

Jesper V. Olsen

List of Publications by Year in Descending Order

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Version: 2024-04-28

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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	A deeper look at carrier proteome effects for single-cell proteomics.. <i>Communications Biology</i> , 2022 , 5, 150	6.7	2
226	Phosphorylation of SHP2 at Tyr62 enables acquired resistance to SHP2 allosteric inhibitors in FLT3-ITD-driven AML.. <i>Cancer Research</i> , 2022 ,	10.1	2
225	SPIN enables high throughput species identification of archaeological bone by proteomics.. <i>Nature Communications</i> , 2022 , 13, 2458	17.4	1
224	A Middle Pleistocene Denisovan molar from the Annamite Chain of northern Laos.. <i>Nature Communications</i> , 2022 , 13, 2557	17.4	3
223	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	20.1	12
222	Proteomic investigation of Cbl and Cbl-b in neuroblastoma cell differentiation highlights roles for SHP-2 and CDK16. <i>iScience</i> , 2021 , 24, 102321	6.1	3
221	Faecal proteomics as a novel method to study mammalian behaviour and physiology. <i>Molecular Ecology Resources</i> , 2021 , 21, 1808-1819	8.4	1
220	Quantitative proteome comparison of human hearts with those of model organisms. <i>PLoS Biology</i> , 2021 , 19, e3001144	9.7	7
219	Proteomics of resistance to Notch1 inhibition in acute lymphoblastic leukemia reveals targetable kinase signatures. <i>Nature Communications</i> , 2021 , 12, 2507	17.4	6
218	GHB analogs confer neuroprotection through specific interaction with the CaMKII α hub domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	8
217	FRMD6 has tumor suppressor functions in prostate cancer. <i>Oncogene</i> , 2021 , 40, 763-776	9.2	11
216	Data Processing and Analysis for DIA-Based Phosphoproteomics Using Spectronaut. <i>Methods in Molecular Biology</i> , 2021 , 2361, 95-107	1.4	1
215	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	17.6	7
214	The methyltransferase METTL9 mediates pervasive 1-methylhistidine modification in mammalian proteomes. <i>Nature Communications</i> , 2021 , 12, 891	17.4	17
213	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. <i>Molecular Systems Biology</i> , 2021 , 17, e9730	12.2	20
212	Spatial-proteomics reveals phospho-signaling dynamics at subcellular resolution. <i>Nature Communications</i> , 2021 , 12, 7113	17.4	5
211	The biomolecular characterization of a finger ring contextually dated to the emergence of the Early Neolithic from Syltholm, Denmark. <i>Royal Society Open Science</i> , 2020 , 7, 191172	3.3	3

210	Quantitative phosphoproteomics to unravel the cellular response to chemical stressors with different modes of action. <i>Archives of Toxicology</i> , 2020 , 94, 1655-1671	5.8	4
209	Proteome and Phosphoproteome Changes Associated with Prognosis in Acute Myeloid Leukemia. <i>Cancers</i> , 2020 , 12,	6.6	12
208	The dental proteome of Homo antecessor. <i>Nature</i> , 2020 , 580, 235-238	50.4	47
207	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
206	Deciphering the human phosphoproteome. <i>Nature Biotechnology</i> , 2020 , 38, 285-286	44.5	3
205	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
204	Quantitative proteomics characterization of acutely isolated primary adult rat cardiomyocytes and fibroblasts. <i>Journal of Molecular and Cellular Cardiology</i> , 2020 , 143, 63-70	5.8	4
203	The human methyltransferase ZCCHC4 catalyses N6-methyladenosine modification of 28S ribosomal RNA. <i>Nucleic Acids Research</i> , 2020 , 48, 830-846	20.1	38
202	ProAlanase is an Effective Alternative to Trypsin for Proteomics Applications and Disulfide Bond Mapping. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 2139-2157	7.6	7
201	Multi-protease analysis of Pleistocene bone proteomes. <i>Journal of Proteomics</i> , 2020 , 228, 103889	3.9	3
200	Effects of active farnesoid X receptor on GLUTag enteroendocrine L cells. <i>Molecular and Cellular Endocrinology</i> , 2020 , 517, 110923	4.4	3
199	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,	4.8	14
198	Multi-omic detection of in archaeological human dental calculus. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020 , 375, 20190584	5.8	13
197	ZAK1Recognizes Stalled Ribosomes through Partially Redundant Sensor Domains. <i>Molecular Cell</i> , 2020 , 78, 700-713.e7	17.6	19
196	Quantitative Proteomics of Human Heart Samples Collected Reveal the Remodeled Protein Landscape of Dilated Left Atrium Without Atrial Fibrillation. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 1132-1144	7.6	11
195	Molecular Basis of the Mechanisms Controlling MASTL. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 326-343	7.6	2
194	Palaeoproteomic identification of breast milk protein residues from the archaeological skeletal remains of a neonatal dog. <i>Scientific Reports</i> , 2019 , 9, 12841	4.9	7
193	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. <i>Nature</i> , 2019 , 574, 103-107	50.4	70

192	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. <i>Cell</i> , 2019 , 179, 543-560.e26	56.2	31
191	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
190	Alternative Translation Initiation Generates a Functionally Distinct Isoform of the Stress-Activated Protein Kinase MK2. <i>Cell Reports</i> , 2019 , 27, 2859-2870.e6	10.6	5
189	Palaeoproteomics resolves sloth relationships. <i>Nature Ecology and Evolution</i> , 2019 , 3, 1121-1130	12.3	47
188	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	20.1	11
187	Protein Aggregation Capture on Microparticles Enables Multipurpose Proteomics Sample Preparation. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1027-1035	7.6	70
186	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
185	Expression and secretion of a lytic polysaccharide monooxygenase by a fast-growing cyanobacterium. <i>Biotechnology for Biofuels</i> , 2019 , 12, 74	7.8	12
184	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
183	Dynamic lineage priming is driven via direct enhancer regulation by ERK. <i>Nature</i> , 2019 , 575, 355-360	50.4	29
182	Enamel proteome shows that Gigantopithecus was an early diverging pongine. <i>Nature</i> , 2019 , 576, 262-265	55.4	41
181	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
180	Large-Scale Phosphoproteomics Reveals Shp-2 Phosphatase-Dependent Regulators of Pdgf Receptor Signaling. <i>Cell Reports</i> , 2018 , 22, 2784-2796	10.6	34
179	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. <i>Angewandte Chemie</i> , 2018 , 130, 7491-7496	3.6	1
178	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
177	Truncated SALL1 Impedes Primary Cilia Function in Townes-Brocks Syndrome. <i>American Journal of Human Genetics</i> , 2018 , 102, 249-265	11	16
176	Control of endothelial cell tube formation by Notch ligand intracellular domain interactions with activator protein 1 (AP-1). <i>Journal of Biological Chemistry</i> , 2018 , 293, 1229-1242	5.4	6
175	Benchmarking common quantification strategies for large-scale phosphoproteomics. <i>Nature Communications</i> , 2018 , 9, 1045	17.4	146

174	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
173	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
172	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
171	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> , 2018 , 90, 8202-8210	7.8	13
170	Performance Evaluation of the Q Exactive HF-X for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018 , 17, 727-738	5.6	160
169	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. <i>Nature Communications</i> , 2018 , 9, 4744	17.4	36
168	Integrated proximal proteomics reveals IRS2 as a determinant of cell survival in ALK-driven neuroblastoma. <i>Science Signaling</i> , 2018 , 11,	8.8	15
167	Ancient proteins from ceramic vessels at Italho West reveal the hidden cuisine of early farmers. <i>Nature Communications</i> , 2018 , 9, 4064	17.4	64
166	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
165	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
164	PKD Phosphorylation as Novel Pathway of KV11.1 Regulation. <i>Cellular Physiology and Biochemistry</i> , 2018 , 47, 1742-1750	3.9	2
163	Molecular basis of Tausled-Like Kinase 2 activation. <i>Nature Communications</i> , 2018 , 9, 2535	17.4	14
162	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
161	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
160	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. <i>Cell Systems</i> , 2017 , 4, 587-599.e4	10.6	255
159	The ubiquitin ligase Cullin5 regulates NDR1/STK38 stability and NF- κ B transactivation. <i>Scientific Reports</i> , 2017 , 7, 42800	4.9	25
158	KIT Induces SRC-Mediated Tyrosine Phosphorylation of MITF and Altered Transcription Program in Melanoma. <i>Molecular Cancer Research</i> , 2017 , 15, 1265-1274	6.6	11
157	Cylindromatosis Tumor Suppressor Protein (CYLD) Deubiquitinase is Necessary for Proper Ubiquitination and Degradation of the Epidermal Growth Factor Receptor. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 1433-1446	7.6	11

156	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. <i>Cell Reports</i> , 2017 , 18, 3242-3256	10.6	59
155	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
154	Proteomic profiling of archaeological human bone. <i>Royal Society Open Science</i> , 2017 , 4, 161004	3.3	50
153	Proteomics insights into DNA damage response and translating this knowledge to clinical strategies. <i>Proteomics</i> , 2017 , 17, 1600018	4.8	10
152	Combinatorial Drug Screening Identifies Ewing Sarcoma-specific Sensitivities. <i>Molecular Cancer Therapeutics</i> , 2017 , 16, 88-101	6.1	13
151	Cetuximab Resistance in Squamous Carcinomas of the Upper Aerodigestive Tract Is Driven by Receptor Tyrosine Kinase Plasticity: Potential for mAb Mixtures. <i>Molecular Cancer Therapeutics</i> , 2016 , 15, 1614-26	6.1	8
150	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 1435-1448	15.1	76
149	A Conserved Motif Provides Binding Specificity to the PP2A-B56 Phosphatase. <i>Molecular Cell</i> , 2016 , 63, 686-695	17.6	145
148	Analytic framework for peptidomics applied to large-scale neuropeptide identification. <i>Nature Communications</i> , 2016 , 7, 11436	17.4	66
147	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
146	Conformation-specific anti-Mad2 monoclonal antibodies for the dissection of checkpoint signaling. <i>MAbs</i> , 2016 , 8, 689-97	6.6	8
145	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
144	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
143	Protein sequences bound to mineral surfaces persist into deep time. <i>ELife</i> , 2016 , 5,	8.9	118
142	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
141	Offline High pH Reversed-Phase Peptide Fractionation for Deep Phosphoproteome Coverage. <i>Methods in Molecular Biology</i> , 2016 , 1355, 179-92	1.4	30
140	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
139	From Phosphosites to Kinases. <i>Methods in Molecular Biology</i> , 2016 , 1355, 307-21	1.4	15

138	Systems Analysis for Interpretation of Phosphoproteomics Data. <i>Methods in Molecular Biology</i> , 2016 , 1355, 341-60	1.4	12
137	Multilayered proteomics reveals molecular switches dictating ligand-dependent EGFR trafficking. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 608-18	17.6	66
136	Ctk1 function is necessary for full translation initiation activity in <i>Saccharomyces cerevisiae</i> . <i>Eukaryotic Cell</i> , 2015 , 14, 86-95		12
135	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
134	SUMO-2 Orchestrates Chromatin Modifiers in Response to DNA Damage. <i>Cell Reports</i> , 2015 , 10, 1778-1791	11.6	90
133	In vivo quantitative phosphoproteomic profiling identifies novel regulators of castration-resistant prostate cancer growth. <i>Oncogene</i> , 2015 , 34, 2764-76	9.2	47
132	Ancient proteins resolve the evolutionary history of Darwin's South American ungulates. <i>Nature</i> , 2015 , 522, 81-4	50.4	210
131	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
130	Recent findings and technological advances in phosphoproteomics for cells and tissues. <i>Expert Review of Proteomics</i> , 2015 , 12, 469-87	4.2	63
129	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
128	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
127	Protein kinase A stimulates Kv7.1 surface expression by regulating Nedd4-2-dependent endocytic trafficking. <i>American Journal of Physiology - Cell Physiology</i> , 2015 , 309, C693-706	5.4	5
126	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
125	Direct evidence of milk consumption from ancient human dental calculus. <i>Scientific Reports</i> , 2014 , 4, 7104	4.9	125
124	Pathogens and host immunity in the ancient human oral cavity. <i>Nature Genetics</i> , 2014 , 46, 336-44	36.3	353
123	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
122	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
121	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

120	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
119	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
118	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014 , 345, 1255832	33.3	204
117	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
116	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
115	The PI3-kinase isoform p110 β is essential for cell transformation induced by the D816V mutant of c-Kit in a lipid-kinase-independent manner. <i>Oncogene</i> , 2014 , 33, 5360-9	9.2	12
114	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
113	Analytical utility of mass spectral binning in proteomic experiments by SPectral Immonium Ion Detection (SPIID). <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1914-24	7.6	15
112	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
111	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
110	Off-line high-pH reversed-phase fractionation for in-depth phosphoproteomics. <i>Journal of Proteome Research</i> , 2014 , 13, 6176-86	5.6	194
109	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
108	Predicting kinase activity in angiotensin receptor phosphoproteomes based on sequence-motifs and interactions. <i>PLoS ONE</i> , 2014 , 9, e94672	3.7	7
107	Comprehensive identification of SUMO2/3 targets and their dynamics during mitosis. <i>PLoS ONE</i> , 2014 , 9, e100692	3.7	17
106	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
105	SILAC-based temporal phosphoproteomics. <i>Methods in Molecular Biology</i> , 2014 , 1188, 125-48	1.4	9
104	Structures of Down syndrome kinases, DYRKs, reveal mechanisms of kinase activation and substrate recognition. <i>Structure</i> , 2013 , 21, 986-96	5.2	99
103	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

102	Functional proteomics defines the molecular switch underlying FGF receptor trafficking and cellular outputs. <i>Molecular Cell</i> , 2013 , 51, 707-22	17.6	105
101	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
100	The SH2 domain interaction landscape. <i>Cell Reports</i> , 2013 , 3, 1293-305	10.6	89
99	RNF4 is required for DNA double-strand break repair in vivo. <i>Cell Death and Differentiation</i> , 2013 , 20, 490-502	12.7	79
98	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
97	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013 , 499, 74-8	50.4	563
96	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
95	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
94	Phosphorylation variation during the cell cycle scales with structural propensities of proteins. <i>PLoS Computational Biology</i> , 2013 , 9, e1002842	5	48
93	In vivo phosphoproteomics analysis reveals the cardiac targets of β adrenergic receptor signaling. <i>Science Signaling</i> , 2013 , 6, rs11	8.8	129
92	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
91	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
90	Correction to Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. <i>Journal of Proteome Research</i> , 2012 , 11, 3506-3508	5.6	10
89	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
88	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
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	Quantitative maps of protein phosphorylation sites across 14 different rat organs and tissues. <i>Nature Communications</i> , 2012 , 3, 876	17.4	248
85	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

84	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
83	Proteomic analyses reveal divergent ubiquitylation site patterns in murine tissues. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1578-85	7.6	214
82	γ -GABA(A) 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, 13404-9	11.5	72
81	GeLCMS for in-depth protein characterization and advanced analysis of proteomes. <i>Methods in Molecular Biology</i> , 2011 , 753, 143-55	1.4	31
80	Proteome-wide mapping of the Drosophila acetylome demonstrates a high degree of conservation of lysine acetylation. <i>Science Signaling</i> , 2011 , 4, ra48	8.8	204
79	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
78	Pre-Clovis mastodon hunting 13,800 years ago at the Manis site, Washington. <i>Science</i> , 2011 , 334, 351-3	33.3	129
77	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
76	Andromeda: a peptide search engine integrated into the MaxQuant environment. <i>Journal of Proteome Research</i> , 2011 , 10, 1794-805	5.6	3402
75	Effective representation and storage of mass spectrometry-based proteomic data sets for the scientific community. <i>Science Signaling</i> , 2011 , 4, pe7	8.8	13
74	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
73	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
72	Phosphorylation of the yeast β -tubulin Tub4 regulates microtubule function. <i>PLoS ONE</i> , 2011 , 6, e19700	3.7	38
71	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
70	MSQuant, an open source platform for mass spectrometry-based quantitative proteomics. <i>Journal of Proteome Research</i> , 2010 , 9, 393-403	5.6	225
69	Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. <i>Science Signaling</i> , 2010 , 3, ra3	8.8	1106
68	Feasibility of large-scale phosphoproteomics with higher energy collisional dissociation fragmentation. <i>Journal of Proteome Research</i> , 2010 , 9, 6786-94	5.6	139
67	Yeast expression proteomics by high-resolution mass spectrometry. <i>Methods in Enzymology</i> , 2010 , 470, 259-80	1.7	8

66	Quantitative interaction proteomics and genome-wide profiling of epigenetic histone marks and their readers. <i>Cell</i> , 2010 , 142, 967-80	56.2	579
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7	A novel LC system embeds analytes in pre-formed gradients for rapid, ultra-robust proteomics		2
6	Limits for resolving tandem mass tag reporter ions with identical integer mass using phase constrained spectrum deconvolution		1
5	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses		5
4	Early Pleistocene enamel proteome sequences from Dmanisi resolve <i>Stephanorhinus</i> phylogeny		5
3	Protein aggregation capture on microparticles enables multi-purpose proteomics sample preparation		1
2	Rapid and site-specific deep phosphoproteome profiling by data-independent acquisition (DIA) without the need for spectral libraries		3
1	A Compact Quadrupole-Orbitrap Mass Spectrometer with FAIMS Interface Improves Proteome Coverage in Short LC Gradients		2