

Karl Mechtler

List of Publications by Year in descending order

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215
papers

30,076
citations

8180

76
h-index

5255

165
g-index

251
all docs

251
docs citations

251
times ranked

30501
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulation of chromatin structure by site-specific histone H3 methyltransferases. <i>Nature</i> , 2000, 406, 593-599.	27.8	2,497
2	Methylation of histone H3 lysine 9 creates a binding site for HP1 proteins. <i>Nature</i> , 2001, 410, 116-120.	27.8	2,481
3	Loss of the Suv39h Histone Methyltransferases Impairs Mammalian Heterochromatin and Genome Stability. <i>Cell</i> , 2001, 107, 323-337.	28.9	1,552
4	Partitioning and Plasticity of Repressive Histone Methylation States in Mammalian Chromatin. <i>Molecular Cell</i> , 2003, 12, 1577-1589.	9.7	1,010
5	Reversal of H3K9me2 by a Small-Molecule Inhibitor for the G9a Histone Methyltransferase. <i>Molecular Cell</i> , 2007, 25, 473-481.	9.7	770
6	Universal and Confident Phosphorylation Site Localization Using phosphoRS. <i>Journal of Proteome Research</i> , 2011, 10, 5354-5362.	3.7	732
7	Activation of the Complement System by Synthetic DNA Complexes: A Potential Barrier for Intravenous Gene Delivery. <i>Human Gene Therapy</i> , 1996, 7, 1437-1446.	2.7	572
8	BAC TransgeneOmics: a high-throughput method for exploration of protein function in mammals. <i>Nature Methods</i> , 2008, 5, 409-415.	19.0	568
9	The size of DNA/transferrin-PEI complexes is an important factor for gene expression in cultured cells. <i>Gene Therapy</i> , 1998, 5, 1425-1433.	4.5	562
10	Wapl Controls the Dynamic Association of Cohesin with Chromatin. <i>Cell</i> , 2006, 127, 955-967.	28.9	550
11	The Par complex directs asymmetric cell division by phosphorylating the cytoskeletal protein Lgl. <i>Nature</i> , 2003, 422, 326-330.	27.8	509
12	Coupling of adenovirus to transferrin-polylysine/DNA complexes greatly enhances receptor-mediated gene delivery and expression of transfected genes.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 6099-6103.	7.1	478
13	Asymmetric Segregation of the Tumor Suppressor Brat Regulates Self-Renewal in <i>Drosophila</i> Neural Stem Cells. <i>Cell</i> , 2006, 124, 1241-1253.	28.9	473
14	Systematic Analysis of Human Protein Complexes Identifies Chromosome Segregation Proteins. <i>Science</i> , 2010, 328, 593-599.	12.6	465
15	A Syd-1 homologue regulates pre- and postsynaptic maturation in <i>Drosophila</i> . <i>Journal of Cell Biology</i> , 2010, 188, 565-579.	5.2	427
16	Protein phosphatase 2A protects centromeric sister chromatid cohesion during meiosis I. <i>Nature</i> , 2006, 441, 53-61.	27.8	419
17	MS Amanda, a Universal Identification Algorithm Optimized for High Accuracy Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2014, 13, 3679-3684.	3.7	416
18	Dissociation of Cohesin from Chromosome Arms and Loss of Arm Cohesion during Early Mitosis Depends on Phosphorylation of SA2. <i>PLoS Biology</i> , 2005, 3, e69.	5.6	382

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19	Phosphorylation of the Cohesin Subunit Scc1 by Polo/Cdc5 Kinase Regulates Sister Chromatid Separation in Yeast. <i>Cell</i> , 2001, 105, 459-472.	28.9	358
20	Recruitment of PRC1 function at the initiation of X inactivation independent of PRC2 and silencing. <i>EMBO Journal</i> , 2006, 25, 3110-3122.	7.8	353
21	Mitotic regulation of the human anaphase-promoting complex by phosphorylation. <i>EMBO Journal</i> , 2003, 22, 6598-6609.	7.8	344
22	Transferrin-polycation-mediated introduction of DNA into human leukemic cells: stimulation by agents that affect the survival of transfected DNA or modulate transferrin receptor levels.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 4033-4037.	7.1	337
23	Gene transfer into hepatocytes using asialoglycoprotein receptor mediated endocytosis of DNA complexed with an artificial tetra-antennary galactose ligand. <i>Bioconjugate Chemistry</i> , 1992, 3, 533-539.	3.6	334
24	Sororin Mediates Sister Chromatid Cohesion by Antagonizing Wapl. <i>Cell</i> , 2010, 143, 737-749.	28.9	325
25	Jmjd2b antagonizes H3K9 trimethylation at pericentric heterochromatin in mammalian cells. <i>Genes and Development</i> , 2006, 20, 1557-1562.	5.9	321
26	Live-cell imaging RNAi screen identifies PP2A ^{B55} and importin- β 1 as key mitotic exit regulators in human cells. <i>Nature Cell Biology</i> , 2010, 12, 886-893.	10.3	315
27	Building Sister Chromatid Cohesion: Smc3 Acetylation Counteracts an Antiestablishment Activity. <i>Molecular Cell</i> , 2009, 33, 763-774.	9.7	294
28	ATP Hydrolysis Is Required for Cohesin's Association with Chromosomes. <i>Current Biology</i> , 2003, 13, 1941-1953.	3.9	254
29	Aurora A phosphorylation of TACC3/maskin is required for centrosome-dependent microtubule assembly in mitosis. <i>Journal of Cell Biology</i> , 2005, 170, 1047-1055.	5.2	248
30	An in vivo RNAi assay identifies major genetic and cellular requirements for primary piRNA biogenesis in <i>Drosophila</i> . <i>EMBO Journal</i> , 2010, 29, 3301-3317.	7.8	242
31	Eco1 Is a Novel Acetyltransferase that Can Acetylate Proteins Involved in Cohesion. <i>Current Biology</i> , 2002, 12, 323-328.	3.9	228
32	Sororin Is Required for Stable Binding of Cohesin to Chromatin and for Sister Chromatid Cohesion in Interphase. <i>Current Biology</i> , 2007, 17, 630-636.	3.9	222
33	Mei-P26 regulates microRNAs and cell growth in the <i>Drosophila</i> ovarian stem cell lineage. <i>Nature</i> , 2008, 454, 241-245.	27.8	222
34	HSPC117 Is the Essential Subunit of a Human tRNA Splicing Ligase Complex. <i>Science</i> , 2011, 331, 760-764.	12.6	215
35	Quantitative Phosphoproteomics of the Ataxia Telangiectasia-Mutated (ATM) and Ataxia Telangiectasia-Mutated and Rad3-related (ATR) Dependent DNA Damage Response in <i>Arabidopsis thaliana</i> *. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 556-571.	3.8	199
36	Structure of the Anaphase-Promoting Complex/Cyclosome Interacting with a Mitotic Checkpoint Complex. <i>Science</i> , 2009, 323, 1477-1481.	12.6	195

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37	Rec8 Phosphorylation by Casein Kinase 1 and Cdc7-Dbf4 Kinase Regulates Cohesin Cleavage by Separase during Meiosis. <i>Developmental Cell</i> , 2010, 18, 397-409.	7.0	192
38	Inter-Homolog Crossing-Over and Synapsis in Arabidopsis Meiosis Are Dependent on the Chromosome Axis Protein AtASY3. <i>PLoS Genetics</i> , 2012, 8, e1002507.	3.5	170
39	Monopolar Attachment of Sister Kinetochores at Meiosis I Requires Casein Kinase 1. <i>Cell</i> , 2006, 126, 1049-1064.	28.9	168
40	Peptide Labeling with Isobaric Tags Yields Higher Identification Rates Using iTRAQ 4-Plex Compared to TMT 6-Plex and iTRAQ 8-Plex on LTQ Orbitrap. <i>Analytical Chemistry</i> , 2010, 82, 6549-6558.	6.5	168
41	CENP-T proteins are conserved centromere receptors of the Ndc80 complex. <i>Nature Cell Biology</i> , 2012, 14, 604-613.	10.3	168
42	Arginine phosphorylation marks proteins for degradation by a Clp protease. <i>Nature</i> , 2016, 539, 48-53.	27.8	168
43	A systematic analysis of <i>Drosophila</i> TUDOR domain-containing proteins identifies Vreteno and the Tdrd12 family as essential primary piRNA pathway factors. <i>EMBO Journal</i> , 2011, 30, 3977-3993.	7.8	163
44	High Precision Quantitative Proteomics Using iTRAQ on an LTQ Orbitrap: A New Mass Spectrometric Method Combining the Benefits of All. <i>Journal of Proteome Research</i> , 2009, 8, 4743-4752.	3.7	158
45	Spatial Exclusivity Combined with Positive and Negative Selection of Phosphorylation Motifs Is the Basis for Context-Dependent Mitotic Signaling. <i>Science Signaling</i> , 2011, 4, ra42.	3.6	155
46	McsB Is a Protein Arginine Kinase That Phosphorylates and Inhibits the Heat-Shock Regulator CtsR. <i>Science</i> , 2009, 324, 1323-1327.	12.6	151
47	Charting the molecular network of the drug target Bcr-Abl. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7414-7419.	7.1	146
48	Unambiguous Phosphosite Localization using Electron-Transfer/Higher-Energy Collision Dissociation (EThcD). <i>Journal of Proteome Research</i> , 2013, 12, 1520-1525.	3.7	145
49	14-3-3 Proteins recognize a histone code at histone H3 and are required for transcriptional activation. <i>EMBO Journal</i> , 2008, 27, 88-99.	7.8	144
50	DNA-binding transferrin conjugates as functional gene-delivery agents: synthesis by linkage of polylysine or ethidium homodimer to the transferrin carbohydrate moiety. <i>Bioconjugate Chemistry</i> , 1991, 2, 226-231.	3.6	140
51	A cross-kingdom conserved ER-phagy receptor maintains endoplasmic reticulum homeostasis during stress. <i>ELife</i> , 2020, 9, .	6.0	139
52	Aurora B and Cdk1 mediate Wapl activation and release of acetylated cohesin from chromosomes by phosphorylating Sororin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13404-13409.	7.1	129
53	A structural basis for kinetochore recruitment of the Ndc80 complex via two distinct centromere receptors. <i>EMBO Journal</i> , 2013, 32, 409-423.	7.8	128
54	Ultra-High-Pressure RPLC Hyphenated to an LTQ-Orbitrap Velos Reveals a Linear Relation between Peak Capacity and Number of Identified Peptides. <i>Analytical Chemistry</i> , 2011, 83, 2699-2704.	6.5	126

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55	Phosphoproteomics strategies for the functional analysis of signal transduction. <i>Proteomics</i> , 2006, 6, 4047-4056.	2.2	124
56	Polysialylation controls dendritic cell trafficking by regulating chemokine recognition. <i>Science</i> , 2016, 351, 186-190.	12.6	123
57	General Statistical Modeling of Data from Protein Relative Expression Isobaric Tags. <i>Journal of Proteome Research</i> , 2011, 10, 2758-2766.	3.7	120
58	Topology and Organization of the Salmonella typhimurium Type III Secretion Needle Complex Components. <i>PLoS Pathogens</i> , 2010, 6, e1000824.	4.7	119
59	Interplay of PDZ and protease domain of DegP ensures efficient elimination of misfolded proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7702-7707.	7.1	118
60	APC15 mediates CDC20 autoubiquitylation by APC/CMCC and disassembly of the mitotic checkpoint complex. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1116-1123.	8.2	118
61	ESCO1 and CTCF enable formation of long chromatin loops by protecting cohesinSTAG1 from WAPL. <i>ELife</i> , 2020, 9, .	6.0	116
62	Receptor-Mediated Gene Transfer into Human T Lymphocytes via Binding of DNA/CD3 Antibody Particles to the CD3 T Cell Receptor Complex. <i>Human Gene Therapy</i> , 1995, 6, 753-761.	2.7	114
63	Mechanism of APC/C ^{CDC20} activation by mitotic phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2570-8.	7.1	112
64	Comparative glycoproteomics of stem cells identifies new players in ricin toxicity. <i>Nature</i> , 2017, 549, 538-542.	27.8	110
65	Phosphoregulation of the budding yeast EB1 homologue Bim1p by Aurora/Ipl1p. <i>Journal of Cell Biology</i> , 2009, 186, 379-391.	5.2	109
66	Titanium dioxide as a chemo-affinity solid phase in offline phosphopeptide chromatography prior to HPLC-MS/MS analysis. <i>Nature Protocols</i> , 2007, 2, 1059-1069.	12.0	108
67	Analysis of protein mixtures from whole-cell extracts by single-run nanoLC-MS/MS using ultralong gradients. <i>Nature Protocols</i> , 2012, 7, 882-890.	12.0	106
68	Quantitative Phosphoproteomics Reveals the Role of Protein Arginine Phosphorylation in the Bacterial Stress Response. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 537-550.	3.8	103
69	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	6.5	100
70	Spatial organization of a ubiquitous eukaryotic kinetochore protein network in Drosophila chromosomes. <i>Chromosoma</i> , 2007, 116, 385-402.	2.2	99
71	A cooperative mechanism drives budding yeast kinetochore assembly downstream of CENP-A. <i>Journal of Cell Biology</i> , 2014, 206, 509-524.	5.2	99
72	Afamin Is a Novel Human Vitamin E-Binding Glycoprotein Characterization and In Vitro Expression. <i>Journal of Proteome Research</i> , 2005, 4, 889-899.	3.7	97

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73	Arabidopsis PCH2 Mediates Meiotic Chromosome Remodeling and Maturation of Crossovers. <i>PLoS Genetics</i> , 2015, 11, e1005372.	3.5	97
74	Lymphatic Microvessels in the Rat Remnant Kidney Model of Renal Fibrosis. <i>Journal of the American Society of Nephrology: JASN</i> , 2003, 14, 1981-1989.	6.1	93
75	Generation and Characterization of Methyl-Lysine Histone Antibodies. <i>Methods in Enzymology</i> , 2003, 376, 234-254.	1.0	90
76	Raman microspectroscopy reveals long-term extracellular activity of chlamydiae. <i>Molecular Microbiology</i> , 2010, 77, 687-700.	2.5	89
77	Systematic Phosphorylation Analysis of Human Mitotic Protein Complexes. <i>Science Signaling</i> , 2011, 4, rs12.	3.6	87
78	Drosophila CPEB Orb2A Mediates Memory Independent of Its RNA-Binding Domain. <i>Neuron</i> , 2012, 76, 383-395.	8.1	86
79	Identification of a Subunit of a Novel Kleisin- β^2 /SMC Complex as a Potential Substrate of Protein Phosphatase 2A. <i>Current Biology</i> , 2003, 13, 2058-2064.	3.9	84
80	Casein kinase 1 is required for efficient removal of Rec8 during meiosis I. <i>Cell Cycle</i> , 2010, 9, 2657-2662.	2.6	83
81	Influence of Membrane-Active Peptides on Lipospermine/DNA Complex Mediated Gene Transfer. <i>Bioconjugate Chemistry</i> , 1997, 8, 213-221.	3.6	82
82	AMPK leads to phosphorylation of the transcription factor Nrf2, tuning transactivation of selected target genes. <i>Redox Biology</i> , 2020, 29, 101393.	9.0	80
83	Absolute quantification of cohesin, CTCF and their regulators in human cells. <i>ELife</i> , 2019, 8, .	6.0	79
84	Regulation of Gene Expression through a Transcriptional Repressor that Senses Acyl-Chain Length in Membrane Phospholipids. <i>Developmental Cell</i> , 2014, 29, 729-739.	7.0	78
85	The nascent RNA binding complex SFINX licenses piRNA-guided heterochromatin formation. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 720-731.	8.2	75
86	The AAA-ATPase molecular chaperone Cdc48/p97 disassembles sumoylated centromeres, decondenses heterochromatin, and activates ribosomal RNA genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16166-16171.	7.1	74
87	Preventing Carryover of Peptides and Proteins in Nano LC-MS Separations. <i>Analytical Chemistry</i> , 2009, 81, 5955-5960.	6.5	73
88	Anion-Exchange Chromatography of Phosphopeptides: Weak Anion Exchange versus Strong Anion Exchange and Anion-Exchange Chromatography versus Electrostatic Repulsion-Hydrophilic Interaction Chromatography. <i>Analytical Chemistry</i> , 2015, 87, 4704-4711.	6.5	73
89	Isotope-labeled cross-linkers and fourier transform ion cyclotron resonance mass spectrometry for structural analysis of a protein/peptide complex. <i>Journal of the American Society for Mass Spectrometry</i> , 2006, 17, 1100-1113.	2.8	72
90	Chemical Cross-Linking and High-Performance Fourier Transform Ion Cyclotron Resonance Mass Spectrometry for Protein Interaction Analysis: Application to a Calmodulin/Target Peptide Complex. <i>Analytical Chemistry</i> , 2005, 77, 495-503.	6.5	70

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91	HPLC techniques for proteomics analysis—a short overview of latest developments. <i>Briefings in Functional Genomics & Proteomics</i> , 2006, 5, 249-260.	3.8	65
92	An improved method for tracking and reducing the void volume in nano HPLC-MS with micro trapping columns. <i>Analytical and Bioanalytical Chemistry</i> , 2003, 376, 946-951.	3.7	64
93	Probing the Phosphoproteome of HeLa Cells Using Nanocast Metal Oxide Microspheres for Phosphopeptide Enrichment. <i>Analytical Chemistry</i> , 2010, 82, 2726-2733.	6.5	63
94	A synthetic peptide library for benchmarking crosslinking-mass spectrometry search engines for proteins and protein complexes. <i>Nature Communications</i> , 2020, 11, 742.	12.8	62
95	Quantitative Phospho-proteomics to Investigate the Polo-like Kinase 1-Dependent Phospho-proteome. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.008540.	3.8	61
96	apQuant: Accurate Label-Free Quantification by Quality Filtering. <i>Journal of Proteome Research</i> , 2019, 18, 535-541.	3.7	61
97	MTHFD1 interaction with BRD4 links folate metabolism to transcriptional regulation. <i>Nature Genetics</i> , 2019, 51, 990-998.	21.4	61
98	Glycerol and Polylysine Synergize in Their Ability to Rupture Vesicular Membranes: A Mechanism for Increased Transferrin- α -Polylysine-Mediated Gene Transfer. <i>Experimental Cell Research</i> , 1997, 232, 137-145.	2.6	58
99	CCAN Assembly Configures Composite Binding Interfaces to Promote Cross-Linking of Ndc80 Complexes at the Kinetochores. <i>Current Biology</i> , 2016, 26, 2370-2378.	3.9	58
100	Tandem affinity purification of functional TAP-tagged proteins from human cells. <i>Nature Protocols</i> , 2007, 2, 1145-1151.	12.0	57
101	A DEK Domain-Containing Protein Modulates Chromatin Structure and Function in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 4328-4344.	6.6	57
102	CharmRT: Boosting Peptide Identifications by Chimeric Spectra Identification and Retention Time Prediction. <i>Journal of Proteome Research</i> , 2018, 17, 2581-2589.	3.7	57
103	Improved Sensitivity in Low-Input Proteomics Using Micropillar Array-Based Chromatography. <i>Analytical Chemistry</i> , 2019, 91, 14203-14207.	6.5	57
104	Automated, on-line two-dimensional nano liquid chromatography tandem mass spectrometry for rapid analysis of complex protein digests. <i>Proteomics</i> , 2004, 4, 2545-2557.	2.2	56
105	Structural prediction of protein models using distance restraints derived from cross-linking mass spectrometry data. <i>Nature Protocols</i> , 2018, 13, 478-494.	12.0	56
106	Optimized Fragmentation Improves the Identification of Peptides Cross-Linked by MS-Cleavable Reagents. <i>Journal of Proteome Research</i> , 2019, 18, 1363-1370.	3.7	55
107	Cleavable Cross-Linkers and Mass Spectrometry for the Ultimate Task of Profiling Protein-Protein Interaction Networks <i>in Vivo</i> . <i>Journal of Proteome Research</i> , 2021, 20, 78-93.	3.7	55
108	AKIRIN2 controls the nuclear import of proteasomes in vertebrates. <i>Nature</i> , 2021, 599, 491-496.	27.8	55

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109	Cell-free tumor antigen peptide-based cancer vaccines. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 3262-3267.	7.1	52
110	Laser microsurgery provides evidence for merotelic kinetochore attachments in fission yeast cells lacking Pcs1 or Clr4. Cell Cycle, 2010, 9, 3997-4004.	2.6	52
111	Improved Precision of iTRAQ and TMT Quantification by an Axial Extraction Field in an Orbitrap HCD Cell. Analytical Chemistry, 2011, 83, 1469-1474.	6.5	52
112	Chasing Phosphoarginine Proteins: Development of a Selective Enrichment Method Using a Phosphatase Trap. Molecular and Cellular Proteomics, 2014, 13, 1953-1964.	3.8	52
113	Transloading of tumor antigen-derived peptides into antigen-presenting cells. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 3256-3261.	7.1	51
114	Affinity proteomics reveals extensive phosphorylation of the Brassica chromosome axis protein <i>ASY1</i> and a network of associated proteins at prophase I of meiosis. Plant Journal, 2018, 93, 17-33.	5.7	51
115	Autophagy mediates temporary reprogramming and dedifferentiation in plant somatic cells. EMBO Journal, 2020, 39, e103315.	7.8	51
116	Molecular basis for cytoplasmic <i>RNA</i> surveillance by uridylation-triggered decay in <i>Drosophila</i> . EMBO Journal, 2016, 35, 2417-2434.	7.8	50
117	The replicative helicase MCM recruits cohesin acetyltransferase ESCO2 to mediate centromeric sister chromatid cohesion. EMBO Journal, 2018, 37, .	7.8	50
118	The biophysical, molecular, and anatomical landscape of pigeon CRY4: A candidate light-based quantal magnetosensor. Science Advances, 2020, 6, eabb9110.	10.3	50
119	Peptide Orientation Affects Selectivity in Ion-Exchange Chromatography. Analytical Chemistry, 2010, 82, 5253-5259.	6.5	49
120	Jagunal homolog 1 is a critical regulator of neutrophil function in fungal host defense. Nature Genetics, 2014, 46, 1028-1033.	21.4	49
121	H3S28 phosphorylation is a hallmark of the transcriptional response to cellular stress. Genome Research, 2014, 24, 1808-1820.	5.5	49
122	Ultrasensitive NanoLC-MS of Subnanogram Protein Samples Using Second Generation Micropillar Array LC Technology with Orbitrap Exploris 480 and FAIMS PRO. Analytical Chemistry, 2021, 93, 8704-8710.	6.5	49
123	Differential cofactor dependencies define distinct types of human enhancers. Nature, 2022, 606, 406-413.	27.8	49
124	A Dam1-based artificial kinetochore is sufficient to promote chromosome segregation in budding yeast. Nature Cell Biology, 2009, 11, 1109-1115.	10.3	48
125	N-terminal \hat{I}^2 -strand underpins biochemical specialization of an ATG8 isoform. PLoS Biology, 2019, 17, e3000373.	5.6	47
126	The 20S proteasome isolated from Alzheimer's disease brain shows post-translational modifications but unchanged proteolytic activity. Journal of Neurochemistry, 2007, 101, 1483-1490.	3.9	46

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127	Stoichiometry Determination of the MP1â”p14 Complex Using a Novel and Cost-Efficient Method To Produce an Equimolar Mixture of Standard Peptides. <i>Analytical Chemistry</i> , 2009, 81, 10254-10261.	6.5	46
128	SIMPATIQCO: A Server-Based Software Suite Which Facilitates Monitoring the Time Course of LCâ”MS Performance Metrics on Orbitrap Instruments. <i>Journal of Proteome Research</i> , 2012, 11, 5540-5547.	3.7	45
129	Casein Kinase 1 and Phosphorylation of Cohesin Subunit Rec11 (SA3) Promote Meiotic Recombination through Linear Element Formation. <i>PLoS Genetics</i> , 2015, 11, e1005225.	3.5	45
130	Phosphoproteomics with Activated Ion Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2017, 89, 6367-6376.	6.5	44
131	Carbohydrate receptor-mediated gene transfer to human T leukaemic cells. <i>Glycobiology</i> , 1994, 4, 429-435.	2.5	43
132	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	3.8	42
133	The rise of singleâ”cell proteomics. <i>Analytical Science Advances</i> , 2021, 2, 84-94.	2.8	41
134	<scp>LSD</scp>1 inhibition induces differentiation and cell death in Merkel cell carcinoma. <i>EMBO Molecular Medicine</i> , 2020, 12, e12525.	6.9	41
135	Transcriptome and proteome quantification of a tumor model provides novel insights into postâ”transcriptional gene regulation. <i>Genome Biology</i> , 2013, 14, r133.	9.6	40
136	Annexin A2/P11 interaction: New insights into annexin A2 tetramer structure by chemical crosslinking, highâ”resolution mass spectrometry, and computational modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 254-269.	2.6	39
137	Optimized Nonlinear Gradients for Reversed-Phase Liquid Chromatography in Shotgun Proteomics. <i>Analytical Chemistry</i> , 2013, 85, 7777-7785.	6.5	39
138	The linear ubiquitin chain assembly complex (LUBAC) generates heterotypic ubiquitin chains. <i>ELife</i> , 2021, 10, .	6.0	38
139	MASPECTRAS: a platform for management and analysis of proteomics LC-MS/MS data. <i>BMC Bioinformatics</i> , 2007, 8, 197.	2.6	37
140	Enhanced detection and identification of multiply phosphorylated peptides using TiO₂ enrichment in combination with MALDI TOF/TOF MS. <i>Proteomics</i> , 2008, 8, 4577-4592.	2.2	37
141	The H3 histone chaperone NASP^{SIM3} escorts CenH3 in Arabidopsis. <i>Plant Journal</i> , 2020, 101, 71-86.	5.7	37
142	Studying the fragmentation behavior of peptides with arginine phosphorylation and its influence on phosphoâ”site localization. <i>Proteomics</i> , 2013, 13, 945-954.	2.2	36
143	Comprehensive Cross-Linking Mass Spectrometry Reveals Parallel Orientation and Flexible Conformations of Plant HOP2â”MND1. <i>Journal of Proteome Research</i> , 2015, 14, 5048-5062.	3.7	36
144	Structure of McsB, a protein kinase for regulated arginine phosphorylation. <i>Nature Chemical Biology</i> , 2019, 15, 510-518.	8.0	36

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145	Cleaning of raw peptide MS/MS spectra: Improved protein identification following deconvolution of multiply charged peaks, isotope clusters, and removal of background noise. <i>Proteomics</i> , 2006, 6, 5117-5131.	2.2	35
146	Quality control in LC-MS/MS. <i>Proteomics</i> , 2011, 11, 1026-1030.	2.2	35
147	A Chemical Proteomics Approach to Phosphatidylinositol 3-Kinase Signaling in Macrophages. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1829-1841.	3.8	34
148	Linear ubiquitination by LUBEL has a role in <i>Drosophila</i> heat stress response. <i>EMBO Reports</i> , 2016, 17, 1624-1640.	4.5	34
149	An improved strategy for tandem affinity purification tagging of <i>Schizosaccharomyces pombe</i> genes. <i>Proteomics</i> , 2009, 9, 4825-4828.	2.2	33
150	SIRT2 regulates nuclear envelope reassembly via ANKLE2 deacetylation. <i>Journal of Cell Science</i> , 2016, 129, 4607-4621.	2.0	32
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