

Matthias Mann

List of Publications by Year in descending order

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829
papers

259,066
citations

226
h-index

475
g-index

908
all docs

908
docs citations

908
times ranked

184144
citing authors

#	ARTICLE	IF	CITATIONS
1	MaxQuant enables high peptide identification rates, individualized p.p.b.-range mass accuracies and proteome-wide protein quantification. <i>Nature Biotechnology</i> , 2008, 26, 1367-1372.	9.4	12,966
2	Mass Spectrometric Sequencing of Proteins from Silver-Stained Polyacrylamide Gels. <i>Analytical Chemistry</i> , 1996, 68, 850-858.	3.2	8,535
3	Electrospray ionization for mass spectrometry of large biomolecules. <i>Science</i> , 1989, 246, 64-71.	6.0	6,875
4	Universal sample preparation method for proteome analysis. <i>Nature Methods</i> , 2009, 6, 359-362.	9.0	6,678
5	Mass spectrometry-based proteomics. <i>Nature</i> , 2003, 422, 198-207.	13.7	6,282
6	The Perseus computational platform for comprehensive analysis of (prote)omics data. <i>Nature Methods</i> , 2016, 13, 731-740.	9.0	6,181
7	Andromeda: A Peptide Search Engine Integrated into the MaxQuant Environment. <i>Journal of Proteome Research</i> , 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. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 376-386.	2.5	4,931
9	In-gel digestion for mass spectrometric characterization of proteins and proteomes. <i>Nature Protocols</i> , 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. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2513-2526.	2.5	4,178
11	Lysine Acetylation Targets Protein Complexes and Co-Regulates Major Cellular Functions. <i>Science</i> , 2009, 325, 834-840.	6.0	3,883
12	Protocol for micro-purification, enrichment, pre-fractionation and storage of peptides for proteomics using StageTips. <i>Nature Protocols</i> , 2007, 2, 1896-1906.	5.5	3,693
13	Systematic identification of protein complexes in <i>Saccharomyces cerevisiae</i> by mass spectrometry. <i>Nature</i> , 2002, 415, 180-183.	13.7	3,445
14	Global, In Vivo, and Site-Specific Phosphorylation Dynamics in Signaling Networks. <i>Cell</i> , 2006, 127, 635-648.	13.5	3,201
15	FLICE, A Novel FADD-Homologous ICE/CED-3-like Protease, Is Recruited to the CD95 (Fas/APO-1) Death-Inducing Signaling Complex. <i>Cell</i> , 1996, 85, 817-827.	13.5	2,944
16	A generic protein purification method for protein complex characterization and proteome exploration. <i>Nature Biotechnology</i> , 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. <i>Analytical Chemistry</i> , 2003, 75, 663-670.	3.2	2,337
18	Proteomics to study genes and genomes. <i>Nature</i> , 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- κ B Activation. <i>Science</i> , 1997, 278, 860-866.	6.0	1,995
20	Analytical Properties of the Nanoelectrospray Ion Source. <i>Analytical Chemistry</i> , 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. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1265-1272.	2.5	1,817
22	Proteomic analysis of post-translational modifications. <i>Nature Biotechnology</i> , 2003, 21, 255-261.	9.4	1,809
23	Femtomole sequencing of proteins from polyacrylamide gels by nano-electrospray mass spectrometry. <i>Nature</i> , 1996, 379, 466-469.	13.7	1,723
24	Mass-spectrometric exploration of proteome structure and function. <i>Nature</i> , 2016, 537, 347-355.	13.7	1,573
25	Error-Tolerant Identification of Peptides in Sequence Databases by Peptide Sequence Tags. <i>Analytical Chemistry</i> , 1994, 66, 4390-4399.	3.2	1,521
26	Electrospray ionization-principles and practice. <i>Mass Spectrometry Reviews</i> , 1990, 9, 37-70.	2.8	1,511
27	Minimal, encapsulated proteomic-sample processing applied to copy-number estimation in eukaryotic cells. <i>Nature Methods</i> , 2014, 11, 319-324.	9.0	1,447
28	Mass spectrometry-based proteomics turns quantitative. <i>Nature Chemical Biology</i> , 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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 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. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 2010-2021.	2.5	1,395
31	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. <i>Science Signaling</i> , 2010, 3, ra3.	1.6	1,319
32	Proteomic characterization of the human centrosome by protein correlation profiling. <i>Nature</i> , 2003, 426, 570-574.	13.7	1,204
33	Reverse Transcriptase Motifs in the Catalytic Subunit of Telomerase. <i>Science</i> , 1997, 276, 561-567.	6.0	1,172
34	The growing landscape of lysine acetylation links metabolism and cell signalling. <i>Nature Reviews Molecular Cell Biology</i> , 2014, 15, 536-550.	16.1	1,153
35	A Human Interactome in Three Quantitative Dimensions Organized by Stoichiometries and Abundances. <i>Cell</i> , 2015, 163, 712-723.	13.5	1,132
36	L-Arginine Modulates T Cell Metabolism and Enhances Survival and Anti-tumor Activity. <i>Cell</i> , 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 3'5' 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	Ultra-deep 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. <i>Biological Mass Spectrometry</i> , 1993, 22, 338-345.	0.5	832
56	Electrospray and Taylor-Cone theory, Dole's beam of macromolecules at last?. <i>International Journal of Mass Spectrometry and Ion Processes</i> , 1994, 136, 167-180.	1.9	828
57	A practical recipe for stable isotope labeling by amino acids in cell culture (SILAC). <i>Nature Protocols</i> , 2006, 1, 2650-2660.	5.5	816
58	Integrated Analysis of Protein Composition, Tissue Diversity, and Gene Regulation in Mouse Mitochondria. <i>Cell</i> , 2003, 115, 629-640.	13.5	815
59	Large-Scale Proteomic Analysis of the Human Spliceosome. <i>Genome Research</i> , 2002, 12, 1231-1245.	2.4	808
60	AU Binding Proteins Recruit the Exosome to Degrade ARE-Containing mRNAs. <i>Cell</i> , 2001, 107, 451-464.	13.5	803
61	Precision Mapping of an In Vivo N-Glycoproteome Reveals Rigid Topological and Sequence Constraints. <i>Cell</i> , 2010, 141, 897-907.	13.5	789
62	Unbiased quantitative proteomics of lipid rafts reveals high specificity for signaling factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5813-5818.	3.3	783
63	Selective Anchoring of TFIID to Nucleosomes by Trimethylation of Histone H3 Lysine 4. <i>Cell</i> , 2007, 131, 58-69.	13.5	769
64	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. <i>Nature Protocols</i> , 2009, 4, 698-705.	5.5	769
65	Phosphoproteomics reveals that Parkinson's disease kinase LRRK2 regulates a subset of Rab GTPases. <i>ELife</i> , 2016, 5, .	2.8	766
66	Mechanism of regulation of WAVE1-induced actin nucleation by Rac1 and Nck. <i>Nature</i> , 2002, 418, 790-793.	13.7	758
67	A Proteome-wide, Quantitative Survey of In Vivo Ubiquitylation Sites Reveals Widespread Regulatory Roles. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.013284.	2.5	754
68	Quantitative Interaction Proteomics and Genome-wide Profiling of Epigenetic Histone Marks and Their Readers. <i>Cell</i> , 2010, 142, 967-980.	13.5	710
69	Quantitative Phosphoproteomics Applied to the Yeast Pheromone Signaling Pathway. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 310-327.	2.5	708
70	A proteomics strategy to elucidate functional protein-protein interactions applied to EGF signaling. <i>Nature Biotechnology</i> , 2003, 21, 315-318.	9.4	702
71	Mass Spectrometry-based Proteomics Using Q Exactive, a High-performance Benchtop Quadrupole Orbitrap Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.011015.	2.5	701
72	Comparative Proteomic Analysis of Eleven Common Cell Lines Reveals Ubiquitous but Varying Expression of Most Proteins. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014050.	2.5	701

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73	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893.	9.4	694
74	Temporal analysis of phosphotyrosine-dependent signaling networks by quantitative proteomics. <i>Nature Biotechnology</i> , 2004, 22, 1139-1145.	9.4	680
75	Improved Resolution and Very High Sensitivity in MALDI TOF of Matrix Surfaces Made by Fast Evaporation. <i>Analytical Chemistry</i> , 1994, 66, 3281-3287.	3.2	679
76	Cell type- and brain region-resolved mouse brain proteome. <i>Nature Neuroscience</i> , 2015, 18, 1819-1831.	7.1	672
77	Identification of the receptor component of the E3 ubiquitin ligase. <i>Nature</i> , 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. <i>Cell</i> , 2008, 134, 353-364.	13.5	631
79	Quantitative, High-Resolution Proteomics for Data-Driven Systems Biology. <i>Annual Review of Biochemistry</i> , 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. <i>Genes and Development</i> , 2002, 16, 1066-1076.	2.7	621
81	Direct identification of clinically relevant neopeptides presented on native human melanoma tissue by mass spectrometry. <i>Nature Communications</i> , 2016, 7, 13404.	5.8	613
82	Online Parallel Accumulation-Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2534-2545.	2.5	602
83	The human urinary proteome contains more than 1500 proteins, including a large proportion of membrane proteins. <i>Genome Biology</i> , 2006, 7, R80.	13.9	598
84	Revisiting biomarker discovery by plasma proteomics. <i>Molecular Systems Biology</i> , 2017, 13, 942.	3.2	597
85	Analysis of the Plasmodium falciparum proteome by high-accuracy mass spectrometry. <i>Nature</i> , 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 LC-MS/MS. <i>Journal of Proteome Research</i> , 2011, 10, 1785-1793.	1.8	595
87	Phosphorylation and Inactivation of BAD by Mitochondria-Anchored Protein Kinase A. <i>Molecular Cell</i> , 1999, 3, 413-422.	4.5	593
88	Proteome-wide Analysis of Chaperonin-Dependent Protein Folding in Escherichia coli. <i>Cell</i> , 2005, 122, 209-220.	13.5	590
89	Interpreting mass spectra of multiply charged ions. <i>Analytical Chemistry</i> , 1989, 61, 1702-1708.	3.2	587
90	Activity of DNA ligase IV stimulated by complex formation with XRCC4 protein in mammalian cells. <i>Nature</i> , 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. <i>Cell</i> , 1998, 93, 1067-1076.	13.5	564
92	Cell-cycle-regulated association of RAD50/MRE11/NBS1 with TRF2 and human telomeres. <i>Nature Genetics</i> , 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. <i>Cell</i> , 1997, 90, 1149-1159.	13.5	552
94	Plasma Proteome Profiling to Assess Human Health and Disease. <i>Cell Systems</i> , 2016, 2, 185-195.	2.9	549
95	Kinase-Selective Enrichment Enables Quantitative Phosphoproteomics of the Kinome across the Cell Cycle. <i>Molecular Cell</i> , 2008, 31, 438-448.	4.5	548
96	Decoding Human Cytomegalovirus. <i>Science</i> , 2012, 338, 1088-1093.	6.0	546
97	Quantitative Proteomics Reveals Subset-Specific Viral Recognition in Dendritic Cells. <i>Immunity</i> , 2010, 32, 279-289.	6.6	544
98	1D and 2D annotation enrichment: a statistical method integrating quantitative proteomics with complementary high-throughput data. <i>BMC Bioinformatics</i> , 2012, 13, S12.	1.2	542
99	A Mammalian Organelle Map by Protein Correlation Profiling. <i>Cell</i> , 2006, 125, 187-199.	13.5	538
100	Gln ⁶³ of Rho is deamidated by Escherichia coli cytotoxic necrotizing factor-1. <i>Nature</i> , 1997, 387, 725-729.	13.7	534
101	Decoding signalling networks by mass spectrometry-based proteomics. <i>Nature Reviews Molecular Cell Biology</i> , 2010, 11, 427-439.	16.1	534
102	Mechanism of Divergent Growth Factor Effects in Mesenchymal Stem Cell Differentiation. <i>Science</i> , 2005, 308, 1472-1477.	6.0	531
103	A "Proteomic Ruler" for Protein Copy Number and Concentration Estimation without Spike-in Standards. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3497-3506.	2.5	530
104	Identification of a gene causing human cytochrome c oxidase deficiency by integrative genomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 605-610.	3.3	526
105	Nucleosome-Interacting Proteins Regulated by DNA and Histone Methylation. <i>Cell</i> , 2010, 143, 470-484.	13.5	524
106	Metabolic priming by a secreted fungal effector. <i>Nature</i> , 2011, 478, 395-398.	13.7	509
107	Combination of FASP and StageTip-Based Fractionation Allows In-Depth Analysis of the Hippocampal Membrane Proteome. <i>Journal of Proteome Research</i> , 2009, 8, 5674-5678.	1.8	507
108	Status of Large-scale Analysis of Post-translational Modifications by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 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. <i>Nature</i> , 2001, 409, 581-588.	13.7	487
110	p70S6 kinase signals cell survival as well as growth, inactivating the pro-apoptotic molecule BAD. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 9666-9670.	3.3	487
111	Chromatin-remodelling factor CHRAC contains the ATPases ISWI and topoisomerase II. <i>Nature</i> , 1997, 388, 598-602.	13.7	484
112	Super-SILAC mix for quantitative proteomics of human tumor tissue. <i>Nature Methods</i> , 2010, 7, 383-385.	9.0	480
113	Widespread Proteome Remodeling and Aggregation in Aging <i>C.Âlegans</i> . <i>Cell</i> , 2015, 161, 919-932.	13.5	478
114	Multilevel proteomics reveals host perturbations by SARS-CoV-2 and SARS-CoV. <i>Nature</i> , 2021, 594, 246-252.	13.7	475
115	Mass spectrometry and EST-database searching allows characterization of the multi-protein spliceosome complex. <i>Nature Genetics</i> , 1998, 20, 46-50.	9.4	470
116	Phosphotyrosine interactome of the ErbBâ€receptor kinase family. <i>Molecular Systems Biology</i> , 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. <i>Cell</i> , 1997, 89, 597-606.	13.5	467
118	Mass spectrometry in high-throughput proteomics: ready for the big time. <i>Nature Methods</i> , 2010, 7, 681-685.	9.0	465
119	Paraspeckles. <i>Current Biology</i> , 2002, 12, 13-25.	1.8	455
120	The Enterotoxin from <i>Clostridium difficile</i> (ToxA) Monoglucosylates the Rho Proteins. <i>Journal of Biological Chemistry</i> , 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. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 658-673.	2.5	445
122	Properties of ¹³ C-Substituted Arginine in Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC). <i>Journal of Proteome Research</i> , 2003, 2, 173-181.	1.8	439
123	Protein abundance profiling of the <i>Escherichia coli</i> cytosol. <i>BMC Genomics</i> , 2008, 9, 102.	1.2	432
124	Identifying and quantifying in vivo methylation sites by heavy methyl SILAC. <i>Nature Methods</i> , 2004, 1, 119-126.	9.0	427
125	Quantitative proteomics combined with BAC TransgeneOmics reveals in vivo protein interactions. <i>Journal of Cell Biology</i> , 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. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 443-450.	2.5	426
128	System-Wide Changes to SUMO Modifications in Response to Heat Shock. <i>Science Signaling</i> , 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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 179-184.	3.3	410
130	Is Proteomics the New Genomics?. <i>Cell</i> , 2007, 130, 395-398.	13.5	410
131	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. <i>Genome Biology</i> , 2007, 8, R250.	13.9	410
132	Phosphatidylcholine Synthesis for Lipid Droplet Expansion Is Mediated by Localized Activation of CTP:Phosphocholine Cytidyltransferase. <i>Cell Metabolism</i> , 2011, 14, 504-515.	7.2	408
133	Uncovering global SUMOylation signaling networks in a site-specific manner. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 927-936.	3.6	408
134	High-throughput phosphoproteomics reveals in vivo insulin signaling dynamics. <i>Nature Biotechnology</i> , 2015, 33, 990-995.	9.4	408
135	An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics. <i>Nature Communications</i> , 2019, 10, 963.	5.8	408
136	Mitotic Regulation of the APC Activator Proteins CDC20 and CDH1. <i>Molecular Biology of the Cell</i> , 2000, 11, 1555-1569.	0.9	405
137	The yeast exosome and human PM-Scl are related complexes of 3' right-arrow 5' exonucleases. <i>Genes and Development</i> , 1999, 13, 2148-2158.	2.7	402
138	Protein Phosphorylation: A Major Switch Mechanism for Metabolic Regulation. <i>Trends in Endocrinology and Metabolism</i> , 2015, 26, 676-687.	3.1	402
139	Pervasive functional translation of noncanonical human open reading frames. <i>Science</i> , 2020, 367, 1140-1146.	6.0	400
140	Mass spectrometric-based approaches in quantitative proteomics. <i>Methods</i> , 2003, 29, 124-130.	1.9	398
141	A Dual Pressure Linear Ion Trap Orbitrap Instrument with Very High Sequencing Speed. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2759-2769.	2.5	398
142	The mitochondrial contact site complex, a determinant of mitochondrial architecture. <i>EMBO Journal</i> , 2011, 30, 4356-4370.	3.5	395
143	System-Wide Temporal Characterization of the Proteome and Phosphoproteome of Human Embryonic Stem Cell Differentiation. <i>Science Signaling</i> , 2011, 4, rs3.	1.6	389
144	In-depth analysis of the membrane and cytosolic proteome of red blood cells. <i>Blood</i> , 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 accumulation ⁺ 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 myosin ^{II} 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 3' 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 spectrometry-based proteomics in cell biology. <i>Journal of Cell Biology</i> , 2010, 190, 491-500.	2.3	348
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