

Jesper V. Olsen

List of Publications by Year in descending order

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229
papers

47,969
citations

3731

89
h-index

1857

209
g-index

247
all docs

247
docs citations

247
times ranked

59826
citing authors

#	ARTICLE	IF	CITATIONS
1	Andromeda: A Peptide Search Engine Integrated into the MaxQuant Environment. <i>Journal of Proteome Research</i> , 2011, 10, 1794-1805.	3.7	4,935
2	In-gel digestion for mass spectrometric characterization of proteins and proteomes. <i>Nature Protocols</i> , 2006, 1, 2856-2860.	12.0	4,265
3	Lysine Acetylation Targets Protein Complexes and Co-Regulates Major Cellular Functions. <i>Science</i> , 2009, 325, 834-840.	12.6	3,883
4	Global, In Vivo, and Site-Specific Phosphorylation Dynamics in Signaling Networks. <i>Cell</i> , 2006, 127, 635-648.	28.9	3,201
5	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.	3.8	1,395
6	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. <i>Science Signaling</i> , 2010, 3, ra3.	3.6	1,319
7	Trypsin Cleaves Exclusively C-terminal to Arginine and Lysine Residues. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 608-614.	3.8	957
8	Higher-energy C-trap dissociation for peptide modification analysis. <i>Nature Methods</i> , 2007, 4, 709-712.	19.0	844
9	Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast. <i>Nature</i> , 2008, 455, 1251-1254.	27.8	835
10	Integrated Analysis of Protein Composition, Tissue Diversity, and Gene Regulation in Mouse Mitochondria. <i>Cell</i> , 2003, 115, 629-640.	28.9	815
11	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. <i>Nature Protocols</i> , 2009, 4, 698-705.	12.0	769
12	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.	27.8	717
13	Quantitative Interaction Proteomics and Genome-wide Profiling of Epigenetic Histone Marks and Their Readers. <i>Cell</i> , 2010, 142, 967-980.	28.9	710
14	Quantitative Phosphoproteomics Applied to the Yeast Pheromone Signaling Pathway. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 310-327.	3.8	708
15	The human urinary proteome contains more than 1500 proteins, including a large proportion of membrane proteins. <i>Genome Biology</i> , 2006, 7, R80.	9.6	598
16	Kinase-Selective Enrichment Enables Quantitative Phosphoproteomics of the Kinome across the Cell Cycle. <i>Molecular Cell</i> , 2008, 31, 438-448.	9.7	548
17	Proteomic Analysis of Lysine Acetylation Sites in Rat Tissues Reveals Organ Specificity and Subcellular Patterns. <i>Cell Reports</i> , 2012, 2, 419-431.	6.4	493
18	Status of Large-scale Analysis of Post-translational Modifications by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3444-3452.	3.8	491

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19	Pathogens and host immunity in the ancient human oral cavity. <i>Nature Genetics</i> , 2014, 46, 336-344.	21.4	482
20	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. <i>Cell Systems</i> , 2017, 4, 587-599.e4.	6.2	413
21	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. <i>Genome Biology</i> , 2007, 8, R250.	9.6	410
22	A Dual Pressure Linear Ion Trap Orbitrap Instrument with Very High Sequencing Speed. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2759-2769.	3.8	398
23	System-Wide Temporal Characterization of the Proteome and Phosphoproteome of Human Embryonic Stem Cell Differentiation. <i>Science Signaling</i> , 2011, 4, rs3.	3.6	389
24	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.	3.8	385
25	Global and Site-Specific Quantitative Phosphoproteomics: Principles and Applications. <i>Annual Review of Pharmacology and Toxicology</i> , 2009, 49, 199-221.	9.4	382
26	The Serine/Threonine/Tyrosine Phosphoproteome of the Model Bacterium <i>Bacillus subtilis</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 697-707.	3.8	359
27	Electron capture dissociation of singly and multiply phosphorylated peptides. <i>Rapid Communications in Mass Spectrometry</i> , 2000, 14, 1793-1800.	1.5	341
28	UbiSite approach for comprehensive mapping of lysine and N-terminal ubiquitination sites. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 631-640.	8.2	341
29	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, 13417-13422.	7.1	317
30	Quantitative maps of protein phosphorylation sites across 14 different rat organs and tissues. <i>Nature Communications</i> , 2012, 3, 876.	12.8	307
31	Proteomic Investigations Reveal a Role for RNA Processing Factor THRAP3 in the DNA Damage Response. <i>Molecular Cell</i> , 2012, 46, 212-225.	9.7	298
32	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.	3.8	284
33	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	21.4	282
34	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014, 46, 826-836.	21.4	281
35	Mislocalized Activation of Oncogenic RTKs Switches Downstream Signaling Outcomes. <i>Molecular Cell</i> , 2009, 36, 326-339.	9.7	278
36	Ancient proteins resolve the evolutionary history of Darwin's South American ungulates. <i>Nature</i> , 2015, 522, 81-84.	27.8	273

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37	Optimized Fast and Sensitive Acquisition Methods for Shotgun Proteomics on a Quadrupole Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2012, 11, 3487-3497.	3.7	270
38	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.	3.8	270
39	A Major Lineage of Enteroendocrine Cells Coexpress CCK, Secretin, GIP, GLP-1, PYY, and Neurotensin but Not Somatostatin. <i>Endocrinology</i> , 2012, 153, 5782-5795.	2.8	269
40	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014, 345, 1255832.	12.6	264
41	Off-Line High-pH Reversed-Phase Fractionation for In-Depth Phosphoproteomics. <i>Journal of Proteome Research</i> , 2014, 13, 6176-6186.	3.7	263
42	Large-scale Proteomics Analysis of the Human Kinome. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1751-1764.	3.8	257
43	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.	7.1	251
44	Rapid and site-specific deep phosphoproteome profiling by data-independent acquisition without the need for spectral libraries. <i>Nature Communications</i> , 2020, 11, 787.	12.8	251
45	Status of complete proteome analysis by mass spectrometry: SILAC labeled yeast as a model system. <i>Genome Biology</i> , 2006, 7, R50.	9.6	244
46	Proteomic Analyses Reveal Divergent Ubiquitylation Site Patterns in Murine Tissues. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1578-1585.	3.8	244
47	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.	3.6	243
48	MSQuant, an Open Source Platform for Mass Spectrometry-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 393-403.	3.7	237
49	A Conserved Motif Provides Binding Specificity to the PP2A-B56 Phosphatase. <i>Molecular Cell</i> , 2016, 63, 686-695.	9.7	235
50	Benchmarking common quantification strategies for large-scale phosphoproteomics. <i>Nature Communications</i> , 2018, 9, 1045.	12.8	232
51	Performance Evaluation of the Q Exactive HF-X for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 727-738.	3.7	221
52	Proteomic Analysis of a Pleistocene Mammoth Femur Reveals More than One Hundred Ancient Bone Proteins. <i>Journal of Proteome Research</i> , 2012, 11, 917-926.	3.7	196
53	Global Effects of Kinase Inhibitors on Signaling Networks Revealed by Quantitative Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2796-2808.	3.8	194
54	Ubc9 Sumoylation Regulates SUMO Target Discrimination. <i>Molecular Cell</i> , 2008, 31, 371-382.	9.7	191

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55	Protein Aggregation Capture on Microparticles Enables Multipurpose Proteomics Sample Preparation*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1027a-1035.	3.8	189
56	Direct evidence of milk consumption from ancient human dental calculus. <i>Scientific Reports</i> , 2014, 4, 7104.	3.3	184
57	Proteomic analysis of the acid-soluble organic matrix of the chicken calcified eggshell layer. <i>Proteomics</i> , 2006, 6, 3801-3810.	2.2	182
58	Top-down Protein Sequencing and MS3 on a Hybrid Linear Quadrupole Ion Trap-Orbitrap Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 949-958.	3.8	179
59	Noncovalent interaction between Ubc9 and SUMO promotes SUMO chain formation. <i>EMBO Journal</i> , 2007, 26, 2797-2807.	7.8	177
60	Protein sequences bound to mineral surfaces persist into deep time. <i>ELife</i> , 2016, 5, .	6.0	176
61	SUMO modification of the ubiquitin-conjugating enzyme E2-25K. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 264-269.	8.2	175
62	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, 6187-6195.	3.7	168
63	In Vivo Phosphoproteomics Analysis Reveals the Cardiac Targets of β_2 -Adrenergic Receptor Signaling. <i>Science Signaling</i> , 2013, 6, rs11.	3.6	164
64	Uncovering SUMOylation Dynamics during Cell-Cycle Progression Reveals FoxM1 as a Key Mitotic SUMO Target Protein. <i>Molecular Cell</i> , 2014, 53, 1053-1066.	9.7	153
65	Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. <i>Journal of Proteome Research</i> , 2010, 9, 6786-6794.	3.7	149
66	Pre-Clovis Mastodon Hunting 13,800 Years Ago at the Manis Site, Washington. <i>Science</i> , 2011, 334, 351-353.	12.6	148
67	Proteomic Mapping of Brain Plasma Membrane Proteins. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 402-408.	3.8	147
68	Functional Proteomics Defines the Molecular Switch Underlying FGF Receptor Trafficking and Cellular Outputs. <i>Molecular Cell</i> , 2013, 51, 707-722.	9.7	145
69	The phosphoproteome of toll-like receptor-activated macrophages. <i>Molecular Systems Biology</i> , 2010, 6, 371.	7.2	142
70	Proteomics strategy for quantitative protein interaction profiling in cell extracts. <i>Nature Methods</i> , 2009, 6, 741-744.	19.0	141
71	Quantitative Phosphoproteomics Dissection of Seven-transmembrane Receptor Signaling Using Full and Biased Agonists. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1540-1553.	3.8	135
72	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. <i>Nature</i> , 2019, 574, 103-107.	27.8	135

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73	High-accuracy identification and bioinformatic analysis of <i>in vivo</i> protein phosphorylation sites in yeast. <i>Proteomics</i> , 2009, 9, 4642-4652.	2.2	132
74	Global analysis of the yeast osmotic stress response by quantitative proteomics. <i>Molecular BioSystems</i> , 2009, 5, 1337.	2.9	128
75	Structures of Down Syndrome Kinases, DYRKs, Reveal Mechanisms of Kinase Activation and Substrate Recognition. <i>Structure</i> , 2013, 21, 986-996.	3.3	127
76	SUMO-2 Orchestrates Chromatin Modifiers in Response to DNA Damage. <i>Cell Reports</i> , 2015, 10, 1778-1791.	6.4	117
77	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	2.8	113
78	Quantitative proteomic assessment of very early cellular signaling events. <i>Nature Biotechnology</i> , 2007, 25, 566-568.	17.5	110
79	The SH2 Domain Interaction Landscape. <i>Cell Reports</i> , 2013, 3, 1293-1305.	6.4	110
80	Advantages of External Accumulation for Electron Capture Dissociation in Fourier Transform Mass Spectrometry. <i>Analytical Chemistry</i> , 2001, 73, 2998-3005.	6.5	106
81	Investigation of Protein-tyrosine Phosphatase 1B Function by Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1763-1777.	3.8	106
82	Ubiquitin-SUMO Circuitry Controls Activated Fanconi Anemia ID Complex Dosage in Response to DNA Damage. <i>Molecular Cell</i> , 2015, 57, 150-164.	9.7	106
83	Ancient proteins from ceramic vessels at Catalhöyük West reveal the hidden cuisine of early farmers. <i>Nature Communications</i> , 2018, 9, 4064.	12.8	105
84	Phosphoproteins of the chicken eggshell calcified layer. <i>Proteomics</i> , 2007, 7, 106-115.	2.2	102
85	RNF4 is required for DNA double-strand break repair <i>in vivo</i> . <i>Cell Death and Differentiation</i> , 2013, 20, 490-502.	11.2	102
86	The dental proteome of Homo antecessor. <i>Nature</i> , 2020, 580, 235-238.	27.8	100
87	Phosphorylation of Histone H3 Thr-45 Is Linked to Apoptosis. <i>Journal of Biological Chemistry</i> , 2009, 284, 16575-16583.	3.4	98
88	Multilayered proteomics reveals molecular switches dictating ligand-dependent EGFR trafficking. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 608-618.	8.2	98
89	Quantitative phosphoproteome analysis of a mouse liver cell line reveals specificity of phosphatase inhibitors. <i>Proteomics</i> , 2008, 8, 4534-4546.	2.2	93
90	Separation of the gluconeogenic and mitochondrial functions of PGC-1 α through S6 kinase. <i>Genes and Development</i> , 2011, 25, 1232-1244.	5.9	93

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91	Analytic framework for peptidomics applied to large-scale neuropeptide identification. <i>Nature Communications</i> , 2016, 7, 11436.	12.8	92
92	Palaeoproteomics resolves sloth relationships. <i>Nature Ecology and Evolution</i> , 2019, 3, 1121-1130.	7.8	91
93	Tyrosine Phosphoproteomics of Fibroblast Growth Factor Signaling. <i>Journal of Biological Chemistry</i> , 2004, 279, 46438-46447.	3.4	90
94	ZAK1± Recognizes Stalled Ribosomes through Partially Redundant Sensor Domains. <i>Molecular Cell</i> , 2020, 78, 700-713.e7.	9.7	90
95	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.	3.8	88
96	The human methyltransferase ZCCHC4 catalyses N6-methyladenosine modification of 28S ribosomal RNA. <i>Nucleic Acids Research</i> , 2020, 48, 830-846.	14.5	88
97	±4±2± GABA _A receptors are high-affinity targets for ±-hydroxybutyric acid (GHB). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13404-13409.	7.1	87
98	Functional characterization of Rad18 domains for Rad6, ubiquitin, DNA binding and PCNA modification. <i>Nucleic Acids Research</i> , 2007, 35, 5819-5830.	14.5	85
99	Quantitative proteomics and single-nucleus transcriptomics of the sinus node elucidates the foundation of cardiac pacemaking. <i>Nature Communications</i> , 2019, 10, 2889.	12.8	84
100	miR-625-3p regulates oxaliplatin resistance by targeting MAP2K6-p38 signalling in human colorectal adenocarcinoma cells. <i>Nature Communications</i> , 2016, 7, 12436.	12.8	82
101	Enamel proteome shows that <i>Cigantopithecus</i> was an early diverging pongine. <i>Nature</i> , 2019, 576, 262-265.	27.8	82
102	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. <i>Cell Reports</i> , 2017, 18, 3242-3256.	6.4	81
103	The dual methyltransferase METTL13 targets N terminus and Lys55 of eEF1A and modulates codon-specific translation rates. <i>Nature Communications</i> , 2018, 9, 3411.	12.8	81
104	Profiling the Phospho-status of the BKCa Channel ± Subunit in Rat Brain Reveals Unexpected Patterns and Complexity. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2188-2198.	3.8	79
105	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, 1419-1434.	3.8	79
106	Causal integration of multi±omics data with prior knowledge to generate mechanistic hypotheses. <i>Molecular Systems Biology</i> , 2021, 17, e9730.	7.2	78
107	Proteomic profiling of archaeological human bone. <i>Royal Society Open Science</i> , 2017, 4, 161004.	2.4	76
108	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 7369-7374.	13.8	76

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109	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.	3.8	73
110	A mass spectrometry-friendly database for cSNP identification. <i>Nature Methods</i> , 2007, 4, 465-466.	19.0	72
111	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. <i>Nature Methods</i> , 2014, 11, 868-874.	19.0	70
112	Recent findings and technological advances in phosphoproteomics for cells and tissues. <i>Expert Review of Proteomics</i> , 2015, 12, 469-487.	3.0	70
113	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.	2.5	70
114	MAPU: Max-Planck Unified database of organellar, cellular, tissue and body fluid proteomes. <i>Nucleic Acids Research</i> , 2007, 35, D771-D779.	14.5	69
115	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.	1.6	68
116	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. <i>Cell</i> , 2019, 179, 543-560.e26.	28.9	65
117	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.	3.6	64
118	Dynamic lineage priming is driven via direct enhancer regulation by ERK. <i>Nature</i> , 2019, 575, 355-360.	27.8	64
119	The Low Molecular Weight Proteome of <i>Halobacterium salinarum</i> . <i>Journal of Proteome Research</i> , 2007, 6, 1510-1518.	3.7	63
120	In vivo quantitative phosphoproteomic profiling identifies novel regulators of castration-resistant prostate cancer growth. <i>Oncogene</i> , 2015, 34, 2764-2776.	5.9	63
121	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. <i>Nature Communications</i> , 2018, 9, 4744.	12.8	63
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.	2.0	62
123	Intramolecular hydrogen atom transfer in hydrogen-deficient polypeptide radical cations. <i>Chemical Physics Letters</i> , 2000, 330, 558-562.	2.6	58
124	A comprehensive platform for the analysis of ubiquitin-like protein modifications using in vivo biotinylation. <i>Scientific Reports</i> , 2017, 7, 40756.	3.3	58
125	Global Phosphoproteome Profiling Reveals Unanticipated Networks Responsive to Cisplatin Treatment of Embryonic Stem Cells. <i>Molecular and Cellular Biology</i> , 2011, 31, 4964-4977.	2.3	56
126	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.	2.0	56

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127	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.	7.0	55
128	Phosphorylation Variation during the Cell Cycle Scales with Structural Propensities of Proteins. <i>PLoS Computational Biology</i> , 2013, 9, e1002842.	3.2	54
129	The methyltransferase METTL9 mediates pervasive 1-methylhistidine modification in mammalian proteomes. <i>Nature Communications</i> , 2021, 12, 891.	12.8	54
130	High Accuracy Mass Spectrometry in Large-Scale Analysis of Protein Phosphorylation. <i>Methods in Molecular Biology</i> , 2009, 492, 131-142.	0.9	54
131	Large-Scale Phosphoproteomics Reveals Shp-2 Phosphatase-Dependent Regulators of Pdgf Receptor Signaling. <i>Cell Reports</i> , 2018, 22, 2784-2796.	6.4	51
132	CDX2 downregulation is associated with poor differentiation and MMR deficiency in colon cancer. <i>Experimental and Molecular Pathology</i> , 2016, 100, 59-66.	2.1	46
133	GIGYF1/2-Driven Cooperation between ZNF598 and TTP in Posttranscriptional Regulation of Inflammatory Signaling. <i>Cell Reports</i> , 2019, 26, 3511-3521.e4.	6.4	44
134	Mass-Spectrometry Based Proteome Comparison of Extracellular Vesicle Isolation Methods: Comparison of ME-kit, Size-Exclusion Chromatography, and High-Speed Centrifugation. <i>Biomedicines</i> , 2020, 8, 246.	3.2	43
135	Can relative cleavage frequencies in peptides provide additional sequence information?. <i>International Journal of Mass Spectrometry</i> , 2002, 219, 283-294.	1.5	42
136	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
137	Phosphorylation of the Yeast $\hat{\beta}$ -Tubulin Tub4 Regulates Microtubule Function. <i>PLoS ONE</i> , 2011, 6, e19700.	2.5	42
138	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.	2.2	41
139	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, 2109-2112.	7.2	39
140	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.	14.5	39
141	Simple and Reproducible Sample Preparation for Single-Shot Phosphoproteomics with High Sensitivity. <i>Methods in Molecular Biology</i> , 2016, 1355, 251-260.	0.9	39
142	A direct role of M^{ad1} in the spindle assembly checkpoint beyond M^{ad2} kinetochore recruitment. <i>EMBO Reports</i> , 2014, 15, 282-290.	4.5	38
143	Spatial-proteomics reveals phospho-signaling dynamics at subcellular resolution. <i>Nature Communications</i> , 2021, 12, 7113.	12.8	38
144	GeLCMS for In-Depth Protein Characterization and Advanced Analysis of Proteomes. <i>Methods in Molecular Biology</i> , 2011, 753, 143-155.	0.9	36

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145	TIMP-1 Increases Expression and Phosphorylation of Proteins Associated with Drug Resistance in Breast Cancer Cells. <i>Journal of Proteome Research</i> , 2013, 12, 4136-4151.	3.7	36
146	Offline High pH Reversed-Phase Peptide Fractionation for Deep Phosphoproteome Coverage. <i>Methods in Molecular Biology</i> , 2016, 1355, 179-192.	0.9	36
147	Electronic Excitation Gives Informative Fragmentation of Polypeptide Cations and Anions. <i>European Journal of Mass Spectrometry</i> , 2002, 8, 117-121.	1.0	35
148	Disulfide Linkage Characterization of Disulfide Bond-Containing Proteins and Peptides by Reducing Electrochemistry and Mass Spectrometry. <i>Analytical Chemistry</i> , 2016, 88, 1585-1592.	6.5	35
149	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.	3.6	34
150	Human METTL18 is a histidine-specific methyltransferase that targets RPL3 and affects ribosome biogenesis and function. <i>Nucleic Acids Research</i> , 2021, 49, 3185-3203.	14.5	34
151	Integrated proximal proteomics reveals IRS2 as a determinant of cell survival in ALK-driven neuroblastoma. <i>Science Signaling</i> , 2018, 11, .	3.6	33
152	Proteome and Phosphoproteome Changes Associated with Prognosis in Acute Myeloid Leukemia. <i>Cancers</i> , 2020, 12, 709.	3.7	33
153	Comparison of electron capture dissociation and collisionally activated dissociation of polycations of peptide nucleic acids. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 969-974.	1.5	32
154	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.	5.4	32
155	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.	3.4	32
156	Molecular evidence of use of hide glue in 4th millennium BC Europe. <i>Journal of Archaeological Science</i> , 2015, 63, 65-71.	2.4	32
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