

# Jesper V Olsen

## List of Publications by Citations

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183  
papers

36,249  
citations

79  
h-index

190  
g-index

191  
ext. papers

42,022  
ext. citations

12.4  
avg, IF

7.12  
L-index

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

166	Proteomic analysis of lysine acetylation sites in rat tissues reveals organ specificity and subcellular patterns. <i>Cell Reports</i> , <b>2012</b> , 2, 419-31	10.6	405
165	A dual pressure linear ion trap Orbitrap instrument with very high sequencing speed. <i>Molecular and Cellular Proteomics</i> , <b>2009</b> , 8, 2759-69	7.6	379
164	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. <i>Genome Biology</i> , <b>2007</b> , 8, R250	18.3	376
163	Pathogens and host immunity in the ancient human oral cavity. <i>Nature Genetics</i> , <b>2014</b> , 46, 336-44	36.3	353
162	Global and site-specific quantitative phosphoproteomics: principles and applications. <i>Annual Review of Pharmacology and Toxicology</i> , <b>2009</b> , 49, 199-221	17.9	350
161	System-wide temporal characterization of the proteome and phosphoproteome of human embryonic stem cell differentiation. <i>Science Signaling</i> , <b>2011</b> , 4, rs3	8.8	347
160	Phosphoproteome analysis of E. coli reveals evolutionary conservation of bacterial Ser/Thr/Tyr phosphorylation. <i>Molecular and Cellular Proteomics</i> , <b>2008</b> , 7, 299-307	7.6	334
159	Electron capture dissociation of singly and multiply phosphorylated peptides. <i>Rapid Communications in Mass Spectrometry</i> , <b>2000</b> , 14, 1793-800	2.2	325
158	The serine/threonine/tyrosine phosphoproteome of the model bacterium <i>Bacillus subtilis</i> . <i>Molecular and Cellular Proteomics</i> , <b>2007</b> , 6, 697-707	7.6	309
157	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> , <b>2004</b> , 101, 13417-22	11.5	288
156	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. <i>Cell Systems</i> , <b>2017</b> , 4, 587-599.e4	10.6	255
155	Quantitative maps of protein phosphorylation sites across 14 different rat organs and tissues. <i>Nature Communications</i> , <b>2012</b> , 3, 876	17.4	248
154	Mislocalized activation of oncogenic RTKs switches downstream signaling outcomes. <i>Molecular Cell</i> , <b>2009</b> , 36, 326-39	17.6	245
153	Proteomic investigations reveal a role for RNA processing factor THRAP3 in the DNA damage response. <i>Molecular Cell</i> , <b>2012</b> , 46, 212-25	17.6	239
152	Large-scale proteomics analysis of the human kinome. <i>Molecular and Cellular Proteomics</i> , <b>2009</b> , 8, 1751-646	17.6	236
151	A major lineage of enteroendocrine cells coexpress CCK, secretin, GIP, GLP-1, PYY, and neurotensin but not somatostatin. <i>Endocrinology</i> , <b>2012</b> , 153, 5782-95	4.8	231
150	MSQuant, an open source platform for mass spectrometry-based quantitative proteomics. <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 393-403	5.6	225
149	Status of complete proteome analysis by mass spectrometry: SILAC labeled yeast as a model system. <i>Genome Biology</i> , <b>2006</b> , 7, R50	18.3	224

148	Optimized fast and sensitive acquisition methods for shotgun proteomics on a quadrupole orbitrap mass spectrometer. <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 3487-97	5.6	221
147	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , <b>2013</b> , 45, 621-31	36.3	219
146	Proteomic analyses reveal divergent ubiquitylation site patterns in murine tissues. <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, 1578-85	7.6	214
145	Ancient proteins resolve the evolutionary history of Darwin's South American ungulates. <i>Nature</i> , <b>2015</b> , 522, 81-4	50.4	210
144	Proteome-wide mapping of the Drosophila acetylome demonstrates a high degree of conservation of lysine acetylation. <i>Science Signaling</i> , <b>2011</b> , 4, ra48	8.8	204
143	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , <b>2014</b> , 46, 826-36	36.3	199
142	Off-line high-pH reversed-phase fractionation for in-depth phosphoproteomics. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 6176-86	5.6	194
141	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> , <b>2014</b> , 111, E4066-75	11.5	185
140	UbiSite approach for comprehensive mapping of lysine and N-terminal ubiquitination sites. <i>Nature Structural and Molecular Biology</i> , <b>2018</b> , 25, 631-640	17.6	178
139	Ubc9 sumoylation regulates SUMO target discrimination. <i>Molecular Cell</i> , <b>2008</b> , 31, 371-82	17.6	169
138	Global effects of kinase inhibitors on signaling networks revealed by quantitative phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , <b>2009</b> , 8, 2796-808	7.6	165
137	Top-down protein sequencing and MS3 on a hybrid linear quadrupole ion trap-orbitrap mass spectrometer. <i>Molecular and Cellular Proteomics</i> , <b>2006</b> , 5, 949-58	7.6	163
136	Proteomic analysis of the acid-soluble organic matrix of the chicken calcified eggshell layer. <i>Proteomics</i> , <b>2006</b> , 6, 3801-10	4.8	162
135	Noncovalent interaction between Ubc9 and SUMO promotes SUMO chain formation. <i>EMBO Journal</i> , <b>2007</b> , 26, 2797-807	13	160
134	Performance Evaluation of the Q Exactive HF-X for Shotgun Proteomics. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 727-738	5.6	160
133	Proteomic analysis of a pleistocene mammoth femur reveals more than one hundred ancient bone proteins. <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 917-26	5.6	150
132	Benchmarking common quantification strategies for large-scale phosphoproteomics. <i>Nature Communications</i> , <b>2018</b> , 9, 1045	17.4	146
131	Proteomic mapping of brain plasma membrane proteins. <i>Molecular and Cellular Proteomics</i> , <b>2005</b> , 4, 402-86	14.1	141

130	Feasibility of large-scale phosphoproteomics with higher energy collisional dissociation fragmentation. <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 6786-94	5.6	139
129	Rapid and deep proteomes by faster sequencing on a benchtop quadrupole ultra-high-field Orbitrap mass spectrometer. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 6187-95	5.6	134
128	A Novel LC System Embeds Analytes in Pre-formed Gradients for Rapid, Ultra-robust Proteomics. <i>Molecular and Cellular Proteomics</i> , <b>2018</b> , 17, 2284-2296	7.6	133
127	Uncovering SUMOylation dynamics during cell-cycle progression reveals FoxM1 as a key mitotic SUMO target protein. <i>Molecular Cell</i> , <b>2014</b> , 53, 1053-66	17.6	132
126	In vivo phosphoproteomics analysis reveals the cardiac targets of $\beta$ adrenergic receptor signaling. <i>Science Signaling</i> , <b>2013</b> , 6, rs11	8.8	129
125	Pre-Clovis mastodon hunting 13,800 years ago at the Manis site, Washington. <i>Science</i> , <b>2011</b> , 334, 351-3	33.3	129
124	Proteomics strategy for quantitative protein interaction profiling in cell extracts. <i>Nature Methods</i> , <b>2009</b> , 6, 741-4	21.6	121
123	Protein sequences bound to mineral surfaces persist into deep time. <i>ELife</i> , <b>2016</b> , 5,	8.9	118
122	Quantitative phosphoproteomics dissection of seven-transmembrane receptor signaling using full and biased agonists. <i>Molecular and Cellular Proteomics</i> , <b>2010</b> , 9, 1540-53	7.6	115
121	The phosphoproteome of toll-like receptor-activated macrophages. <i>Molecular Systems Biology</i> , <b>2010</b> , 6, 371	12.2	113
120	A Compact Quadrupole-Orbitrap Mass Spectrometer with FAIMS Interface Improves Proteome Coverage in Short LC Gradients. <i>Molecular and Cellular Proteomics</i> , <b>2020</b> , 19, 716-729	7.6	112
119	Rapid and site-specific deep phosphoproteome profiling by data-independent acquisition without the need for spectral libraries. <i>Nature Communications</i> , <b>2020</b> , 11, 787	17.4	108
118	Global analysis of the yeast osmotic stress response by quantitative proteomics. <i>Molecular BioSystems</i> , <b>2009</b> , 5, 1337-46		108
117	Functional proteomics defines the molecular switch underlying FGF receptor trafficking and cellular outputs. <i>Molecular Cell</i> , <b>2013</b> , 51, 707-22	17.6	105
116	High-accuracy identification and bioinformatic analysis of in vivo protein phosphorylation sites in yeast. <i>Proteomics</i> , <b>2009</b> , 9, 4642-52	4.8	103
115	Quantitative proteomic assessment of very early cellular signaling events. <i>Nature Biotechnology</i> , <b>2007</b> , 25, 566-8	44.5	103
114	Advantages of external accumulation for electron capture dissociation in Fourier transform mass spectrometry. <i>Analytical Chemistry</i> , <b>2001</b> , 73, 2998-3005	7.8	101
113	Structures of Down syndrome kinases, DYRKs, reveal mechanisms of kinase activation and substrate recognition. <i>Structure</i> , <b>2013</b> , 21, 986-96	5.2	99

112	Phosphoproteins of the chicken eggshell calcified layer. <i>Proteomics</i> , <b>2007</b> , 7, 106-15	4.8	95
111	Investigation of protein-tyrosine phosphatase 1B function by quantitative proteomics. <i>Molecular and Cellular Proteomics</i> , <b>2008</b> , 7, 1763-77	7.6	91
110	SUMO-2 Orchestrates Chromatin Modifiers in Response to DNA Damage. <i>Cell Reports</i> , <b>2015</b> , 10, 1778-1791	10.6	90
109	The SH2 domain interaction landscape. <i>Cell Reports</i> , <b>2013</b> , 3, 1293-305	10.6	89
108	Quantitative phosphoproteome analysis of a mouse liver cell line reveals specificity of phosphatase inhibitors. <i>Proteomics</i> , <b>2008</b> , 8, 4534-46	4.8	89
107	Phosphorylation of histone H3 Thr-45 is linked to apoptosis. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 16575-16583	5.4	85
106	Tyrosine phosphoproteomics of fibroblast growth factor signaling: a role for insulin receptor substrate-4. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 46438-47	5.4	84
105	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> , <b>2004</b> , 3, 82-92	7.6	79
104	$\gamma$ -GABA(A) receptors are high-affinity targets for $\gamma$ -hydroxybutyric acid (GHB). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 13404-9	11.5	72
103	Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , <b>2019</b> , 574, 103-107	50.4	70
102	Protein Aggregation Capture on Microparticles Enables Multipurpose Proteomics Sample Preparation. <i>Molecular and Cellular Proteomics</i> , <b>2019</b> , 18, 1027-1035	7.6	70
101	Profiling the phospho-status of the BKCa channel alpha subunit in rat brain reveals unexpected patterns and complexity. <i>Molecular and Cellular Proteomics</i> , <b>2008</b> , 7, 2188-98	7.6	70
100	Signaling initiated by overexpression of the fibroblast growth factor receptor-1 investigated by mass spectrometry. <i>Molecular and Cellular Proteomics</i> , <b>2003</b> , 2, 29-36	7.6	67
99	Analytic framework for peptidomics applied to large-scale neuropeptide identification. <i>Nature Communications</i> , <b>2016</b> , 7, 11436	17.4	66
98	Multilayered proteomics reveals molecular switches dictating ligand-dependent EGFR trafficking. <i>Nature Structural and Molecular Biology</i> , <b>2016</b> , 23, 608-18	17.6	66
97	Ancient proteins from ceramic vessels at Italth West reveal the hidden cuisine of early farmers. <i>Nature Communications</i> , <b>2018</b> , 9, 4064	17.4	64
96	Recent findings and technological advances in phosphoproteomics for cells and tissues. <i>Expert Review of Proteomics</i> , <b>2015</b> , 12, 469-87	4.2	63
95	The low molecular weight proteome of <i>Halobacterium salinarum</i> . <i>Journal of Proteome Research</i> , <b>2007</b> , 6, 1510-8	5.6	60

94	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. <i>Cell Reports</i> , <b>2017</b> , 18, 3242-3256	10.6	59
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> , <b>2015</b> , 14, 1419-34	7.6	59
92	A mass spectrometry-friendly database for cSNP identification. <i>Nature Methods</i> , <b>2007</b> , 4, 465-6	21.6	57
91	MAPU: Max-Planck Unified database of organellar, cellular, tissue and body fluid proteomes. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D771-9	20.1	56
90	Temporal proteomics of NGF-TrkA signaling identifies an inhibitory role for the E3 ligase Cbl-b in neuroblastoma cell differentiation. <i>Science Signaling</i> , <b>2015</b> , 8, ra40	8.8	52
89	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> , <b>2012</b> , 125, 3243-53	5.3	52
88	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. <i>Nature Methods</i> , <b>2014</b> , 11, 868-74	21.6	50
87	Proteomic profiling of archaeological human bone. <i>Royal Society Open Science</i> , <b>2017</b> , 4, 161004	3.3	50
86	Global phosphoproteome profiling reveals unanticipated networks responsive to cisplatin treatment of embryonic stem cells. <i>Molecular and Cellular Biology</i> , <b>2011</b> , 31, 4964-77	4.8	49
85	Species identification of archaeological skin objects from Danish bogs: comparison between mass spectrometry-based peptide sequencing and microscopy-based methods. <i>PLoS ONE</i> , <b>2014</b> , 9, e106875	3.7	49
84	Palaeoproteomics resolves sloth relationships. <i>Nature Ecology and Evolution</i> , <b>2019</b> , 3, 1121-1130	12.3	47
83	The dental proteome of Homo antecessor. <i>Nature</i> , <b>2020</b> , 580, 235-238	50.4	47
82	Metaproteomics of saliva identifies human protein markers specific for individuals with periodontitis and dental caries compared to orally healthy controls. <i>PeerJ</i> , <b>2016</b> , 4, e2433	3.1	44
81	High accuracy mass spectrometry in large-scale analysis of protein phosphorylation. <i>Methods in Molecular Biology</i> , <b>2009</b> , 492, 131-42	1.4	43
80	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. <i>Angewandte Chemie - International Edition</i> , <b>2018</b> , 57, 7369-7374	16.4	41
79	Enamel proteome shows that Gigantopithecus was an early diverging pongine. <i>Nature</i> , <b>2019</b> , 576, 262-265	50.4	41
78	The dual methyltransferase METTL13 targets N terminus and Lys55 of eEF1A and modulates codon-specific translation rates. <i>Nature Communications</i> , <b>2018</b> , 9, 3411	17.4	40
77	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> , <b>2007</b> , 1134, 95-106	3.7	39

76	Phosphorylation of the yeast $\beta$ tubulin Tub4 regulates microtubule function. <i>PLoS ONE</i> , <b>2011</b> , 6, e19700	3.7	38
75	The human methyltransferase ZCCHC4 catalyses N6-methyladenosine modification of 28S ribosomal RNA. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 830-846	20.1	38
74	Can relative cleavage frequencies in peptides provide additional sequence information?. <i>International Journal of Mass Spectrometry</i> , <b>2002</b> , 219, 283-294	1.9	37
73	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. <i>Nature Communications</i> , <b>2018</b> , 9, 4744	17.4	36
72	A comprehensive platform for the analysis of ubiquitin-like protein modifications using in vivo biotinylation. <i>Scientific Reports</i> , <b>2017</b> , 7, 40756	4.9	34
71	Large-Scale Phosphoproteomics Reveals Shp-2 Phosphatase-Dependent Regulators of Pdgf Receptor Signaling. <i>Cell Reports</i> , <b>2018</b> , 22, 2784-2796	10.6	34
70	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. <i>Cell</i> , <b>2019</b> , 179, 543-560.e26	56.2	31
69	GeLCMS for in-depth protein characterization and advanced analysis of proteomes. <i>Methods in Molecular Biology</i> , <b>2011</b> , 753, 143-55	1.4	31
68	Comparison of electron capture dissociation and collisionally activated dissociation of polycations of peptide nucleic acids. <i>Rapid Communications in Mass Spectrometry</i> , <b>2001</b> , 15, 969-74	2.2	30
67	Offline High pH Reversed-Phase Peptide Fractionation for Deep Phosphoproteome Coverage. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1355, 179-92	1.4	30
66	Dynamic lineage priming is driven via direct enhancer regulation by ERK. <i>Nature</i> , <b>2019</b> , 575, 355-360	50.4	29
65	A direct role of Mad1 in the spindle assembly checkpoint beyond Mad2 kinetochore recruitment. <i>EMBO Reports</i> , <b>2014</b> , 15, 282-90	6.5	29
64	Disulfide Linkage Characterization of Disulfide Bond-Containing Proteins and Peptides by Reducing Electrochemistry and Mass Spectrometry. <i>Analytical Chemistry</i> , <b>2016</b> , 88, 1585-92	7.8	28
63	Simple and Reproducible Sample Preparation for Single-Shot Phosphoproteomics with High Sensitivity. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1355, 251-60	1.4	28
62	TIMP-1 increases expression and phosphorylation of proteins associated with drug resistance in breast cancer cells. <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 4136-51	5.6	26
61	Complete Mapping of Complex Disulfide Patterns with Closely-Spaced Cysteines by In-Source Reduction and Data-Dependent Mass Spectrometry. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 5949-5957	7.8	25
60	The ubiquitin ligase Cullin5 regulates NDR1/STK38 stability and NF- $\kappa$ B transactivation. <i>Scientific Reports</i> , <b>2017</b> , 7, 42800	4.9	25
59	Multi-spectra peptide sequencing and its applications to multistage mass spectrometry. <i>Bioinformatics</i> , <b>2008</b> , 24, i416-23	7.2	25



58	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> , <b>2014</b> , 170, 222-232	2.4	24
57	Pinpointing phosphorylation sites: Quantitative filtering and a novel site-specific x-ion fragment. <i>Journal of Proteome Research</i> , <b>2011</b> , 10, 2937-48	5.6	24
56	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> , <b>2015</b> , 290, 15526-15537	5.4	22
55	Analysis of changes in SUMO-2/3 modification during breast cancer progression and metastasis. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 3905-18	5.6	22
54	Systems biology approach identifies the kinase Csnk1a1 as a regulator of the DNA damage response in embryonic stem cells. <i>Science Signaling</i> , <b>2013</b> , 6, ra5	8.8	22
53	Molecular evidence of use of hide glue in 4th millennium BC Europe. <i>Journal of Archaeological Science</i> , <b>2015</b> , 63, 65-71	2.9	21
52	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. <i>Molecular Systems Biology</i> , <b>2021</b> , 17, e9730	12.2	20
51	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> , <b>2014</b> , 170, 222-232	2.4	18
50	Comprehensive identification of SUMO2/3 targets and their dynamics during mitosis. <i>PLoS ONE</i> , <b>2014</b> , 9, e100692	3.7	17
49	The methyltransferase METTL9 mediates pervasive 1-methylhistidine modification in mammalian proteomes. <i>Nature Communications</i> , <b>2021</b> , 12, 891	17.4	17
48	Limits for Resolving Isobaric Tandem Mass Tag Reporter Ions Using Phase-Constrained Spectrum Deconvolution. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 4008-4016	5.6	17
47	Analytical utility of mass spectral binning in proteomic experiments by SPECTRAL Immonium Ion Detection (SPIID). <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 1914-24	7.6	15
46	From Phosphosites to Kinases. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1355, 307-21	1.4	15
45	Integrated proximal proteomics reveals IRS2 as a determinant of cell survival in ALK-driven neuroblastoma. <i>Science Signaling</i> , <b>2018</b> , 11,	8.8	15
44	Mass-Spectrometry Based Proteome Comparison of Extracellular Vesicle Isolation Methods: Comparison of ME-kit, Size-Exclusion Chromatography, and High-Speed Centrifugation. <i>Biomedicines</i> , <b>2020</b> , 8,	4.8	14
43	Molecular basis of Tausled-Like Kinase 2 activation. <i>Nature Communications</i> , <b>2018</b> , 9, 2535	17.4	14
42	Generic Workflow for Mapping of Complex Disulfide Bonds Using In-Source Reduction and Extracted Ion Chromatograms from Data-Dependent Mass Spectrometry. <i>Analytical Chemistry</i> , <b>2018</b> , 90, 8202-8210	7.8	13
41	Combinatorial Drug Screening Identifies Ewing Sarcoma-specific Sensitivities. <i>Molecular Cancer Therapeutics</i> , <b>2017</b> , 16, 88-101	6.1	13

40	Effective representation and storage of mass spectrometry-based proteomic data sets for the scientific community. <i>Science Signaling</i> , <b>2011</b> , 4, pe7	8.8	13
39	Multi-omic detection of in archaeological human dental calculus. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2020</b> , 375, 20190584	5.8	13
38	Proteome and Phosphoproteome Changes Associated with Prognosis in Acute Myeloid Leukemia. <i>Cancers</i> , <b>2020</b> , 12,	6.6	12
37	Human METTL18 is a histidine-specific methyltransferase that targets RPL3 and affects ribosome biogenesis and function. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 3185-3203	20.1	12
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