesticated transposon mediates the effects of a singleâ€nucleotide polymorphism responsible for enhanced muscle growth. EMBO Reports, 2010, 11, 305-311.	2.0	53
582	Dicer-dependent and -independent Argonaute2 Protein Interaction Networks in Mammalian Cells. Molecular and Cellular Proteomics, 2012, 11, 1442-1456.	2.5	53
583	The Impact of High-Fat Diet on Metabolism and Immune Defense in Small Intestine Mucosa. Journal of Proteome Research, 2015, 14, 353-365.	1.8	53
584	Oxyntomodulin Identified as a Marker of Type 2 Diabetes and Gastric Bypass Surgery by Mass-spectrometry Based Profiling of Human Plasma. EBioMedicine, 2016, 7, 112-120.	2.7	53
585	UBL3 modification influences protein sorting to small extracellular vesicles. Nature Communications, 2018, 9, 3936.	5.8	53
586	Cortical circuit alterations precede motor impairments in Huntingtonâ€™s disease mice. Scientific Reports, 2019, 9, 6634.	1.6	53
587	Quantitative and Dynamic Catalogs of Proteins Released during Apoptotic and Necroptotic Cell Death. Cell Reports, 2020, 30, 1260-1270.e5.	2.9	53
588	Integrative analysis of cell state changes in lung fibrosis with peripheral protein biomarkers. EMBO Molecular Medicine, 2021, 13, e12871.	3.3	53
589	Nup116p Associates with the Nup82p-Nsp1p-Nup159p Nucleoporin Complex. Journal of Biological Chemistry, 2000, 275, 23540-23548.	1.6	52
590	Overexpression of Q-rich prion-like proteins suppresses polyQ cytotoxicity and alters the polyQ interactome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18219-18224.	3.3	52
591	Deep Proteomic Evaluation of Primary and Cell Line Motoneuron Disease Models Delineates Major Differences in Neuronal Characteristics. Molecular and Cellular Proteomics, 2014, 13, 3410-3420.	2.5	51
592	A Proteomics Approach to the Protein Normalization Problem: Selection of Unvarying Proteins for MS-Based Proteomics and Western Blotting. Journal of Proteome Research, 2016, 15, 2321-2326.	1.8	51
593	A Framework for Intelligent Data Acquisition and Real-Time Database Searching for Shotgun Proteomics. Molecular and Cellular Proteomics, 2012, 11, M111.013185.	2.5	50
594	Quantitative Proteomics Identifies Serum Response Factor Binding Protein 1 as a Host Factor for Hepatitis C Virus Entry. Cell Reports, 2015, 12, 864-878.	2.9	50

#	Article	IF	Citations
595	Interconversion between Anticipatory and Active GID E3ÂUbiquitin Ligase Conformations via Metabolically Driven Substrate Receptor Assembly. Molecular Cell, 2020, 77, 150-163.e9.	4.5	50
596	The structural context of posttranslational modifications at a proteome-wide scale. PLoS Biology, 2022, 20, e3001636.	2.6	50
597	Anaphase specific auto-cleavage of separase. FEBS Letters, 2002, 528, 246-250.	1.3	49
598	Cloning of a novel phosphotyrosine binding domain containing molecule, Odin, involved in signaling by receptor tyrosine kinases. Oncogene, 2002, 21, 8029-8036.	2.6	48
599	Computational and experimental analysis reveals a novel Src family kinase in the C. elegans genome. Bioinformatics, 2003, 19, 169-172.	1.8	48
600	Induction of membrane circular dorsal ruffles requires co-signalling of integrinâ€"ILK-complex and EGF receptor. Journal of Cell Science, 2012, 125, 435-448.	1.2	48
601	Multivalent binding of PWWP2A to H2A.Z regulates mitosis and neural crest differentiation. EMBO Journal, 2017, 36, 2263-2279.	3.5	48
602	Proteome profiling of cerebrospinal fluid reveals biomarker candidates for Parkinsonâ€™s disease. Cell Reports Medicine, 2022, 3, 100661.	3.3	48
603	Identification of components oftrans-Golgi network-derived transport vesicles and detergent-insoluble complexes by nanoelectrospray tandem mass spectrometry. Electrophoresis, 1997, 18, 2591-2600.	1.3	47
604	Regulation of Liver Metabolism by the Endosomal GTPase Rab5. Cell Reports, 2015, 11, 884-892.	2.9	47
605	Two Chromatin Remodeling Activities Cooperate during Activation of Hormone Responsive Promoters. PLoS Genetics, 2009, 5, e1000567.	1.5	47
606	Large scale discovery of coronavirus-host factor protein interaction motifs reveals SARS-CoV-2 specific mechanisms and vulnerabilities. Nature Communications, 2021, 12, 6761.	5.8	47
607	Phosphotyrosine Mapping in Bcr/Abl Oncoprotein Using Phosphotyrosine-specific Immonium Ion Scanning. Molecular and Cellular Proteomics, 2003, 2, 138-145.	2.5	46
608	PWWP2A binds distinct chromatin moieties and interacts with an MTA1-specific core NuRD complex. Nature Communications, 2018, 9, 4300.	5.8	46
609	Quantitative mass spectrometry and PAR-CLIP to identify RNA-protein interactions. Nucleic Acids Research, 2012, 40, 9897-9902.	6.5	45
610	Minimal amounts of kindlin-3 suffice for basal platelet and leukocyte functions in mice. Blood, 2015, 126, 2592-2600.	0.6	45
611	Histone monoubiquitination by Clockâ€"Bmal1 complex marks Per1 and Per2 genes for circadian feedback. Nature Structural and Molecular Biology, 2015, 22, 759-766.	3.6	45
612	Accurate MS-based Rab10 Phosphorylation Stoichiometry Determination as Readout for LRRK2 Activity in Parkinson's Disease. Molecular and Cellular Proteomics, 2020, 19, 1546-1560.	2.5	45

#	Article	IF	Citations
613	The tumor suppressor kinase DAPK3 drives tumor-intrinsic immunity through the STINGâ€"IFN-Î² pathway. Nature Immunology, 2021, 22, 485-496.	7.0	45
614	Rapid Protein Sequencing by Tandem Mass Spectrometry and cDNA Cloning of p20-CGGBP. Journal of Biological Chemistry, 1997, 272, 16761-16768.	1.6	44
615	Large-scale De Novo Prediction of Physical Protein-Protein Association. Molecular and Cellular Proteomics, 2011, 10, M111.010629.	2.5	44
616	GID E3 ligase supramolecular chelate assembly configures multipronged ubiquitin targeting of an oligomeric metabolic enzyme. Molecular Cell, 2021, 81, 2445-2459.e13.	4.5	44
617	Identification and characterization of PaMTH1, a putative O -methyltransferase accumulating during senescence of Podospora anserina cultures. Current Genetics, 2000, 37, 200-208.	0.8	43
618	Mass spectrometric analysis of a UV-cross-linked protein-DNA complex: Tryptophans 54 and 88 ofE. coliSSB cross-link to DNA. Protein Science, 2001, 10, 1989-2001.	3.1	43
619	SPF30 Is an Essential Human Splicing Factor Required for Assembly of the U4/U5/U6 Tri-small Nuclear Ribonucleoprotein into the Spliceosome. Journal of Biological Chemistry, 2001, 276, 31142-31150.	1.6	43
620	Constitutive and dynamic phosphorylation and acetylation sites on NUCKS, a hypermodified nuclear protein, studied by quantitative proteomics. Proteins: Structure, Function and Bioinformatics, 2008, 73, 710-718.	1.5	43
621	High Performance Computational Analysis of Large-scale Proteome Data Sets to Assess Incremental Contribution to Coverage of the Human Genome. Journal of Proteome Research, 2013, 12, 2858-2868.	1.8	43
622	Characterization of glycosylphosphatidylinositol-linked molecule CD55/decay-accelerating factor as the receptor for antibody SC-1-induced apoptosis. Cancer Research, 1999, 59, 5299-306.	0.4	43
623	The proteogenomic subtypes of acute myeloid leukemia. Cancer Cell, 2022, 40, 301-317.e12.	7.7	43
624	Detailed Analysis of the Phosphorylation of the Human La (SS-B) Autoantigen. (De)phosphorylation Does Not Affect Its Subcellular Distributionâ€. Biochemistry, 2000, 39, 3023-3033.	1.2	42
625	Reply to â€œSpin filterâ€"based sample preparation for shotgun proteomicsâ€• Nature Methods, 2009, 6, 785-786.	9.0	42
626	Quantitative Proteome and Transcriptome Analysis of the Archaeon Thermoplasma acidophilum Cultured under Aerobic and Anaerobic Conditions. Journal of Proteome Research, 2010, 9, 4839-4850.	1.8	42
627	Polycomb group ring finger 1 cooperates with Runx1 in regulating differentiation and self-renewal of hematopoietic cells. Blood, 2012, 119, 4152-4161.	0.6	42
628	Fractionation profiling: a fast and versatile approach for mapping vesicle proteomes and proteinâ€"protein interactions. Molecular Biology of the Cell, 2014, 25, 3178-3194.	0.9	42
629	A proteomic atlas of insulin signalling reveals tissueâ€specific mechanisms of longevity assurance. Molecular Systems Biology, 2017, 13, 939.	3.2	42
630	Automated protein preparation techniques using a digest robot. The Protein Journal, 1997, 16, 343-348.	1.1	41

#	Article	IF	Citations
631	Posttranslational modification of GÂo1 generates GÂo3, an abundant G protein in brain. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 1327-1332.	3.3	41
632	Analysis of Bromotryptophan and Hydroxyproline Modifications by High-Resolution, High-Accuracy Precursor Ion Scanning Utilizing Fragment Ions with Mass-Deficient Mass Tags. Analytical Chemistry, 2002, 74, 6230-6236.	3.2	41
633	Quantitative proteomic profiling of membrane proteins from the mouse brain cortex, hippocampus, and cerebellum using the HysTag reagent: Mapping of neurotransmitter receptors and ion channels. Brain Research, 2007, 1134, 95-106.	1.1	41
634	Differential substrate specificity of group I and group II chaperonins in the archaeon Methanosarcina mazei. Molecular Microbiology, 2009, 74, 1152-1168.	1.2	41
635	The human proteome â€“ a scientific opportunity for transforming diagnostics, therapeutics, and healthcare. Clinical Proteomics, 2012, 9, 6.	1.1	41
636	The proteome of the calcified layer organic matrix of turkey (Meleagris gallopavo) eggshell. Proteome Science, 2013, 11, 40.	0.7	41
637	Distinct signaling by insulin and IGF-1 receptors and their extra- and intracellular domains. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	41
638	Fibro-adipogenic progenitors of dystrophic mice are insensitive to NOTCH regulation of adipogenesis. Life Science Alliance, 2019, 2, e201900437.	1.3	41
639	Hippocampal disruptions of synaptic and astrocyte metabolism are primary events of early amyloid pathology in the 5xFAD mouse model of Alzheimerâ€™s disease. Cell Death and Disease, 2021, 12, 954.	2.7	41
640	Compartment-resolved Proteomic Analysis of Mouse Aorta during Atherosclerotic Plaque Formation Reveals Osteoclast-specific Protein Expression. Molecular and Cellular Proteomics, 2018, 17, 321-334.	2.5	40
641	The Transcription Factor ETV1 Induces Atrial Remodeling and Arrhythmia. Circulation Research, 2018, 123, 550-563.	2.0	40
642	Trends in trapped ion mobility â€“ Mass spectrometry instrumentation. TrAC - Trends in Analytical Chemistry, 2019, 116, 324-331.	5.8	40
643	Common pitfalls in bioinformatics-based analyses: look before you leap. Trends in Genetics, 2001, 17, 541-545.	2.9	39
644	Time-resolved dissection of early phosphoproteome and ensuing proteome changes in response to TGF-Î². Science Signaling, 2014, 7, rs5.	1.6	39
645	A Double-Barrel Liquid Chromatography-Tandem Mass Spectrometry (LC-MS/MS) System to Quantify 96 Interactomes per Day*. Molecular and Cellular Proteomics, 2015, 14, 2030-2041.	2.5	39
646	Why is it so difficult to measure glucagon-like peptide-1 in a mouse?. Diabetologia, 2017, 60, 2066-2075.	2.9	39
647	Identification of Phosphorylation Sites in Native Lamina-Associated Polypeptide 2Î²â€. Biochemistry, 1999, 38, 9426-9434.	1.2	38
648	Ephrin B1 Is Expressed on Neuroepithelial Cells in Correlation with Neocortical Neurogenesis. Journal of Neuroscience, 2001, 21, 2726-2737.	1.7	38

#	Article	IF	Citations
649	Analysis of Tyrosine Phosphorylation Sites in Signaling Molecules by a Phosphotyrosine-Specific Immonium Ion Scanning Method. Science Signaling, 2002, 2002, pl16-pl16.	1.6	38
650	The Atherosclerosis Risk Variant rs2107595 Mediates Allele-Specific Transcriptional Regulation of HDAC9 via E2F3 and Rb1. Stroke, 2019, 50, 2651-2660.	1.0	38
651	<scp>STAT</scp> 3 â€dependent analysis reveals <scp>PDK</scp> 4 as independent predictor of recurrence in prostate cancer. Molecular Systems Biology, 2020, 16, e9247.	3.2	38
652	Homology-directed repair protects the replicating genome from metabolic assaults. Developmental Cell, 2021, 56, 461-477.e7.	3.1	38
653	Design and performance of an electrospray ionization source for a doubly-focusing magnetic sector mass spectrometer. Rapid Communications in Mass Spectrometry, 1990, 4, 369-372.	0.7	37
654	Cloning of a novel signaling molecule, AMSH-2, that potentiates transforming growth factor beta signaling. BMC Cell Biology, 2004, 5, 2.	3.0	37
655	FAM111 protease activity undermines cellular fitness and is amplified by gainâ€ofâ€function mutations in human disease. EMBO Reports, 2020, 21, e50662.	2.0	37
656	The Purification and Characterization of the Catalytic Domain of Src Expressed in Schizosaccharomyces Pombe. Comparison of Unphosphorylated and Tyrosine Phosphorylated Species. FEBS Journal, 1996, 240, 756-764.	0.2	36
657	A Novel Src Homology 2 Domain-containing Molecule, Src-like Adapter Protein-2 (SLAP-2), Which Negatively Regulates T Cell Receptor Signaling. Journal of Biological Chemistry, 2002, 277, 19131-19138.	1.6	36
658	Phosphorylation of SUMO-1 Occurs in Vivo and Is Conserved through Evolution. Journal of Proteome Research, 2008, 7, 4050-4057.	1.8	36
659	Proteomic analysis of quail calcified eggshell matrix: a comparison to chicken and turkey eggshell proteomes. Proteome Science, 2015, 13, 22.	0.7	36
660	A beginnerâ€™s guide to mass spectrometryâ€“based proteomics. Biochemist, 2020, 42, 64-69.	0.2	35
661	Peptide End Sequencing by Orthogonal MALDI Tandem Mass Spectrometry. Journal of Proteome Research, 2002, 1, 63-71.	1.8	34
662	Mediator Phosphorylation Prevents Stress Response Transcription During Non-stress Conditions. Journal of Biological Chemistry, 2012, 287, 44017-44026.	1.6	33
663	The ETS family member GABPÎ± modulates androgen receptor signalling and mediates an aggressive phenotype in prostate cancer. Nucleic Acids Research, 2014, 42, 6256-6269.	6.5	33
664	In-depth proteomic analyses of Haliotis laevigata (greenlip abalone) nacre and prismatic organic shell matrix. Proteome Science, 2018, 16, 11.	0.7	33
665	Ethical Principles, Constraints, and Opportunities in Clinical Proteomics. Molecular and Cellular Proteomics, 2021, 20, 100046.	2.5	33
666	Integrative Analysis Identifies Key Molecular Signatures Underlying Neurodevelopmental Deficits in Fragile X Syndrome. Biological Psychiatry, 2020, 88, 500-511.	0.7	33

#	Article	IF	Citations
667	Red Blood Cell (RBC) membrane proteomics â€" Part II: Comparative proteomics and RBC patho-physiology. Journal of Proteomics, 2010, 73, 421-435.	1.2	32
668	SCAI promotes DNA double-strand break repair in distinct chromosomal contexts. Nature Cell Biology, 2016, 18, 1357-1366.	4.6	32
669	Tumor Necrosis Factor-induced Microtubule Stabilization Mediated by Hyperphosphorylated Oncoprotein 18 Promotes Cell Death. Journal of Biological Chemistry, 2000, 275, 33876-33882.	1.6	31
670	Phosphoproteomes of Strongylocentrotus purpuratus shell and tooth matrix: identification of a major acidic sea urchin tooth phosphoprotein, phosphodontin. Proteome Science, 2010, 8, 6.	0.7	31
671	Î²1 integrin cytoplasmic tyrosines promote skin tumorigenesis independent of their phosphorylation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15213-15218.	3.3	31
672	The unfolded protein response affects readthrough of premature termination codons. EMBO Molecular Medicine, 2014, 6, 685-701.	3.3	31
673	TheCaenorhabditiseleganspericentriolar material components SPD-2 and SPD-5 are monomeric in the cytoplasm before incorporation into the PCM matrix. Molecular Biology of the Cell, 2014, 25, 2984-2992.	0.9	31
674	Mitochondrial specialization revealed by single muscle fiber proteomics: focus on the Krebs cycle. Scandinavian Journal of Medicine and Science in Sports, 2015, 25, 41-48.	1.3	31
675	Phosphoproteome profiling uncovers a key role for CDKs in TNF signaling. Nature Communications, 2021, 12, 6053.	5.8	31
676	Glutathione peroxidase 3 localizes to the epithelial lining fluid and the extracellular matrix in interstitial lung disease. Scientific Reports, 2016, 6, 29952.	1.6	30
677	The Hippo pathway controls myofibril assembly and muscle fiber growth by regulating sarcomeric gene expression. ELife, 2021, 10, .	2.8	29
678	Sequential Defects in Cardiac Lineage Commitment and Maturation Cause Hypoplastic Left Heart Syndrome. Circulation, 2021, 144, 1409-1428.	1.6	29
679	Cotranslational N-degron masking by acetylation promotes proteome stability in plants. Nature Communications, 2022, 13, 810.	5.8	29
680	Labile sulfogroup allows differentiation of sulfotyrosine and phosphotyrosine in peptides. Journal of Mass Spectrometry, 2001, 36, 832-833.	0.7	28
681	How much peptide sequence information is contained in ion trap tandem mass spectra?. Journal of the American Society for Mass Spectrometry, 2008, 19, 1813-1820.	1.2	28
682	Identification of new chicken egg proteins by mass spectrometry-based proteomic analysis. World's Poultry Science Journal, 2008, 64, 209-218.	1.4	28
683	PLEKHA7 Recruits PDZD11 to Adherens Junctions to Stabilize Nectins. Journal of Biological Chemistry, 2016, 291, 11016-11029.	1.6	28
684	Fifteen Years of Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC). Methods in Molecular Biology, 2014, 1188, 1-7.	0.4	28

#	Article	IF	Citations
685	Gelâ€like inclusions of Câ€terminal fragments of TDPâ€43 sequester stalled proteasomes in neurons. EMBO Reports, 2022, 23, e53890.	2.0	28
686	A Novel Proliferation-Associated Variant of CFR-1 Defined by a Human Monoclonal Antibody. Laboratory Investigation, 2001, 81, 1097-1108.	1.7	27
687	A Novel Chromatographic Method Allows On-line Reanalysis of the Proteome. Molecular and Cellular Proteomics, 2008, 7, 1452-1459.	2.5	27
688	A SILAC-based Approach Identifies Substrates of Caspase-dependent Cleavage upon TRAIL-induced Apoptosis. Molecular and Cellular Proteomics, 2013, 12, 1436-1450.	2.5	27
689	Immunoproteomics Using Polyclonal Antibodies and Stable Isotopeâ€"labeled Affinity-purified Recombinant Proteins. Molecular and Cellular Proteomics, 2014, 13, 1611-1624.	2.5	27
690	Hepatic Rab24 controls blood glucose homeostasis via improving mitochondrial plasticity. Nature Metabolism, 2019, 1, 1009-1026.	5.1	27
691	Functional identity of hypothalamic melanocortin neurons depends on Tbx3. Nature Metabolism, 2019, 1, 222-235.	5.1	27
692	Signaling defects associated with insulin resistance in nondiabetic and diabetic individuals and modification by sex. Journal of Clinical Investigation, 2021, 131, .	3.9	27
693	Isoprenylation of the G Protein Î³ Subunit Is both Necessary and Sufficient for Î²Î³ Dimer-Mediated Stimulation of Phospholipase Câ€. Biochemistry, 1996, 35, 15174-15182.	1.2	26
694	A DNA-Centric Protein Interaction Map of Ultraconserved Elements Reveals Contribution of Transcription Factor Binding Hubs to Conservation. Cell Reports, 2013, 5, 531-545.	2.9	26
695	TLR3-Mediated CD8+ Dendritic Cell Activation Is Coupled with Establishment of a Cell-Intrinsic Antiviral State. Journal of Immunology, 2015, 195, 1025-1033.	0.4	26
696	Phylointeractomics reconstructs functional evolution of protein binding. Nature Communications, 2017, 8, 14334.	5.8	26
697	Mesothelial Cell HIF1Î± Expression Is Metabolically Downregulated by Metformin to Prevent Oncogenic Tumor-Stromal Crosstalk. Cell Reports, 2019, 29, 4086-4098.e6.	2.9	26
698	A Multi-Omics Approach to Liver Diseases: Integration of Single Nuclei Transcriptomics with Proteomics and HiCap Bulk Data in Human Liver. OMICS A Journal of Integrative Biology, 2020, 24, 180-194.	1.0	26
699	Linkage-specific ubiquitin chain formation depends on a lysine hydrocarbon ruler. Nature Chemical Biology, 2021, 17, 272-279.	3.9	26
700	Mild Protease Treatment as a Small-Scale Biochemical Method for Mitochondria Purification and Proteomic Mapping of Cytoplasm-Exposed Mitochondrial Proteins. Journal of Proteome Research, 2006, 5, 3277-3287.	1.8	25
701	Multi-spectra peptide sequencing and its applications to multistage mass spectrometry. Bioinformatics, 2008, 24, i416-i423.	1.8	25
702	Origins of mass spectrometry-based proteomics. Nature Reviews Molecular Cell Biology, 2016, 17, 678-678.	16.1	25

#	Article	IF	Citations
703	Rapid proteomic analysis for solid tumors reveals <scp>LSD</scp>1 as a drug target in an endâ€stage cancer patient. Molecular Oncology, 2018, 12, 1296-1307.	2.1	25
704	The ever expanding scope of electrospray mass spectrometryâ€"a 30 year journey. Nature Communications, 2019, 10, 3744.	5.8	25
705	Identifying and Quantifying Sites of Protein Methylation by Heavy Methyl SILAC. Current Protocols in Protein Science, 2006, 46, Unit 14.9.	2.8	24
706	Mapping of Lysine Monomethylation of Linker Histones in Human Breast and Its Cancer. Journal of Proteome Research, 2009, 8, 4207-4215.	1.8	24
707	Interaction of 7SK with the Smn complex modulates snRNP production. Nature Communications, 2021, 12, 1278.	5.8	23
708	AlphaTims: Indexing Trapped Ion Mobility Spectrometryâ€"TOF Data for Fast and Easy Accession and Visualization. Molecular and Cellular Proteomics, 2021, 20, 100149.	2.5	23
709	Defining the RBPome of primary T helper cells to elucidate higher-order Roquin-mediated mRNA regulation. Nature Communications, 2021, 12, 5208.	5.8	23
710	The focal adhesion protein PINCH-1 associates with EPLIN at integrin adhesion sites. Journal of Cell Science, 2015, 128, 1023-33.	1.2	22
711	HCD Fragmentation of Glycated Peptides. Journal of Proteome Research, 2016, 15, 2881-2890.	1.8	22
712	Dynamic human liver proteome atlas reveals functional insights into disease pathways. Molecular Systems Biology, 2022, 18, e10947.	3.2	22
713	Signatures of muscle disuse in spaceflight and bed rest revealed by single muscle fiber proteomics. , 2022, 1, .		22
714	Sequence Database Searching by Mass Spectrometric Data. , 0, , 223-245.		21
715	New carbamate supports for the preparation of 3â€²-amino-modified oligonucleotides. Bioorganic and Medicinal Chemistry, 1996, 4, 1649-1658.	1.4	21
716	Parent Ion Scans of Large Molecules. Journal of Mass Spectrometry, 1997, 32, 94-98.	0.7	21
717	Integrative proteomics reveals principles of dynamic phosphosignaling networks in human erythropoiesis. Molecular Systems Biology, 2020, 16, e9813.	3.2	21
718	Preparation of oligonucleotide-dexamethasone conjugates. Bioorganic and Medicinal Chemistry Letters, 1995, 5, 1577-1580.	1.0	20
719	The Rise of Mass Spectrometry and the Fall of Edman Degradation. Clinical Chemistry, 2016, 62, 293-294.	1.5	20
720	Dimethyl-Labeling-Based Quantification of the Lysine Acetylome and Proteome of Plants. Methods in Molecular Biology, 2017, 1653, 65-81.	0.4	20

#	Article	IF	Citations
721	Plasma Proteomes Can Be Reidentifiable and Potentially Contain Personally Sensitive and Incidental Findings. Molecular and Cellular Proteomics, 2021, 20, 100035.	2.5	20
722	The non-classical nuclear import carrier Transportin 1 modulates circadian rhythms through its effect on PER1 nuclear localization. PLoS Genetics, 2018, 14, e1007189.	1.5	20
723	Hepatocyte-specific perturbation of NAD+ biosynthetic pathways in mice induces reversible nonalcoholic steatohepatitisâ€"like phenotypes. Journal of Biological Chemistry, 2021, 297, 101388.	1.6	20
724	Red blood cell proteomics. Transfusion Clinique Et Biologique, 2010, 17, 151-164.	0.2	19
725	PhosphoSiteAnalyzer: A Bioinformatic Platform for Deciphering Phospho Proteomes Using Kinase Predictions Retrieved from NetworKIN. Journal of Proteome Research, 2012, 11, 3480-3486.	1.8	19
726	On the extent and role of the small proteome in the parasitic eukaryote Trypanosoma brucei. BMC Biology, 2014, 12, 14.	1.7	19
727	H3.Y discriminates between HIRA and DAXX chaperone complexes and reveals unexpected insights into human DAXX-H3.3-H4 binding and deposition requirements. Nucleic Acids Research, 2017, 45, 5691-5706.	6.5	19
728	MAPU 2.0: high-accuracy proteomes mapped to genomes. Nucleic Acids Research, 2009, 37, D902-D906.	6.5	18
729	YBX1 mediates translation of oncogenic transcripts to control cell competition in AML. Leukemia, 2022, 36, 426-437.	3.3	18
730	HAX1-dependent control of mitochondrial proteostasis governs neutrophil granulocyte differentiation. Journal of Clinical Investigation, 2022, 132, .	3.9	18
731	Effective Representation and Storage of Mass Spectrometryâ€"Based Proteomic Data Sets for the Scientific Community. Science Signaling, 2011, 4, pe7.	1.6	17
732	Proteomics of Cytochrome c Oxidase-Negative versus -Positive Muscle Fiber Sections in Mitochondrial Myopathy. Cell Reports, 2019, 29, 3825-3834.e4.	2.9	17
733	DIA-based systems biology approach unveils E3 ubiquitin ligase-dependent responses to a metabolic shift. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32806-32815.	3.3	17
734	Is mass spectrometry ready for proteome-wide protein expression analysis?. Genome Biology, 2002, 3, comment2008.1.	13.9	16
735	Advocating for science progress as a human right. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10820-10823.	3.3	16
736	JAZF1, A Novel p400/TIP60/NuA4 Complex Member, Regulates H2A.Z Acetylation at Regulatory Regions. International Journal of Molecular Sciences, 2021, 22, 678.	1.8	16
737	PLCG1 is required for AML1-ETO leukemia stem cell self-renewal. Blood, 2022, 139, 1080-1097.	0.6	16
738	Actin: A Target of Lipopolysaccharid-Induced Phosphorylation in Human Monocytes. Biochemical and Biophysical Research Communications, 1997, 241, 670-674.	1.0	15

#	Article	IF	Citations
739	Purification of Protein A-tagged Yeast Ran Reveals Association with a Novel Karyopherin Î² Family Member, Pdr6p. Journal of Biological Chemistry, 2000, 275, 467-471.	1.6	15
740	Motif Decomposition of the Phosphotyrosine Proteome Reveals a New N-terminal Binding Motif for SHIP2. Molecular and Cellular Proteomics, 2008, 7, 181-192.	2.5	15
741	Proteomic Analysis of Cellular Systems. , 2013, , 3-25.		15
742	Proteomic Approaches in Circadian Biology. Handbook of Experimental Pharmacology, 2013, , 389-407.	0.9	15
743	Systems Analyses Reveal Shared and Diverse Attributes of Oct4 Regulation in Pluripotent Cells. Cell Systems, 2015, 1, 141-151.	2.9	15
744	Fam20C regulates protein secretion by Cab45 phosphorylation. Journal of Cell Biology, 2020, 219, .	2.3	15
745	Association of Complement and MAPK Activation With SARS-CoV-2â€“Associated Myocardial Inflammation. JAMA Cardiology, 2022, 7, 286.	3.0	15
746	Temporal resolution of gene derepression and proteome changes upon PROTAC-mediated degradation of BCL11A protein in erythroid cells. Cell Chemical Biology, 2022, 29, 1273-1287.e8.	2.5	14
747	Mass tool for diagnosis. Nature, 2002, 418, 731-732.	13.7	13
748	Resources for proteomics in mouse embryonic stem cells. Nature Methods, 2011, 8, 103-104.	9.0	13
749	A New Parallel High-Pressure Packing System Enables Rapid Multiplexed Production of Capillary Columns. Molecular and Cellular Proteomics, 2021, 20, 100082.	2.5	13
750	Molecular Origin of Bloodâ€Based Infrared Spectroscopic Fingerprints**. Angewandte Chemie - International Edition, 2021, 60, 17060-17069.	7.2	13
751	Amyloid-like aggregating proteins cause lysosomal defects in neurons via gain-of-function toxicity. Life Science Alliance, 2022, 5, e202101185.	1.3	13
752	Evidence for Insertional RNA Editing in Humans. Current Biology, 2008, 18, 1760-1765.	1.8	12
753	Plasma proteome profiles treatment efficacy of incretin dual agonism in dietâ€induced obese female and male mice. Diabetes, Obesity and Metabolism, 2021, 23, 195-207.	2.2	12
754	Tissue-specific modulation of gene expression in response to lowered insulin signalling in Drosophila. ELife, 2021, 10, .	2.8	12
755	AlphaMap: an open-source Python package for the visual annotation of proteomics data with sequence-specific knowledge. Bioinformatics, 2022, 38, 849-852.	1.8	12
756	DEAD Box Protein DDX1 Regulates Cytoplasmic Localization of KSRP. PLoS ONE, 2013, 8, e73752.	1.1	12

#	Article	IF	Citations
757	Synthesis of oligodeoxynucleotides containing 5-aminouracil and its N-acetyl derivative. Journal of the Chemical Society Perkin Transactions 1, 1997, , 2051-2058.	0.9	11
758	Correction to Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. Journal of Proteome Research, 2012, 11, 3506-3508.	1.8	11
759	Metallopeptidase inhibitor 1 (TIMPâ€1) promotes receptor tyrosine kinase câ€Kit signaling in colorectal cancer. Molecular Oncology, 2019, 13, 2646-2662.	2.1	11
760	A20 and ABIN-1 cooperate in balancing CBM complex-triggered NF-ÎºB signaling in activated T cells. Cellular and Molecular Life Sciences, 2022, 79, 112.	2.4	11
761	HYPK promotes the activity of the N ^{Î±} -acetyltransferase A complex to determine proteostasis of nonAc-X ² /N-degronâ€"containing proteins. Science Advances, 2022, 8, .	4.7	11
762	Nanoelectrospray peptide mapping revisited: Composite survey spectra allow high dynamic range protein characterization without LCMS on an orbitrap mass spectrometer. International Journal of Mass Spectrometry, 2007, 268, 158-167.	0.7	10
763	Identification and characterization of a novel ubiquitous nucleolar protein â€˜NARRâ€™ encoded by a gene overlapping the rab34 oncogene. Nucleic Acids Research, 2011, 39, 7103-7113.	6.5	10
764	SILAC-based quantitative mass spectrometry-based proteomics quantifies endoplasmic reticulum stress in whole HeLa cells. DMM Disease Models and Mechanisms, 2019, 12, .	1.2	10
765	Loss of full-length hnRNP R isoform impairs DNA damage response in motoneurons by inhibiting Yb1 recruitment to chromatin. Nucleic Acids Research, 2021, 49, 12284-12305.	6.5	10
766	Deep-coverage rhesus red blood cell proteome: a first comparison with the human and mouse red blood cell. Blood Transfusion, 2010, 8 Suppl 3, s126-39.	0.3	10
767	Gene-selective transcription promotes the inhibition of tissue reparative macrophages by TNF. Life Science Alliance, 2022, 5, e202101315.	1.3	10
768	Mass spectrometry of proteins: studies of parvalbumins by plasma desorption, laser desorption and electrospray mass spectrometry. International Journal of Mass Spectrometry and Ion Processes, 1991, 111, 151-172.	1.9	9
769	Applications of sustained off-resonance irradiation (SORI) and quadrupolar excitation axialization (QEA) for the characterization of biomolecules by Fourier-transform mass spectrometry (FTMS). Biochemical Society Transactions, 1996, 24, 943-947.	1.6	9
770	The Origins of Organellar Mapping by Protein Correlation Profiling. Proteomics, 2020, 20, 1900330.	1.3	9
771	Atomic-resolution mapping of transcription factor-DNA interactions by femtosecond laser crosslinking and mass spectrometry. Nature Communications, 2020, 11, 3019.	5.8	9
772	Towards Precision Dermatology: Emerging Role of Proteomic Analysis of the Skin. Dermatology, 2022, 238, 185-194.	0.9	9
773	Approaches to the Practical Use of MS/MS in a Protein Sequencing Facility. , 1996, , 245-265.		9
774	Electrospray Mass Spectrometry. , 1992, , 1-35.		9

#	Article	IF	Citations
775	Defining NASH from a Multi-Omics Systems Biology Perspective. Journal of Clinical Medicine, 2021, 10, 4673.	1.0	9
776	A GID E3 ligase assembly ubiquitinates an Rsp5 E3 adaptor and regulates plasma membrane transporters. EMBO Reports, 2022, 23, e53835.	2.0	9
777	Molecular Cloning of pTAC12 an Alternative Splicing Product of the CD3Î³ Chain as a Component of the Pre-T Cell Antigen-Receptor Complex. Journal of Biological Chemistry, 1998, 273, 30675-30679.	1.6	8
778	Phosphorylation of the Human Full-Length Protein Kinase CÎ¹. Journal of Proteome Research, 2008, 7, 2928-2935.	1.8	8
779	Yeast Expression Proteomics by High-Resolution Mass Spectrometry. Methods in Enzymology, 2010, 470, 259-280.	0.4	8
780	Identification of the transcription factor MAZ as a regulator of erythropoiesis. Blood Advances, 2021, 5, 3002-3015.	2.5	8
781	Distinction Between Phosphorylated and Sulfated Peptides by Matrix Assisted Laser Desorption Ionization Reflector Mass Spectrometry at the Sub Picomole Level. Techniques in Protein Chemistry, 1994, 5, 105-113.	0.3	8
782	The application of robotics and mass spectrometry to the characterisation of theDrosophila melanogaster indirect flight muscle proteome. International Journal of Peptide Research and Therapeutics, 1997, 4, 57-65.	0.1	7
783	Use of Mass Spectrometric Methods for Protein Identification in Receptor Research. Journal of Receptor and Signal Transduction Research, 1999, 19, 659-672.	1.3	7
784	Proteomics for biomedicine: a halfâ€completed journey. EMBO Molecular Medicine, 2012, 4, 75-77.	3.3	7
785	A mass spectrometry guided approach for the identification of novel vaccine candidates in gram-negative pathogens. Scientific Reports, 2019, 9, 17401.	1.6	7
786	SHP1 regulates a STAT6â€"ITGB3 axis in FLT3ITD-positive AML cells. Leukemia, 2020, 34, 1444-1449.	3.3	7
787	Delayed Extraction Improves Specificity in Database Searches by Matrixâ€assisted Laser Desorption/Ionization Peptide Maps. Rapid Communications in Mass Spectrometry, 1996, 10, 1371-1378.	0.7	7
788	Proteomic Analysis Identifies NDUFS1 and ATP5O as Novel Markers for Survival Outcome in Prostate Cancer. Cancers, 2021, 13, 6036.	1.7	7
789	Title is missing!. International Journal of Peptide Research and Therapeutics, 1997, 4, 57-65.	0.1	6
790	A Proteomic Approach to the Inventory of the Human Centrosome. , 2005, , 123-142.		6
791	Myosin binding protein H-like (MYBPHL): a promising biomarker to predict atrial damage. Scientific Reports, 2019, 9, 9986.	1.6	6
792	Catching Lipid Droplet Contacts by Proteomics. Contact (Thousand Oaks (Ventura County, Calif)), 2019, 2, 251525641985918.	0.4	6

#	Article	IF	Citations
793	Identification of covalent modifications regulatingÂimmune signaling complex composition and phenotype. Molecular Systems Biology, 2021, 17, e10125.	3.2	6
794	Response to Raaijmakers & Medema. EMBO Journal, 2019, 38, e103547.	3.5	6
795	Pharmacological and phosphoproteomic approaches to roles of protein kinase C in kappa opioid receptor-mediated effects in mice. Neuropharmacology, 2020, 181, 108324.	2.0	5
796	Proteomics in the Study of Liver Diseases. , 2019, , 165-193.		4
797	A boundless future for proteomics?. Trends in Biotechnology, 2001, 19, S1-S2.	4.9	3
798	Identification of yeast proteins by mass spectrometry. Methods in Enzymology, 2002, 351, 296-321.	0.4	3
799	Requirement of ATM-Dependent Monoubiquitylation of Histone H2B for Timely Repair of DNA Double-Strand Breaks. Molecular Cell, 2011, 42, 137.	4.5	3
800	Electrospray Mass Spectrometry. , 1992, , 145-163.		3
801	Phosphorylation of serine-893 in CARD11 suppresses the formation and activity of the CARD11-BCL10-MALT1 complex in T and B cells. Science Signaling, 2022, 15, eabk3083.	1.6	3
802	Cryo-EM structures of Gid12-bound GID E3 reveal steric blockade as a mechanism inhibiting substrate ubiquitylation. Nature Communications, 2022, 13, .	5.8	3
803	Some biochemical applications of electrospray-magnetic sector mass spectrometry. Biochemical Society Transactions, 1991, 19, 940-943.	1.6	2
804	John Bennett Fenn, 1917â€“2010. Journal of the American Society for Mass Spectrometry, 2011, 22, 602-603.	1.2	2
805	Quick and clean: Cracking sentences encoded in E. coli by LCâ€“MS/MS, de novo sequencing, and dictionary search. EuPA Open Proteomics, 2019, 22-23, 30-35.	2.5	2
806	Cohort profile: the MUNICH Preterm and Term Clinical study (MUNICH-PreTCl), a neonatal birth cohort with focus on prenatal and postnatal determinants of infant and childhood morbidity. BMJ Open, 2021, 11, e050652.	0.8	2
807	Reply to â€œQuality control requirements for the correct annotation of lipidomics dataâ€. Nature Communications, 2021, 12, 4772.	5.8	2
808	Protein-interaction mapping for functional proteomics. Trends in Biotechnology, 2000, 18, 43-47.	4.9	1
809	The Post-Genomic World.. Analytical Chemistry, 2000, 72, 565 A-565 A.	3.2	1
810	Corrigendum to: Anaphase specific auto-cleavage of separase (FEBS 26464). FEBS Letters, 2002, 531, 381-381.	1.3	1

#	Article	IF	Citations
811	Multi-Protein Complexes Studied by Mass Spectrometry. Scientific World Journal, The, 2002, 2, 91-92.	0.8	1
812	A home for proteomics data?. Nature, 2002, 420, 21-21.	13.7	1
813	Proteomics, the red blood cell and transfusion medicine. ISBT Science Series, 2010, 5, 63-72.	1.1	1
814	Sequencing of the First Draft of the Human Acetylome. Clinical Chemistry, 2020, 66, 852-853.	1.5	1
815	Temporal Dynamics of EGF Receptor Signaling by Quantitative Proteomics. , 2008, , 190-198.		1
816	Cbf5p, a potential pseudouridine synthase, and Nhp2p, a putative RNA-binding protein, are present together with Gar1p in all H BOX/ACA-motif snoRNPs and constitute a common bipartite structure. , 0, .		1
817	Deciphering Functionally Important Multiprotein Complexes by Mass Spectrometry. , 2000, , 237-269.		1
818	Ethical principles, opportunities and constraints in clinical proteomics. Molecular and Cellular Proteomics, 2021, , .	2.5	1
819	MPSA short communications. The Protein Journal, 1994, 13, 431-512.	1.1	0
820	Biochemie und Molekulargenetik 2001. Nachrichten Aus Der Chemie, 2002, 50, 312-326.	0.0	0
821	Protein Identification and Sequencing by Mass Spectrometry. , 2006, , 363-369.		0
822	Stable Isotope Labeling by Amino Acids in Cell Culture for Quantitative Proteomics. , 2006, , 427-436.		0
823	Mass Spectrometry Resurrects Protein-based Approaches in Functional Genomics. Novartis Foundation Symposium, 2008, 229, 27-32.	1.2	0
824	DDRE-22. TARGETING SERINE SYNTHESIS IN BRAIN METASTASIS. Neuro-Oncology Advances, 2021, 3, i11-i11.	0.4	0
825	Molecular Origin of Bloodâ€Based Infrared Spectroscopic Fingerprints**. Angewandte Chemie, 2021, 133, 17197-17206.	1.6	0
826	InnenrÃ¼cktitelbild: Molecular Origin of Bloodâ€Based Infrared Spectroscopic Fingerprints (Angew.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.6	0
827	OS12.7.A Characterization of intra-tumoral heterogeneity and differential immune activation during malignant progression of meningiomas on single cell level. Neuro-Oncology, 2021, 23, ii15-ii16.	0.6	0
828	Protein Interaction Mapping by Coprecipitation and Mass Spectrometric Identification. , 2003, , 295-300.		0

#	Article	IF	Citations
829	microRNA-mediated regulation of mTOR complex components facilitates discrimination between activation and anergy in CD4 T cells. Journal of Cell Biology, 2014, 207, 2072OIA191.	2.3	0