

Jesper V Olsen

List of Publications by Year in descending order

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181
papers

45,397
citations

4960

84
h-index

3650

180
g-index

191
all docs

191
docs citations

191
times ranked

56631
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	Off-Line High-pH Reversed-Phase Fractionation for In-Depth Phosphoproteomics. <i>Journal of Proteome Research</i> , 2014, 13, 6176-6186.	3.7	263
41	Large-scale Proteomics Analysis of the Human Kinome. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1751-1764.	3.8	257
42	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
43	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
44	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
45	Proteomic Analyses Reveal Divergent Ubiquitylation Site Patterns in Murine Tissues. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1578-1585.	3.8	244
46	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
47	MSQuant, an Open Source Platform for Mass Spectrometry-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 393-403.	3.7	237
48	Benchmarking common quantification strategies for large-scale phosphoproteomics. <i>Nature Communications</i> , 2018, 9, 1045.	12.8	232
49	Performance Evaluation of the Q Exactive HF-X for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 727-738.	3.7	221
50	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
51	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
52	Ubc9 Sumoylation Regulates SUMO Target Discrimination. <i>Molecular Cell</i> , 2008, 31, 371-382.	9.7	191
53	Protein Aggregation Capture on Microparticles Enables Multipurpose Proteomics Sample Preparation*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1027a-1035.	3.8	189
54	Proteomic analysis of the acid-soluble organic matrix of the chicken calcified eggshell layer. <i>Proteomics</i> , 2006, 6, 3801-3810.	2.2	182

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55	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
56	Noncovalent interaction between Ubc9 and SUMO promotes SUMO chain formation. <i>EMBO Journal</i> , 2007, 26, 2797-2807.	7.8	177
57	Protein sequences bound to mineral surfaces persist into deep time. <i>ELife</i> , 2016, 5, .	6.0	176
58	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
59	In Vivo Phosphoproteomics Analysis Reveals the Cardiac Targets of β^2 -Adrenergic Receptor Signaling. <i>Science Signaling</i> , 2013, 6, rs11.	3.6	164
60	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
61	Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. <i>Journal of Proteome Research</i> , 2010, 9, 6786-6794.	3.7	149
62	Pre-Clovis Mastodon Hunting 13,800 Years Ago at the Manis Site, Washington. <i>Science</i> , 2011, 334, 351-353.	12.6	148
63	Proteomic Mapping of Brain Plasma Membrane Proteins. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 402-408.	3.8	147
64	Functional Proteomics Defines the Molecular Switch Underlying FGF Receptor Trafficking and Cellular Outputs. <i>Molecular Cell</i> , 2013, 51, 707-722.	9.7	145
65	The phosphoproteome of toll-like receptor-activated macrophages. <i>Molecular Systems Biology</i> , 2010, 6, 371.	7.2	142
66	Proteomics strategy for quantitative protein interaction profiling in cell extracts. <i>Nature Methods</i> , 2009, 6, 741-744.	19.0	141
67	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
68	Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , 2019, 574, 103-107.	27.8	135
69	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
70	Global analysis of the yeast osmotic stress response by quantitative proteomics. <i>Molecular BioSystems</i> , 2009, 5, 1337.	2.9	128
71	Structures of Down Syndrome Kinases, DYRKs, Reveal Mechanisms of Kinase Activation and Substrate Recognition. <i>Structure</i> , 2013, 21, 986-996.	3.3	127
72	SUMO-2 Orchestrates Chromatin Modifiers in Response to DNA Damage. <i>Cell Reports</i> , 2015, 10, 1778-1791.	6.4	117

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73	Quantitative proteomic assessment of very early cellular signaling events. <i>Nature Biotechnology</i> , 2007, 25, 566-568.	17.5	110
74	The SH2 Domain Interaction Landscape. <i>Cell Reports</i> , 2013, 3, 1293-1305.	6.4	110
75	Advantages of External Accumulation for Electron Capture Dissociation in Fourier Transform Mass Spectrometry. <i>Analytical Chemistry</i> , 2001, 73, 2998-3005.	6.5	106
76	Investigation of Protein-tyrosine Phosphatase 1B Function by Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1763-1777.	3.8	106
77	Ancient proteins from ceramic vessels at Neolithic West reveal the hidden cuisine of early farmers. <i>Nature Communications</i> , 2018, 9, 4064.	12.8	105
78	Phosphoproteins of the chicken eggshell calcified layer. <i>Proteomics</i> , 2007, 7, 106-115.	2.2	102
79	The dental proteome of Homo antecessor. <i>Nature</i> , 2020, 580, 235-238.	27.8	100
80	Phosphorylation of Histone H3 Thr-45 Is Linked to Apoptosis. <i>Journal of Biological Chemistry</i> , 2009, 284, 16575-16583.	3.4	98
81	Multilayered proteomics reveals molecular switches dictating ligand-dependent EGFR trafficking. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 608-618.	8.2	98
82	Quantitative phosphoproteome analysis of a mouse liver cell line reveals specificity of phosphatase inhibitors. <i>Proteomics</i> , 2008, 8, 4534-4546.	2.2	93
83	Analytic framework for peptidomics applied to large-scale neuropeptide identification. <i>Nature Communications</i> , 2016, 7, 11436.	12.8	92
84	Palaeoproteomics resolves sloth relationships. <i>Nature Ecology and Evolution</i> , 2019, 3, 1121-1130.	7.8	91
85	Tyrosine Phosphoproteomics of Fibroblast Growth Factor Signaling. <i>Journal of Biological Chemistry</i> , 2004, 279, 46438-46447.	3.4	90
86	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
87	The human methyltransferase ZCCHC4 catalyses N6-methyladenosine modification of 28S ribosomal RNA. <i>Nucleic Acids Research</i> , 2020, 48, 830-846.	14.5	88
88	α -GABA receptors are high-affinity targets for γ -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
89	Enamel proteome shows that Gigantopithecus was an early diverging pongine. <i>Nature</i> , 2019, 576, 262-265.	27.8	82
90	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. <i>Cell Reports</i> , 2017, 18, 3242-3256.	6.4	81

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91	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
92	Profiling the Phospho-status of the BKCa Channel β Subunit in Rat Brain Reveals Unexpected Patterns and Complexity. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2188-2198.	3.8	79
93	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
94	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. <i>Molecular Systems Biology</i> , 2021, 17, e9730.	7.2	78
95	Proteomic profiling of archaeological human bone. <i>Royal Society Open Science</i> , 2017, 4, 161004.	2.4	76
96	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
97	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
98	A mass spectrometry-friendly database for cSNP identification. <i>Nature Methods</i> , 2007, 4, 465-466.	19.0	72
99	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
100	Recent findings and technological advances in phosphoproteomics for cells and tissues. <i>Expert Review of Proteomics</i> , 2015, 12, 469-487.	3.0	70
101	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
102	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
103	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. <i>Cell</i> , 2019, 179, 543-560.e26.	28.9	65
104	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
105	Dynamic lineage priming is driven via direct enhancer regulation by ERK. <i>Nature</i> , 2019, 575, 355-360.	27.8	64
106	The Low Molecular Weight Proteome of <i>Halobacterium salinarum</i> . <i>Journal of Proteome Research</i> , 2007, 6, 1510-1518.	3.7	63
107	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. <i>Nature Communications</i> , 2018, 9, 4744.	12.8	63
108	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

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109	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
110	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
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.	2.0	56
112	The methyltransferase METTL9 mediates pervasive 1-methylhistidine modification in mammalian proteomes. <i>Nature Communications</i> , 2021, 12, 891.	12.8	54
113	High Accuracy Mass Spectrometry in Large-Scale Analysis of Protein Phosphorylation. <i>Methods in Molecular Biology</i> , 2009, 492, 131-142.	0.9	54
114	Large-Scale Phosphoproteomics Reveals Shp-2 Phosphatase-Dependent Regulators of Pdgf Receptor Signaling. <i>Cell Reports</i> , 2018, 22, 2784-2796.	6.4	51
115	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
116	Can relative cleavage frequencies in peptides provide additional sequence information?. <i>International Journal of Mass Spectrometry</i> , 2002, 219, 283-294.	1.5	42
117	Phosphorylation of the Yeast $\hat{\beta}$ -Tubulin Tub4 Regulates Microtubule Function. <i>PLoS ONE</i> , 2011, 6, e19700.	2.5	42
118	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
119	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
120	A direct role of $\text{Mad}1$ in the spindle assembly checkpoint beyond $\text{Mad}2$ kinetochore recruitment. <i>EMBO Reports</i> , 2014, 15, 282-290.	4.5	38
121	Spatial-proteomics reveals phospho-signaling dynamics at subcellular resolution. <i>Nature Communications</i> , 2021, 12, 7113.	12.8	38
122	GeLCMS for In-Depth Protein Characterization and Advanced Analysis of Proteomes. <i>Methods in Molecular Biology</i> , 2011, 753, 143-155.	0.9	36
123	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
124	Offline High pH Reversed-Phase Peptide Fractionation for Deep Phosphoproteome Coverage. <i>Methods in Molecular Biology</i> , 2016, 1355, 179-192.	0.9	36
125	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
126	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

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127	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
128	Integrated proximal proteomics reveals IRS2 as a determinant of cell survival in ALK-driven neuroblastoma. <i>Science Signaling</i> , 2018, 11, .	3.6	33
129	Proteome and Phosphoproteome Changes Associated with Prognosis in Acute Myeloid Leukemia. <i>Cancers</i> , 2020, 12, 709.	3.7	33
130	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
131	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
132	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
133	The ubiquitin ligase Cullin5SOCS2 regulates NDR1/STK38 stability and NF- κ B transactivation. <i>Scientific Reports</i> , 2017, 7, 42800.	3.3	32
134	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.	2.3	31
135	Multi-omic detection of <i>Mycobacterium leprae</i> in archaeological human dental calculus. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190584.	4.0	31
136	GHB analogs confer neuroprotection through specific interaction with the CaMKII β hub domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	31
137	A deeper look at carrier proteome effects for single-cell proteomics. <i>Communications Biology</i> , 2022, 5, 150.	4.4	31
138	Limits for Resolving Isobaric Tandem Mass Tag Reporter Ions Using Phase-Constrained Spectrum Deconvolution. <i>Journal of Proteome Research</i> , 2018, 17, 4008-4016.	3.7	29
139	Pinpointing Phosphorylation Sites: Quantitative Filtering and a Novel Site-specific x-Ion Fragment. <i>Journal of Proteome Research</i> , 2011, 10, 2937-2948.	3.7	27
140	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.	6.5	27
141	ProAlanase is an Effective Alternative to Trypsin for Proteomics Applications and Disulfide Bond Mapping. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 2139-2157.	3.8	27
142	Multi-spectra peptide sequencing and its applications to multistage mass spectrometry. <i>Bioinformatics</i> , 2008, 24, i416-i423.	4.1	25
143	Analysis of Changes in SUMO-2/3 Modification during Breast Cancer Progression and Metastasis. <i>Journal of Proteome Research</i> , 2014, 13, 3905-3918.	3.7	25
144	Proteomic characterization of chromosomal common fragile site (CFS)-associated proteins uncovers ATRX as a regulator of CFS stability. <i>Nucleic Acids Research</i> , 2019, 47, 8004-8018.	14.5	25

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145	Molecular basis of Tausled-Like Kinase 2 activation. <i>Nature Communications</i> , 2018, 9, 2535.	12.8	24
146	Quantitative proteome comparison of human hearts with those of model organisms. <i>PLoS Biology</i> , 2021, 19, e3001144.	5.6	23
147	Analytical Utility of Mass Spectral Binning in Proteomic Experiments by SPectral Immonium Ion Detection (SPIID). <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1914-1924.	3.8	22
148	Resolution of the type material of the Asian elephant, <i>Elephas maximus</i> Linnaeus, 1758 (Proboscidea). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	2.8	22
149	Proteomics of resistance to Notch1 inhibition in acute lymphoblastic leukemia reveals targetable kinase signatures. <i>Nature Communications</i> , 2021, 12, 2507.	12.8	22
150	Human DDK rescues stalled forks and counteracts checkpoint inhibition at unfired origins to complete DNA replication. <i>Molecular Cell</i> , 2021, 81, 426-441.e8.	9.7	21
151	From Phosphosites to Kinases. <i>Methods in Molecular Biology</i> , 2016, 1355, 307-321.	0.9	21
152	A Middle Pleistocene Denisovan molar from the Annamite Chain of northern Laos. <i>Nature Communications</i> , 2022, 13, 2557.	12.8	20
153	Comprehensive Identification of SUMO2/3 Targets and Their Dynamics during Mitosis. <i>PLoS ONE</i> , 2014, 9, e100692.	2.5	19
154	Proteomics insights into DNA damage response and translating this knowledge to clinical strategies. <i>Proteomics</i> , 2017, 17, 1600018.	2.2	18
155	Multi-protease analysis of Pleistocene bone proteomes. <i>Journal of Proteomics</i> , 2020, 228, 103889.	2.4	18
156	Effective Representation and Storage of Mass Spectrometry-Based Proteomic Data Sets for the Scientific Community. <i>Science Signaling</i> , 2011, 4, pe7.	3.6	17
157	Combinatorial Drug Screening Identifies Ewing Sarcoma-specific Sensitivities. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 88-101.	4.1	17
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