

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

227 papers	38,043 citations	83 h-index	194 g-index
247 ext. papers	44,264 ext. citations	11.8 avg, IF	7.17 L-index

#	Paper	IF	Citations
227	In-gel digestion for mass spectrometric characterization of proteins and proteomes. <i>Nature Protocols</i> , 2006 , 1, 2856-60	18.8	3440
226	Andromeda: a peptide search engine integrated into the MaxQuant environment. <i>Journal of Proteome Research</i> , 2011 , 10, 1794-805	5.6	3402
225	Lysine acetylation targets protein complexes and co-regulates major cellular functions. <i>Science</i> , 2009 , 325, 834-40	33.3	3316
224	Global, in vivo, and site-specific phosphorylation dynamics in signaling networks. <i>Cell</i> , 2006 , 127, 635-48	56.2	2797
223	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, 2010-21	7.6	1233
222	Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. <i>Science Signaling</i> , 2010 , 3, ra3	8.8	1106
221	Trypsin cleaves exclusively C-terminal to arginine and lysine residues. <i>Molecular and Cellular Proteomics</i> , 2004 , 3, 608-14	7.6	804
220	Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast. <i>Nature</i> , 2008 , 455, 1251-4	50.4	745
219	Integrated analysis of protein composition, tissue diversity, and gene regulation in mouse mitochondria. <i>Cell</i> , 2003 , 115, 629-40	56.2	742
218	Higher-energy C-trap dissociation for peptide modification analysis. <i>Nature Methods</i> , 2007 , 4, 709-12	21.6	727
217	Quantitative phosphoproteomics applied to the yeast pheromone signaling pathway. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 310-27	7.6	665
216	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. <i>Nature Protocols</i> , 2009 , 4, 698-705	18.8	637
215	Quantitative interaction proteomics and genome-wide profiling of epigenetic histone marks and their readers. <i>Cell</i> , 2010 , 142, 967-80	56.2	579
214	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013 , 499, 74-8	50.4	563
213	The human urinary proteome contains more than 1500 proteins, including a large proportion of membrane proteins. <i>Genome Biology</i> , 2006 , 7, R80	18.3	514
212	Kinase-selective enrichment enables quantitative phosphoproteomics of the kinome across the cell cycle. <i>Molecular Cell</i> , 2008 , 31, 438-48	17.6	495
211	Status of large-scale analysis of post-translational modifications by mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 3444-52	7.6	406

210	Proteomic analysis of lysine acetylation sites in rat tissues reveals organ specificity and subcellular patterns. <i>Cell Reports</i> , 2012 , 2, 419-31	10.6	405
209	A dual pressure linear ion trap Orbitrap instrument with very high sequencing speed. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 2759-69	7.6	379
208	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. <i>Genome Biology</i> , 2007 , 8, R250	18.3	376
207	Pathogens and host immunity in the ancient human oral cavity. <i>Nature Genetics</i> , 2014 , 46, 336-44	36.3	353
206	Global and site-specific quantitative phosphoproteomics: principles and applications. <i>Annual Review of Pharmacology and Toxicology</i> , 2009 , 49, 199-221	17.9	350
205	System-wide temporal characterization of the proteome and phosphoproteome of human embryonic stem cell differentiation. <i>Science Signaling</i> , 2011 , 4, rs3	8.8	347
204	Phosphoproteome analysis of E. coli reveals evolutionary conservation of bacterial Ser/Thr/Tyr phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 299-307	7.6	334
203	Electron capture dissociation of singly and multiply phosphorylated peptides. <i>Rapid Communications in Mass Spectrometry</i> , 2000 , 14, 1793-800	2.2	325
202	The serine/threonine/tyrosine phosphoproteome of the model bacterium <i>Bacillus subtilis</i> . <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 697-707	7.6	309
201	Improved peptide identification in proteomics by two consecutive stages of mass spectrometric fragmentation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 13417-22	11.5	288
200	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. <i>Cell Systems</i> , 2017 , 4, 587-599.e4	10.6	255
199	Quantitative maps of protein phosphorylation sites across 14 different rat organs and tissues. <i>Nature Communications</i> , 2012 , 3, 876	17.4	248
198	Mislocalized activation of oncogenic RTKs switches downstream signaling outcomes. <i>Molecular Cell</i> , 2009 , 36, 326-39	17.6	245
197	Proteomic investigations reveal a role for RNA processing factor THRAP3 in the DNA damage response. <i>Molecular Cell</i> , 2012 , 46, 212-25	17.6	239
196	Large-scale proteomics analysis of the human kinome. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 1751-64	17.6	236
195	A major lineage of enteroendocrine cells coexpress CCK, secretin, GIP, GLP-1, PYY, and neurotensin but not somatostatin. <i>Endocrinology</i> , 2012 , 153, 5782-95	4.8	231
194	MSQuant, an open source platform for mass spectrometry-based quantitative proteomics. <i>Journal of Proteome Research</i> , 2010 , 9, 393-403	5.6	225
193	Status of complete proteome analysis by mass spectrometry: SILAC labeled yeast as a model system. <i>Genome Biology</i> , 2006 , 7, R50	18.3	224

192	Optimized fast and sensitive acquisition methods for shotgun proteomics on a quadrupole orbitrap mass spectrometer. <i>Journal of Proteome Research</i> , 2012 , 11, 3487-97	5.6	221
191	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013 , 45, 621-31	36.3	219
190	Proteomic analyses reveal divergent ubiquitylation site patterns in murine tissues. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1578-85	7.6	214
189	Ancient proteins resolve the evolutionary history of Darwin's South American ungulates. <i>Nature</i> , 2015 , 522, 81-4	50.4	210
188	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014 , 345, 1255832	33.3	204
187	Proteome-wide mapping of the <i>Drosophila</i> acetylome demonstrates a high degree of conservation of lysine acetylation. <i>Science Signaling</i> , 2011 , 4, ra48	8.8	204
186	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014 , 46, 826-36	36.3	199
185	Off-line high-pH reversed-phase fractionation for in-depth phosphoproteomics. <i>Journal of Proteome Research</i> , 2014 , 13, 6176-86	5.6	194
184	Immature truncated O-glycophenotype of cancer directly induces oncogenic features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E4066-75	11.5	185
183	UbiSite approach for comprehensive mapping of lysine and N-terminal ubiquitination sites. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 631-640	17.6	178
182	Ubc9 sumoylation regulates SUMO target discrimination. <i>Molecular Cell</i> , 2008 , 31, 371-82	17.6	169
181	Global effects of kinase inhibitors on signaling networks revealed by quantitative phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 2796-808	7.6	165
180	Top-down protein sequencing and MS3 on a hybrid linear quadrupole ion trap-orbitrap mass spectrometer. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 949-58	7.6	163
179	Proteomic analysis of the acid-soluble organic matrix of the chicken calcified eggshell layer. <i>Proteomics</i> , 2006 , 6, 3801-10	4.8	162
178	Noncovalent interaction between Ubc9 and SUMO promotes SUMO chain formation. <i>EMBO Journal</i> , 2007 , 26, 2797-807	13	160
177	Performance Evaluation of the Q Exactive HF-X for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018 , 17, 727-738	5.6	160
176	SUMO modification of the ubiquitin-conjugating enzyme E2-25K. <i>Nature Structural and Molecular Biology</i> , 2005 , 12, 264-9	17.6	158
175	Proteomic analysis of a pleistocene mammoth femur reveals more than one hundred ancient bone proteins. <i>Journal of Proteome Research</i> , 2012 , 11, 917-26	5.6	150

174	Benchmarking common quantification strategies for large-scale phosphoproteomics. <i>Nature Communications</i> , 2018 , 9, 1045	17.4	146
173	A Conserved Motif Provides Binding Specificity to the PP2A-B56 Phosphatase. <i>Molecular Cell</i> , 2016 , 63, 686-695	17.6	145
172	Proteomic mapping of brain plasma membrane proteins. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 402-406	17.6	141
171	Feasibility of large-scale phosphoproteomics with higher energy collisional dissociation fragmentation. <i>Journal of Proteome Research</i> , 2010 , 9, 6786-94	5.6	139
170	Rapid and deep proteomes by faster sequencing on a benchtop quadrupole ultra-high-field Orbitrap mass spectrometer. <i>Journal of Proteome Research</i> , 2014 , 13, 6187-95	5.6	134
169	A Novel LC System Embeds Analytes in Pre-formed Gradients for Rapid, Ultra-robust Proteomics. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2284-2296	7.6	133
168	Uncovering SUMOylation dynamics during cell-cycle progression reveals FoxM1 as a key mitotic SUMO target protein. <i>Molecular Cell</i> , 2014 , 53, 1053-66	17.6	132
167	In vivo phosphoproteomics analysis reveals the cardiac targets of β -adrenergic receptor signaling. <i>Science Signaling</i> , 2013 , 6, rs11	8.8	129
166	Pre-Clovis mastodon hunting 13,800 years ago at the Manis site, Washington. <i>Science</i> , 2011 , 334, 351-3	33.3	129
165	Direct evidence of milk consumption from ancient human dental calculus. <i>Scientific Reports</i> , 2014 , 4, 7104	4.9	125
164	Proteomics strategy for quantitative protein interaction profiling in cell extracts. <i>Nature Methods</i> , 2009 , 6, 741-4	21.6	121
163	Protein sequences bound to mineral surfaces persist into deep time. <i>ELife</i> , 2016 , 5,	8.9	118
162	Quantitative phosphoproteomics dissection of seven-transmembrane receptor signaling using full and biased agonists. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1540-53	7.6	115
161	The phosphoproteome of toll-like receptor-activated macrophages. <i>Molecular Systems Biology</i> , 2010 , 6, 371	12.2	113
160	A Compact Quadrupole-Orbitrap Mass Spectrometer with FAIMS Interface Improves Proteome Coverage in Short LC Gradients. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 716-729	7.6	112
159	Rapid and site-specific deep phosphoproteome profiling by data-independent acquisition without the need for spectral libraries. <i>Nature Communications</i> , 2020 , 11, 787	17.4	108
158	Global analysis of the yeast osmotic stress response by quantitative proteomics. <i>Molecular BioSystems</i> , 2009 , 5, 1337-46		108
157	Functional proteomics defines the molecular switch underlying FGF receptor trafficking and cellular outputs. <i>Molecular Cell</i> , 2013 , 51, 707-22	17.6	105

156	High-accuracy identification and bioinformatic analysis of in vivo protein phosphorylation sites in yeast. <i>Proteomics</i> , 2009 , 9, 4642-52	4.8	103
155	Quantitative proteomic assessment of very early cellular signaling events. <i>Nature Biotechnology</i> , 2007 , 25, 566-8	44.5	103
154	Advantages of external accumulation for electron capture dissociation in Fourier transform mass spectrometry. <i>Analytical Chemistry</i> , 2001 , 73, 2998-3005	7.8	101
153	Structures of Down syndrome kinases, DYRKs, reveal mechanisms of kinase activation and substrate recognition. <i>Structure</i> , 2013 , 21, 986-96	5.2	99
152	Phosphoproteins of the chicken eggshell calcified layer. <i>Proteomics</i> , 2007 , 7, 106-15	4.8	95
151	Investigation of protein-tyrosine phosphatase 1B function by quantitative proteomics. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1763-77	7.6	91
150	SUMO-2 Orchestrates Chromatin Modifiers in Response to DNA Damage. <i>Cell Reports</i> , 2015 , 10, 1778-1791	10.6	90
149	The SH2 domain interaction landscape. <i>Cell Reports</i> , 2013 , 3, 1293-305	10.6	89
148	Ubiquitin-SUMO circuitry controls activated fanconi anemia ID complex dosage in response to DNA damage. <i>Molecular Cell</i> , 2015 , 57, 150-64	17.6	89
147	Quantitative phosphoproteome analysis of a mouse liver cell line reveals specificity of phosphatase inhibitors. <i>Proteomics</i> , 2008 , 8, 4534-46	4.8	89
146	Phosphorylation of histone H3 Thr-45 is linked to apoptosis. <i>Journal of Biological Chemistry</i> , 2009 , 284, 16575-16583	5.4	85
145	Tyrosine phosphoproteomics of fibroblast growth factor signaling: a role for insulin receptor substrate-4. <i>Journal of Biological Chemistry</i> , 2004 , 279, 46438-47	5.4	84
144	Separation of the gluconeogenic and mitochondrial functions of PGC-1{alpha} through S6 kinase. <i>Genes and Development</i> , 2011 , 25, 1232-44	12.6	83
143	RNF4 is required for DNA double-strand break repair in vivo. <i>Cell Death and Differentiation</i> , 2013 , 20, 490-502	12.7	79
142	HysTag--a novel proteomic quantification tool applied to differential display analysis of membrane proteins from distinct areas of mouse brain. <i>Molecular and Cellular Proteomics</i> , 2004 , 3, 82-92	7.6	79
141	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 1435-1448	15.1	76
140	Functional characterization of Rad18 domains for Rad6, ubiquitin, DNA binding and PCNA modification. <i>Nucleic Acids Research</i> , 2007 , 35, 5819-30	20.1	76
139	GABA(A) receptors are high-affinity targets for G-hydroxybutyric acid (GHB). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 13404-9	11.5	72

138	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. <i>Nature</i> , 2019 , 574, 103-107	50.4	70
137	Protein Aggregation Capture on Microparticles Enables Multipurpose Proteomics Sample Preparation. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1027-1035	7.6	70
136	Profiling the phospho-status of the BKCa channel alpha subunit in rat brain reveals unexpected patterns and complexity. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 2188-98	7.6	70
135	Signaling initiated by overexpression of the fibroblast growth factor receptor-1 investigated by mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2003 , 2, 29-36	7.6	67
134	Analytic framework for peptidomics applied to large-scale neuropeptide identification. <i>Nature Communications</i> , 2016 , 7, 11436	17.4	66
133	Multilayered proteomics reveals molecular switches dictating ligand-dependent EGFR trafficking. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 608-18	17.6	66
132	Ancient proteins from ceramic vessels at Atlhik West reveal the hidden cuisine of early farmers. <i>Nature Communications</i> , 2018 , 9, 4064	17.4	64
131	Recent findings and technological advances in phosphoproteomics for cells and tissues. <i>Expert Review of Proteomics</i> , 2015 , 12, 469-87	4.2	63
130	De novo sequencing of antimicrobial peptides isolated from the venom glands of the wolf spider <i>Lycosa singoriensis</i> . <i>Journal of Mass Spectrometry</i> , 2004 , 39, 193-201	2.2	62
129	The low molecular weight proteome of <i>Halobacterium salinarum</i> . <i>Journal of Proteome Research</i> , 2007 , 6, 1510-8	5.6	60
128	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. <i>Cell Reports</i> , 2017 , 18, 3242-3256	10.6	59
127	System-wide Analysis of SUMOylation Dynamics in Response to Replication Stress Reveals Novel Small Ubiquitin-like Modified Target Proteins and Acceptor Lysines Relevant for Genome Stability. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1419-34	7.6	59
126	A mass spectrometry-friendly database for cSNP identification. <i>Nature Methods</i> , 2007 , 4, 465-6	21.6	57
125	MAPU: Max-Planck Unified database of organellar, cellular, tissue and body fluid proteomes. <i>Nucleic Acids Research</i> , 2007 , 35, D771-9	20.1	56
124	miR-625-3p regulates oxaliplatin resistance by targeting MAP2K6-p38 signalling in human colorectal adenocarcinoma cells. <i>Nature Communications</i> , 2016 , 7, 12436	17.4	52
123	Temporal proteomics of NGF-TrkA signaling identifies an inhibitory role for the E3 ligase Cbl-b in neuroblastoma cell differentiation. <i>Science Signaling</i> , 2015 , 8, ra40	8.8	52
122	The Ndc80 internal loop is required for recruitment of the Ska complex to establish end-on microtubule attachment to kinetochores. <i>Journal of Cell Science</i> , 2012 , 125, 3243-53	5.3	52
121	Quantitative proteomics and single-nucleus transcriptomics of the sinus node elucidates the foundation of cardiac pacemaking. <i>Nature Communications</i> , 2019 , 10, 2889	17.4	51

120	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. <i>Nature Methods</i> , 2014 , 11, 868-74	21.6	50
119	Proteomic profiling of archaeological human bone. <i>Royal Society Open Science</i> , 2017 , 4, 161004	3.3	50
118	Global phosphoproteome profiling reveals unanticipated networks responsive to cisplatin treatment of embryonic stem cells. <i>Molecular and Cellular Biology</i> , 2011 , 31, 4964-77	4.8	49
117	Species identification of archaeological skin objects from Danish bogs: comparison between mass spectrometry-based peptide sequencing and microscopy-based methods. <i>PLoS ONE</i> , 2014 , 9, e106875	3.7	49
116	Phosphorylation variation during the cell cycle scales with structural propensities of proteins. <i>PLoS Computational Biology</i> , 2013 , 9, e1002842	5	48
115	Intramolecular hydrogen atom transfer in hydrogen-deficient polypeptide radical cations. <i>Chemical Physics Letters</i> , 2000 , 330, 558-562	2.5	48
114	Palaeoproteomics resolves sloth relationships. <i>Nature Ecology and Evolution</i> , 2019 , 3, 1121-1130	12.3	47
113	In vivo quantitative phosphoproteomic profiling identifies novel regulators of castration-resistant prostate cancer growth. <i>Oncogene</i> , 2015 , 34, 2764-76	9.2	47
112	The dental proteome of Homo antecessor. <i>Nature</i> , 2020 , 580, 235-238	50.4	47
111	Metaproteomics of saliva identifies human protein markers specific for individuals with periodontitis and dental caries compared to orally healthy controls. <i>PeerJ</i> , 2016 , 4, e2433	3.1	44
110	High accuracy mass spectrometry in large-scale analysis of protein phosphorylation. <i>Methods in Molecular Biology</i> , 2009 , 492, 131-42	1.4	43
109	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. <i>Angewandte Chemie - International Edition</i> , 2018 , 57, 7369-7374	16.4	41
108	Enamel proteome shows that Gigantopithecus was an early diverging pongine. <i>Nature</i> , 2019 , 576, 262-265	50.4	41
107	The dual methyltransferase METTL13 targets N terminus and Lys55 of eEF1A and modulates codon-specific translation rates. <i>Nature Communications</i> , 2018 , 9, 3411	17.4	40
106	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. <i>Brain Research</i> , 2007 , 1134, 95-106	3.7	39
105	Phosphorylation of the yeast β -tubulin Tub4 regulates microtubule function. <i>PLoS ONE</i> , 2011 , 6, e19700	3.7	38
104	The human methyltransferase ZCCHC4 catalyses N6-methyladenosine modification of 28S ribosomal RNA. <i>Nucleic Acids Research</i> , 2020 , 48, 830-846	20.1	38
103	Can relative cleavage frequencies in peptides provide additional sequence information?. <i>International Journal of Mass Spectrometry</i> , 2002 , 219, 283-294	1.9	37

102	qcML: an exchange format for quality control metrics from mass spectrometry experiments. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1905-13	7.6	36
101	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. <i>Nature Communications</i> , 2018 , 9, 4744	17.4	36
100	A comprehensive platform for the analysis of ubiquitin-like protein modifications using in vivo biotinylation. <i>Scientific Reports</i> , 2017 , 7, 40756	4.9	34
99	Large-Scale Phosphoproteomics Reveals Shp-2 Phosphatase-Dependent Regulators of Pdgf Receptor Signaling. <i>Cell Reports</i> , 2018 , 22, 2784-2796	10.6	34
98	CDX2 downregulation is associated with poor differentiation and MMR deficiency in colon cancer. <i>Experimental and Molecular Pathology</i> , 2016 , 100, 59-66	4.4	34
97	Electronic Excitation Gives Informative Fragmentation of Polypeptide Cations and Anions. <i>European Journal of Mass Spectrometry</i> , 2002 , 8, 117-121	1.1	32
96	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. <i>Cell</i> , 2019 , 179, 543-560.e26	56.2	31
95	GeLCMS for in-depth protein characterization and advanced analysis of proteomes. <i>Methods in Molecular Biology</i> , 2011 , 753, 143-55	1.4	31
94	Comparison of electron capture dissociation and collisionally activated dissociation of polycations of peptide nucleic acids. <i>Rapid Communications in Mass Spectrometry</i> , 2001 , 15, 969-74	2.2	30
93	Offline High pH Reversed-Phase Peptide Fractionation for Deep Phosphoproteome Coverage. <i>Methods in Molecular Biology</i> , 2016 , 1355, 179-92	1.4	30
92	Dynamic lineage priming is driven via direct enhancer regulation by ERK. <i>Nature</i> , 2019 , 575, 355-360	50.4	29
91	A direct role of Mad1 in the spindle assembly checkpoint beyond Mad2 kinetochore recruitment. <i>EMBO Reports</i> , 2014 , 15, 282-90	6.5	29
90	Proteogenomic Characterization of Patient-Derived Xenografts Highlights the Role of REST in Neuroendocrine Differentiation of Castration-Resistant Prostate Cancer. <i>Clinical Cancer Research</i> , 2019 , 25, 595-608	12.9	29
89	Disulfide Linkage Characterization of Disulfide Bond-Containing Proteins and Peptides by Reducing Electrochemistry and Mass Spectrometry. <i>Analytical Chemistry</i> , 2016 , 88, 1585-92	7.8	28
88	Simple and Reproducible Sample Preparation for Single-Shot Phosphoproteomics with High Sensitivity. <i>Methods in Molecular Biology</i> , 2016 , 1355, 251-60	1.4	28
87	Development of an analytical methodology for the determination of the antiparasitic drug toltrazuril and its two metabolites in surface water, soil and animal manure. <i>Analytica Chimica Acta</i> , 2012 , 755, 69-76	6.6	27
86	TIMP-1 increases expression and phosphorylation of proteins associated with drug resistance in breast cancer cells. <i>Journal of Proteome Research</i> , 2013 , 12, 4136-51	5.6	26
85	Complete Mapping of Complex Disulfide Patterns with Closely-Spaced Cysteines by In-Source Reduction and Data-Dependent Mass Spectrometry. <i>Analytical Chemistry</i> , 2017 , 89, 5949-5957	7.8	25

84	The ubiquitin ligase Cullin5 regulates NDR1/STK38 stability and NF- κ B transactivation. <i>Scientific Reports</i> , 2017 , 7, 42800	4.9	25
83	Multi-spectra peptide sequencing and its applications to multistage mass spectrometry. <i>Bioinformatics</i> , 2008 , 24, i416-23	7.2	25
82	GIGYF1/2-Driven Cooperation between ZNF598 and TTP in Posttranscriptional Regulation of Inflammatory Signaling. <i>Cell Reports</i> , 2019 , 26, 3511-3521.e4	10.6	24
81	SPOP promotes transcriptional expression of DNA repair and replication factors to prevent replication stress and genomic instability. <i>Nucleic Acids Research</i> , 2018 , 46, 9484-9495	20.1	24
80	Resolution of the type material of the Asian elephant, <i>Elephas maximus</i> Linnaeus, 1758 (Proboscidea, Elephantidae). <i>Zoological Journal of the Linnean Society</i> , 2014 , 170, 222-232	2.4	24
79	Genomic and proteomic analyses of Prdm5 reveal interactions with insulator binding proteins in embryonic stem cells. <i>Molecular and Cellular Biology</i> , 2013 , 33, 4504-16	4.8	24
78	Pinpointing phosphorylation sites: Quantitative filtering and a novel site-specific x-ion fragment. <i>Journal of Proteome Research</i> , 2011 , 10, 2937-48	5.6	24
77	B-lymphoid tyrosine kinase (Blk) is an oncogene and a potential target for therapy with dasatinib in cutaneous T-cell lymphoma (CTCL). <i>Leukemia</i> , 2014 , 28, 2109-12	10.7	23
76	Ubiquitin-specific Protease 11 (USP11) Deubiquitinates Hybrid Small Ubiquitin-like Modifier (SUMO)-Ubiquitin Chains to Counteract RING Finger Protein 4 (RNF4). <i>Journal of Biological Chemistry</i> , 2015 , 290, 15526-15537	5.4	22
75	Analysis of changes in SUMO-2/3 modification during breast cancer progression and metastasis. <i>Journal of Proteome Research</i> , 2014 , 13, 3905-18	5.6	22
74	Systems biology approach identifies the kinase Csnk1a1 as a regulator of the DNA damage response in embryonic stem cells. <i>Science Signaling</i> , 2013 , 6, ra5	8.8	22
73	Identification of new chicken egg proteins by mass spectrometry-based proteomic analysis. <i>World's Poultry Science Journal</i> , 2008 , 64, 209-218	3	22
72	Molecular evidence of use of hide glue in 4th millennium BC Europe. <i>Journal of Archaeological Science</i> , 2015 , 63, 65-71	2.9	21
71	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. <i>Molecular Systems Biology</i> , 2021 , 17, e9730	12.2	20
70	ZAK1 Recognizes Stalled Ribosomes through Partially Redundant Sensor Domains. <i>Molecular Cell</i> , 2020 , 78, 700-713.e7	17.6	19
69	Resolution of the type material of the Asian elephant, <i>Elephas maximus</i> Linnaeus, 1758 (Proboscidea, Elephantidae). <i>Zoological Journal of the Linnean Society</i> , 2014 , 170, 222-232	2.4	18
68	Proteomics Reveals Global Regulation of Protein SUMOylation by ATM and ATR Kinases during Replication Stress. <i>Cell Reports</i> , 2017 , 21, 546-558	10.6	17
67	Comprehensive identification of SUMO2/3 targets and their dynamics during mitosis. <i>PLoS ONE</i> , 2014 , 9, e100692	3.7	17

66	The methyltransferase METTL9 mediates pervasive 1-methylhistidine modification in mammalian proteomes. <i>Nature Communications</i> , 2021 , 12, 891	17.4	17
65	Limits for Resolving Isobaric Tandem Mass Tag Reporter Ions Using Phase-Constrained Spectrum Deconvolution. <i>Journal of Proteome Research</i> , 2018 , 17, 4008-4016	5.6	17
64	The Role of TTP Phosphorylation in the Regulation of Inflammatory Cytokine Production by MK2/3. <i>Journal of Immunology</i> , 2019 , 203, 2291-2300	5.3	16
63	Truncated SALL1 Impedes Primary Cilia Function in Townes-Brocks Syndrome. <i>American Journal of Human Genetics</i> , 2018 , 102, 249-265	11	16
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