

# Matthias Mann

## List of Publications by Year in descending order

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972  
papers

251,722  
citations

<sup>2</sup>  
224  
h-index

<sup>10</sup>  
465  
g-index

1191  
all docs

1191  
docs citations

1191  
times ranked

194653  
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.	20.8	13,477
2	Mass Spectrometric Sequencing of Proteins from Silver-Stained Polyacrylamide Gels. <i>Analytical Chemistry</i> , 1996, 68, 850-858.	6.8	8,591
3	Universal sample preparation method for proteome analysis. <i>Nature Methods</i> , 2009, 6, 359-362.	19.6	6,978
4	Mass spectrometry-based proteomics. <i>Nature</i> , 2003, 422, 198-207.	36.2	6,859
5	Andromeda: A Peptide Search Engine Integrated into the MaxQuant Environment. <i>Journal of Proteome Research</i> , 2011, 10, 1794-1805.	3.8	5,142
6	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.	3.9	4,988
7	Lysine Acetylation Targets Protein Complexes and Co-Regulates Major Cellular Functions. <i>Science</i> , 2009, 325, 834-840.	20.9	3,944
8	Systematic identification of protein complexes in <i>Saccharomyces cerevisiae</i> by mass spectrometry. <i>Nature</i> , 2002, 415, 180-183.	36.2	3,463
9	Global, In Vivo, and Site-Specific Phosphorylation Dynamics in Signaling Networks. <i>Cell</i> , 2006, 127, 635-648.	27.8	3,245
10	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.	27.8	2,957
11	A generic protein purification method for protein complex characterization and proteome exploration. <i>Nature Biotechnology</i> , 1999, 17, 1030-1032.	20.8	2,558
12	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.	6.8	2,435
13	Proteomics to study genes and genomes. <i>Nature</i> , 2000, 405, 837-846.	36.2	2,199
14	IKK-1 and IKK-2: Cytokine-Activated I $\kappa$ B Kinases Essential for NF- $\kappa$ B Activation. <i>Science</i> , 1997, 278, 860-866.	20.9	2,010
15	Analytical Properties of the Nanoelectrospray Ion Source. <i>Analytical Chemistry</i> , 1996, 68, 1-8.	6.8	1,852
16	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.	3.9	1,845
17	Proteomic analysis of post-translational modifications. <i>Nature Biotechnology</i> , 2003, 21, 255-261.	20.8	1,844
18	Femtomole sequencing of proteins from polyacrylamide gels by nano-electrospray mass spectrometry. <i>Nature</i> , 1996, 379, 466-469.	36.2	1,730

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19	Electrospray ionization-principles and practice. <i>Mass Spectrometry Reviews</i> , 1990, 9, 37-70.	6.1	1,525
20	Error-Tolerant Identification of Peptides in Sequence Databases by Peptide Sequence Tags. <i>Analytical Chemistry</i> , 1994, 66, 4390-4399.	6.8	1,524
21	Mass spectrometry-based proteomics turns quantitative. <i>Nature Chemical Biology</i> , 2005, 1, 252-262.	8.0	1,439
22	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.	7.6	1,421
23	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.	3.9	1,411
24	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. <i>Science Signaling</i> , 2010, 3, ra3.	5.1	1,348
25	Proteomic characterization of the human centrosome by protein correlation profiling. <i>Nature</i> , 2003, 426, 570-574.	36.2	1,222
26	A Human Interactome in Three Quantitative Dimensions Organized by Stoichiometries and Abundances. <i>Cell</i> , 2015, 163, 712-723.	27.8	1,181
27	L-Arginine Modulates T Cell Metabolism and Enhances Survival and Anti-tumor Activity. <i>Cell</i> , 2016, 167, 829-842.e13.	27.8	1,168
28	FLICE is activated by association with the CD95 death-inducing signaling complex (DISC). <i>EMBO Journal</i> , 1997, 16, 2794-2804.	8.2	1,079
29	Nucleolar proteome dynamics. <i>Nature</i> , 2005, 433, 77-83.	36.2	1,072
30	Analysis of Proteins and Proteomes by Mass Spectrometry. <i>Annual Review of Biochemistry</i> , 2001, 70, 437-473.	11.2	1,057
31	Glucosylation of Rho proteins by <i>Clostridium difficile</i> toxin B. <i>Nature</i> , 1995, 375, 500-503.	36.2	1,037
32	Trypsin Cleaves Exclusively C-terminal to Arginine and Lysine Residues. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 608-614.	3.9	976
33	Directed Proteomic Analysis of the Human Nucleolus. <i>Current Biology</i> , 2002, 12, 1-11.	4.0	968
34	The abc's (and xyz's) of peptide sequencing. <i>Nature Reviews Molecular Cell Biology</i> , 2004, 5, 699-711.	37.3	956
35	miRNPs: a novel class of ribonucleoproteins containing numerous microRNAs. <i>Genes and Development</i> , 2002, 16, 720-728.	5.9	930
36	Circular non-coding RNA ANRIL modulates ribosomal RNA maturation and atherosclerosis in humans. <i>Nature Communications</i> , 2016, 7, 12429.	13.2	905

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37	From genomics to proteomics. <i>Nature</i> , 2003, 422, 193-197.	36.2	897
38	Deep proteome and transcriptome mapping of a human cancer cell line. <i>Molecular Systems Biology</i> , 2011, 7, 548.	7.5	895
39	Analysis of protein phosphorylation using mass spectrometry: deciphering the phosphoproteome. <i>Trends in Biotechnology</i> , 2002, 20, 261-268.	9.5	883
40	Functional and quantitative proteomics using SILAC. <i>Nature Reviews Molecular Cell Biology</i> , 2006, 7, 952-958.	37.3	873
41	Ultradeep Human Phosphoproteome Reveals a Distinct Regulatory Nature of Tyr and Ser/Thr-Based Signaling. <i>Cell Reports</i> , 2014, 8, 1583-1594.	6.3	871
42	Higher-energy C-trap dissociation for peptide modification analysis. <i>Nature Methods</i> , 2007, 4, 709-712.	19.6	870
43	The Exosome: A Conserved Eukaryotic RNA Processing Complex Containing Multiple 3'â€²5' Exoribonucleases. <i>Cell</i> , 1997, 91, 457-466.	27.8	869
44	Specificity in Toll-like receptor signalling through distinct effector functions of TRAF3 and TRAF6. <i>Nature</i> , 2006, 439, 204-207.	36.2	855
45	Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast. <i>Nature</i> , 2008, 455, 1251-1254.	36.2	843
46	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	840
47	Use of mass spectrometric molecular weight information to identify proteins in sequence databases. <i>Biological Mass Spectrometry</i> , 1993, 22, 338-345.	0.5	837
48	Integrated Analysis of Protein Composition, Tissue Diversity, and Gene Regulation in Mouse Mitochondria. <i>Cell</i> , 2003, 115, 629-640.	27.8	822
49	Phosphoproteomics reveals that Parkinson's disease kinase LRRK2 regulates a subset of Rab GTPases. <i>ELife</i> , 2016, 5, .	5.9	818
50	Large-Scale Proteomic Analysis of the Human Spliceosome. <i>Genome Research</i> , 2002, 12, 1231-1245.	5.6	812
51	AU Binding Proteins Recruit the Exosome to Degrade ARE-Containing mRNAs. <i>Cell</i> , 2001, 107, 451-464.	27.8	809
52	Precision Mapping of an In Vivo N-Glycoproteome Reveals Rigid Topological and Sequence Constraints. <i>Cell</i> , 2010, 141, 897-907.	27.8	804
53	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.	7.6	784
54	Selective Anchoring of TFIID to Nucleosomes by Trimethylation of Histone H3 Lysine 4. <i>Cell</i> , 2007, 131, 58-69.	27.8	784

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55	A Proteome-wide, Quantitative Survey of In Vivo Ubiquitylation Sites Reveals Widespread Regulatory Roles. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.013284.	3.9	769
56	Mechanism of regulation of WAVE1-induced actin nucleation by Rac1 and Nck. <i>Nature</i> , 2002, 418, 790-793.	36.2	762
57	Rapid, Sensitive, and Specific Thiobarbituric Acid Method for Measuring Lipid Peroxidation in Animal Tissue, Food, and Feedstuff Samples. <i>Journal of Agricultural and Food Chemistry</i> , 1994, 42, 1931-1937.	5.3	753
58	Quantitative Interaction Proteomics and Genome-wide Profiling of Epigenetic Histone Marks and Their Readers. <i>Cell</i> , 2010, 142, 967-980.	27.8	724
59	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.	3.9	713
60	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.	3.9	712
61	Quantitative Phosphoproteomics Applied to the Yeast Pheromone Signaling Pathway. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 310-327.	3.9	711
62	Cell type- and brain region- resolved mouse brain proteome. <i>Nature Neuroscience</i> , 2015, 18, 1819-1831.	14.5	707
63	A proteomics strategy to elucidate functional protein-protein interactions applied to EGF signaling. <i>Nature Biotechnology</i> , 2003, 21, 315-318.	20.8	705
64	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893.	20.8	702
65	Online Parallel Accumulation-Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2534-2545.	3.9	686
66	Temporal analysis of phosphotyrosine-dependent signaling networks by quantitative proteomics. <i>Nature Biotechnology</i> , 2004, 22, 1139-1145.	20.8	683
67	Improved Resolution and Very High Sensitivity in MALDI TOF of Matrix Surfaces Made by Fast Evaporation. <i>Analytical Chemistry</i> , 1994, 66, 3281-3287.	6.8	681
68	Identification of the receptor component of the $\text{E}3^{\text{ubiquitin}}$ ubiquitin ligase. <i>Nature</i> , 1998, 396, 590-594.	36.2	652
69	Revisiting biomarker discovery by plasma proteomics. <i>Molecular Systems Biology</i> , 2017, 13, 942.	7.5	649
70	SILAC Mouse for Quantitative Proteomics Uncovers Kindlin-3 as an Essential Factor for Red Blood Cell Function. <i>Cell</i> , 2008, 134, 353-364.	27.8	637
71	Quantitative, High-Resolution Proteomics for Data-Driven Systems Biology. <i>Annual Review of Biochemistry</i> , 2011, 80, 273-299.	11.2	635
72	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.	5.9	633

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73	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.	3.8	605
74	The human urinary proteome contains more than 1500 proteins, including a large proportion of membrane proteins. <i>Genome Biology</i> , 2006, 7, R80.	7.3	603
75	Analysis of the <i>Plasmodium falciparum</i> proteome by high-accuracy mass spectrometry. <i>Nature</i> , 2002, 419, 537-542.	36.2	599
76	Proteome-wide Analysis of Chaperonin-Dependent Protein Folding in <i>Escherichia coli</i> . <i>Cell</i> , 2005, 122, 209-220.	27.8	599
77	Phosphorylation and Inactivation of BAD by Mitochondria-Anchored Protein Kinase A. <i>Molecular Cell</i> , 1999, 3, 413-422.	9.6	596
78	Interpreting mass spectra of multiply charged ions. <i>Analytical Chemistry</i> , 1989, 61, 1702-1708.	6.8	591
79	Activity of DNA ligase IV stimulated by complex formation with XRCC4 protein in mammalian cells. <i>Nature</i> , 1997, 388, 492-495.	36.2	590
80	Plasma Proteome Profiling to Assess Human Health and Disease. <i>Cell Systems</i> , 2016, 2, 185-195.	6.2	581
81	A "Proteomic Ruler" for Protein Copy Number and Concentration Estimation without Spike-in Standards. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3497-3506.	3.9	574
82	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.	27.8	568
83	Cell-cycle-regulated association of RAD50/MRE11/NBS1 with TRF2 and human telomeres. <i>Nature Genetics</i> , 2000, 25, 347-352.	20.4	566
84	1D and 2D annotation enrichment: a statistical method integrating quantitative proteomics with complementary high-throughput data. <i>BMC Bioinformatics</i> , 2012, 13, S12.	2.7	564
85	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.	27.8	559
86	Kinase-Selective Enrichment Enables Quantitative Phosphoproteomics of the Kinome across the Cell Cycle. <i>Molecular Cell</i> , 2008, 31, 438-448.	9.6	557
87	Quantitative Proteomics Reveals Subset-Specific Viral Recognition in Dendritic Cells. <i>Immunity</i> , 2010, 32, 279-289.	14.2	556
88	A Mammalian Organelle Map by Protein Correlation Profiling. <i>Cell</i> , 2006, 125, 187-199.	27.8	544
89	Multilevel proteomics reveals host perturbations by SARS-CoV-2 and SARS-CoV. <i>Nature</i> , 2021, 594, 246-252.	36.2	543
90	Decoding signalling networks by mass spectrometry-based proteomics. <i>Nature Reviews Molecular Cell Biology</i> , 2010, 11, 427-439.	37.3	540

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91	Gln <sup>63</sup> of Rho is deamidated by Escherichia coli cytotoxic necrotizing factor-1. <i>Nature</i> , 1997, 387, 725-729.	36.2	539
92	Identification of a gene causing human cytochrome <i>c</i> oxidase deficiency by integrative genomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 605-610.	7.6	537
93	Mechanism of Divergent Growth Factor Effects in Mesenchymal Stem Cell Differentiation. <i>Science</i> , 2005, 308, 1472-1477.	20.9	534
94	Nucleosome-Interacting Proteins Regulated by DNA and Histone Methylation. <i>Cell</i> , 2010, 143, 470-484.	27.8	531
95	Metabolic priming by a secreted fungal effector. <i>Nature</i> , 2011, 478, 395-398.	36.2	529
96	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.	3.8	517
97	Status of Large-scale Analysis of Post-translational Modifications by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3444-3452.	3.9	501
98	Widespread Proteome Remodeling and Aggregation in Aging <i>C.Âlegans</i> . <i>Cell</i> , 2015, 161, 919-932.	27.8	501
99	Trans-complex formation by proteolipid channels in the terminal phase of membrane fusion. <i>Nature</i> , 2001, 409, 581-588.	36.2	494
100	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.	7.6	490
101	Super-SILAC mix for quantitative proteomics of human tumor tissue. <i>Nature Methods</i> , 2010, 7, 383-385.	19.6	487
102	Chromatin-remodelling factor CHRAC contains the ATPases ISWI and topoisomerase II. <i>Nature</i> , 1997, 388, 598-602.	36.2	485
103	Phosphotyrosine interactome of the ErbB receptor kinase family. <i>Molecular Systems Biology</i> , 2005, 1, 2005.0008.	7.5	475
104	diaPASEF: parallel accumulation serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 2020, 17, 1229-1236.	19.6	474
105	Mass spectrometry and EST-database searching allows characterization of the multi-protein spliceosome complex. <i>Nature Genetics</i> , 1998, 20, 46-50.	20.4	472
106	Mass spectrometry in high-throughput proteomics: ready for the big time. <i>Nature Methods</i> , 2010, 7, 681-685.	19.6	471
107	mRNA Silencing in Erythroid Differentiation: hnRNP K and hnRNP E1 Regulate 15-Lipoxygenase Translation from the 3' End. <i>Cell</i> , 1997, 89, 597-606.	27.8	470
108	Paraspeckles. <i>Current Biology</i> , 2002, 12, 13-25.	4.0	470

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109	Flagellar motility is required for the viability of the bloodstream trypanosome. <i>Nature</i> , 2006, 440, 224-227.	36.2	460
110	The Enterotoxin from <i>Clostridium difficile</i> (ToxA) Monoglucosylates the Rho Proteins. <i>Journal of Biological Chemistry</i> , 1995, 270, 13932-13936.	3.5	453
111	An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics. <i>Nature Communications</i> , 2019, 10, 963.	13.2	442
112	Properties of <sup>13</sup> C-Substituted Arginine in Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC). <i>Journal of Proteome Research</i> , 2003, 2, 173-181.	3.8	440
113	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.	3.9	440
114	Protein abundance profiling of the <i>Escherichia coli</i> cytosol. <i>BMC Genomics</i> , 2008, 9, 102.	2.9	438
115	Quantitative proteomics combined with BAC TransgeneOmics reveals in vivo protein interactions. <i>Journal of Cell Biology</i> , 2010, 189, 739-754.	5.2	436
116	Protein Phosphorylation: A Major Switch Mechanism for Metabolic Regulation. <i>Trends in Endocrinology and Metabolism</i> , 2015, 26, 676-687.	7.0	436
117	Identifying and quantifying in vivo methylation sites by heavy methyl SILAC. <i>Nature Methods</i> , 2004, 1, 119-126.	19.6	431
118	Rapid <i>de novo</i> ™ peptide sequencing by a combination of nanoelectrospray, isotopic labeling and a quadrupole/time-of-flight mass spectrometer. <i>Rapid Communications in Mass Spectrometry</i> , 1997, 11, 1015-1024.	1.5	428
119	Phosphatidylcholine Synthesis for Lipid Droplet Expansion Is Mediated by Localized Activation of CTP:Phosphocholine Cytidylyltransferase. <i>Cell Metabolism</i> , 2011, 14, 504-515.	15.8	428
120	System-Wide Changes to SUMO Modifications in Response to Heat Shock. <i>Science Signaling</i> , 2009, 2, ra24.	5.1	426
121	High-throughput phosphoproteomics reveals in vivo insulin signaling dynamics. <i>Nature Biotechnology</i> , 2015, 33, 990-995.	20.8	422
122	Uncovering global SUMOylation signaling networks in a site-specific manner. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 927-936.	8.1	419
123	Is Proteomics the New Genomics?. <i>Cell</i> , 2007, 130, 395-398.	27.8	417
124	Mitotic Regulation of the APC Activator Proteins CDC20 and CDH1. <i>Molecular Biology of the Cell</i> , 2000, 11, 1555-1569.	2.5	414
125	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.	7.6	412
126	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. <i>Genome Biology</i> , 2007, 8, R250.	7.3	410



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127	The mitochondrial contact site complex, a determinant of mitochondrial architecture. <i>EMBO Journal</i> , 2011, 30, 4356-4370.	8.2	408
128	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.	5.9	404
129	Mass spectrometric-based approaches in quantitative proteomics. <i>Methods</i> , 2003, 29, 124-130.	3.9	403
130	A Dual Pressure Linear Ion Trap Orbitrap Instrument with Very High Sequencing Speed. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2759-2769.	3.9	403
131	System-Wide Temporal Characterization of the Proteome and Phosphoproteome of Human Embryonic Stem Cell Differentiation. <i>Science Signaling</i> , 2011, 4, rs3.	5.1	398
132	Global analysis of genome, transcriptome and proteome reveals the response to aneuploidy in human cells. <i>Molecular Systems Biology</i> , 2012, 8, 608.	7.5	398
133	The Mex67p-mediated nuclear mRNA export pathway is conserved from yeast to human. <i>EMBO Journal</i> , 1999, 18, 2593-2609.	8.2	396
134	Precision proteomics: The case for high resolution and high mass accuracy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18132-18138.	7.6	394
135	In-depth analysis of the membrane and cytosolic proteome of red blood cells. <i>Blood</i> , 2006, 108, 791-801.	1.4	392
136	Phosphoproteome Analysis of <i>E. coli</i> Reveals Evolutionary Conservation of Bacterial Ser/Thr/Tyr Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 299-307.	3.9	392
137	$\beta$ 1- and $\beta$ v-class integrins cooperate to regulate myosin <sup>II</sup> during rigidity sensing of fibronectin-based microenvironments. <i>Nature Cell Biology</i> , 2013, 15, 625-636.	10.0	392
138	Global and Site-Specific Quantitative Phosphoproteomics: Principles and Applications. <i>Annual Review of Pharmacology and Toxicology</i> , 2009, 49, 199-221.	9.6	385
139	Identification of Proteins in the Postsynaptic Density Fraction by Mass Spectrometry. <i>Journal of Neuroscience</i> , 2000, 20, 4069-4080.	3.8	380
140	Systematic proteomic analysis of LRRK2-mediated Rab GTPase phosphorylation establishes a connection to ciliogenesis. <i>ELife</i> , 2017, 6, .	5.9	374
141	The Methylosome, a 20S Complex Containing JBP1 and pICln, Produces Dimethylarginine-Modified Sm Proteins. <i>Molecular and Cellular Biology</i> , 2001, 21, 8289-8300.	2.5	370
142	PHOSIDA 2011: the posttranslational modification database. <i>Nucleic Acids Research</i> , 2011, 39, D253-D260.	14.0	366
143	In-Vivo Quantitative Proteomics Reveals a Key Contribution of Post-Transcriptional Mechanisms to the Circadian Regulation of Liver Metabolism. <i>PLoS Genetics</i> , 2014, 10, e1004047.	3.4	366
144	The Serine/Threonine/Tyrosine Phosphoproteome of the Model Bacterium <i>Bacillus subtilis</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 697-707.	3.9	361

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145	Chromatin-Remodeling Components of the BAF Complex Facilitate Reprogramming. <i>Cell</i> , 2010, 141, 943-955.	27.8	360
146	Requirement of ATM-Dependent Monoubiquitylation of Histone H2B for Timely Repair of DNA Double-Strand Breaks. <i>Molecular Cell</i> , 2011, 41, 529-542.	9.6	358
147	System-wide Perturbation Analysis with Nearly Complete Coverage of the Yeast Proteome by Single-shot Ultra HPLC Runs on a Bench Top Orbitrap. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013722.	3.9	357
148	A Mass Spectrometry-based Proteomic Approach for Identification of Serine/Threonine-phosphorylated Proteins by Enrichment with Phospho-specific Antibodies. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 517-527.	3.9	356
149	Proteomic Analysis of the Arabidopsis Nucleolus Suggests Novel Nucleolar Functions. <i>Molecular Biology of the Cell</i> , 2005, 16, 260-269.	2.5	355
150	Identification of 491 proteins in the tear fluid proteome reveals a large number of proteases and protease inhibitors. <i>Genome Biology</i> , 2006, 7, R72.	7.3	354
151	ERCC1/XPF Removes the 3' Overhang from Uncapped Telomeres and Represses Formation of Telomeric DNA-Containing Double Minute Chromosomes. <i>Molecular Cell</i> , 2003, 12, 1489-1498.	9.6	352
152	Mass spectrometry-based proteomics in cell biology. <i>Journal of Cell Biology</i> , 2010, 190, 491-500.	5.2	352
153	Pre-mRNA splicing and mRNA export linked by direct interactions between UAP56 and Aly. <i>Nature</i> , 2001, 413, 644-647.	36.2	348
154	Observation of the diphoton decay of the Higgs boson and measurement of its properties. <i>European Physical Journal C</i> , 2014, 74, 3076.	4.0	348
155	Proteome Analysis of Separated Male and Female Gametocytes Reveals Novel Sex-Specific Plasmodium Biology. <i>Cell</i> , 2005, 121, 675-687.	27.8	345
156	A Systematic Mammalian Genetic Interaction Map Reveals Pathways Underlying Ricin Susceptibility. <i>Cell</i> , 2013, 152, 909-922.	27.8	340
157	Microcolumns with self-assembled particle frits for proteomics. <i>Journal of Chromatography A</i> , 2002, 979, 233-239.	3.8	334
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