

Jesper V Olsen

List of Publications by Year in Descending Order

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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.

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	A deeper look at carrier proteome effects for single-cell proteomics.. <i>Communications Biology</i> , 2022 , 5, 150	6.7	2
182	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
181	A Middle Pleistocene Denisovan molar from the Annamite Chain of northern Laos.. <i>Nature Communications</i> , 2022 , 13, 2557	17.4	3
180	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
179	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
178	Faecal proteomics as a novel method to study mammalian behaviour and physiology. <i>Molecular Ecology Resources</i> , 2021 , 21, 1808-1819	8.4	1
177	Quantitative proteome comparison of human hearts with those of model organisms. <i>PLoS Biology</i> , 2021 , 19, e3001144	9.7	7
176	Proteomics of resistance to Notch1 inhibition in acute lymphoblastic leukemia reveals targetable kinase signatures. <i>Nature Communications</i> , 2021 , 12, 2507	17.4	6
175	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
174	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
173	The methyltransferase METTL9 mediates pervasive 1-methylhistidine modification in mammalian proteomes. <i>Nature Communications</i> , 2021 , 12, 891	17.4	17
172	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. <i>Molecular Systems Biology</i> , 2021 , 17, e9730	12.2	20
171	Spatial-proteomics reveals phospho-signaling dynamics at subcellular resolution. <i>Nature Communications</i> , 2021 , 12, 7113	17.4	5
170	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
169	Proteome and Phosphoproteome Changes Associated with Prognosis in Acute Myeloid Leukemia. <i>Cancers</i> , 2020 , 12,	6.6	12
168	The dental proteome of Homo antecessor. <i>Nature</i> , 2020 , 580, 235-238	50.4	47
167	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

166	Deciphering the human phosphoproteome. <i>Nature Biotechnology</i> , 2020 , 38, 285-286	44.5	3
165	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
164	The human methyltransferase ZCCHC4 catalyses N6-methyladenosine modification of 28S ribosomal RNA. <i>Nucleic Acids Research</i> , 2020 , 48, 830-846	20.1	38
163	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
162	Multi-protease analysis of Pleistocene bone proteomes. <i>Journal of Proteomics</i> , 2020 , 228, 103889	3.9	3
161	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
160	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
159	Molecular Basis of the Mechanisms Controlling MASTL. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 326-343	3.4	2
158	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
157	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. <i>Nature</i> , 2019 , 574, 103-107	50.4	70
156	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. <i>Cell</i> , 2019 , 179, 543-560.e26	56.2	31
155	Palaeoproteomics resolves sloth relationships. <i>Nature Ecology and Evolution</i> , 2019 , 3, 1121-1130	12.3	47
154	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
153	Protein Aggregation Capture on Microparticles Enables Multipurpose Proteomics Sample Preparation. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1027-1035	7.6	70
152	Dynamic lineage priming is driven via direct enhancer regulation by ERK. <i>Nature</i> , 2019 , 575, 355-360	50.4	29
151	Enamel proteome shows that Gigantopithecus was an early diverging pongine. <i>Nature</i> , 2019 , 576, 262-265	50.4	41
150	Large-Scale Phosphoproteomics Reveals Shp-2 Phosphatase-Dependent Regulators of Pdgf Receptor Signaling. <i>Cell Reports</i> , 2018 , 22, 2784-2796	10.6	34
149	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. <i>Angewandte Chemie</i> , 2018 , 130, 7491-7496	3.6	1

148	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
147	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
146	Benchmarking common quantification strategies for large-scale phosphoproteomics. <i>Nature Communications</i> , 2018 , 9, 1045	17.4	146
145	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
144	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
143	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
142	Performance Evaluation of the Q Exactive HF-X for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018 , 17, 727-738	5.6	160
141	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. <i>Nature Communications</i> , 2018 , 9, 4744	17.4	36
140	Integrated proximal proteomics reveals IRS2 as a determinant of cell survival in ALK-driven neuroblastoma. <i>Science Signaling</i> , 2018 , 11,	8.8	15
139	Ancient proteins from ceramic vessels at Italy West reveal the hidden cuisine of early farmers. <i>Nature Communications</i> , 2018 , 9, 4064	17.4	64
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	5.6	17
137	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
136	Molecular basis of Tausled-Like Kinase 2 activation. <i>Nature Communications</i> , 2018 , 9, 2535	17.4	14
135	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
134	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
133	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. <i>Cell Systems</i> , 2017 , 4, 587-599.e4	10.6	255
132	The ubiquitin ligase Cullin5 regulates NDR1/STK38 stability and NF- κ B transactivation. <i>Scientific Reports</i> , 2017 , 7, 42800	4.9	25
131	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

130	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
129	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. <i>Cell Reports</i> , 2017 , 18, 3242-3256	10.6	59
128	Proteomic profiling of archaeological human bone. <i>Royal Society Open Science</i> , 2017 , 4, 161004	3.3	50
127	Proteomics insights into DNA damage response and translating this knowledge to clinical strategies. <i>Proteomics</i> , 2017 , 17, 1600018	4.8	10
126	Combinatorial Drug Screening Identifies Ewing Sarcoma-specific Sensitivities. <i>Molecular Cancer Therapeutics</i> , 2017 , 16, 88-101	6.1	13
125	Analytic framework for peptidomics applied to large-scale neuropeptide identification. <i>Nature Communications</i> , 2016 , 7, 11436	17.4	66
124	Conformation-specific anti-Mad2 monoclonal antibodies for the dissection of checkpoint signaling. <i>MAbs</i> , 2016 , 8, 689-97	6.6	8
123	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
122	Protein sequences bound to mineral surfaces persist into deep time. <i>ELife</i> , 2016 , 5,	8.9	118
121	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
120	Offline High pH Reversed-Phase Peptide Fractionation for Deep Phosphoproteome Coverage. <i>Methods in Molecular Biology</i> , 2016 , 1355, 179-92	1.4	30
119	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
118	From Phosphosites to Kinases. <i>Methods in Molecular Biology</i> , 2016 , 1355, 307-21	1.4	15
117	Multilayered proteomics reveals molecular switches dictating ligand-dependent EGFR trafficking. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 608-18	17.6	66
116	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
115	SUMO-2 Orchestrates Chromatin Modifiers in Response to DNA Damage. <i>Cell Reports</i> , 2015 , 10, 1778-1791	11.6	90
114	Ancient proteins resolve the evolutionary history of Darwin's South American ungulates. <i>Nature</i> , 2015 , 522, 81-4	50.4	210
113	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

112	Recent findings and technological advances in phosphoproteomics for cells and tissues. <i>Expert Review of Proteomics</i> , 2015 , 12, 469-87	4.2	63
111	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
110	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
109	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
108	Pathogens and host immunity in the ancient human oral cavity. <i>Nature Genetics</i> , 2014 , 46, 336-44	36.3	353
107	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
106	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
105	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
104	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
103	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
102	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
101	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
100	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
99	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
98	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
97	Off-line high-pH reversed-phase fractionation for in-depth phosphoproteomics. <i>Journal of Proteome Research</i> , 2014 , 13, 6176-86	5.6	194
96	Predicting kinase activity in angiotensin receptor phosphoproteomes based on sequence-motifs and interactions. <i>PLoS ONE</i> , 2014 , 9, e94672	3.7	7
95	Comprehensive identification of SUMO2/3 targets and their dynamics during mitosis. <i>PLoS ONE</i> , 2014 , 9, e100692	3.7	17

94	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
93	SILAC-based temporal phosphoproteomics. <i>Methods in Molecular Biology</i> , 2014 , 1188, 125-48	1.4	9
92	Structures of Down syndrome kinases, DYRKs, reveal mechanisms of kinase activation and substrate recognition. <i>Structure</i> , 2013 , 21, 986-96	5.2	99
91	Functional proteomics defines the molecular switch underlying FGF receptor trafficking and cellular outputs. <i>Molecular Cell</i> , 2013 , 51, 707-22	17.6	105
90	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
89	The SH2 domain interaction landscape. <i>Cell Reports</i> , 2013 , 3, 1293-305	10.6	89
88	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
87	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013 , 499, 74-8	50.4	563
86	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
85	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
84	In vivo phosphoproteomics analysis reveals the cardiac targets of β adrenergic receptor signaling. <i>Science Signaling</i> , 2013 , 6, rs11	8.8	129
83	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
82	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
81	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
80	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
79	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
78	Quantitative maps of protein phosphorylation sites across 14 different rat organs and tissues. <i>Nature Communications</i> , 2012 , 3, 876	17.4	248
77	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

76	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
75	Proteomic analyses reveal divergent ubiquitylation site patterns in murine tissues. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1578-85	7.6	214
74	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
73	GeLCMS for in-depth protein characterization and advanced analysis of proteomes. <i>Methods in Molecular Biology</i> , 2011 , 753, 143-55	1.4	31
72	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
71	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
70	Pre-Clovis mastodon hunting 13,800 years ago at the Manis site, Washington. <i>Science</i> , 2011 , 334, 351-3	33.3	129
69	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
68	Andromeda: a peptide search engine integrated into the MaxQuant environment. <i>Journal of Proteome Research</i> , 2011 , 10, 1794-805	5.6	3402
67	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
66	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
65	Phosphorylation of the yeast β-tubulin Tub4 regulates microtubule function. <i>PLoS ONE</i> , 2011 , 6, e19700	3.7	38
64	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
63	MSQuant, an open source platform for mass spectrometry-based quantitative proteomics. <i>Journal of Proteome Research</i> , 2010 , 9, 393-403	5.6	225
62	Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. <i>Science Signaling</i> , 2010 , 3, ra3	8.8	1106
61	Feasibility of large-scale phosphoproteomics with higher energy collisional dissociation fragmentation. <i>Journal of Proteome Research</i> , 2010 , 9, 6786-94	5.6	139
60	Yeast expression proteomics by high-resolution mass spectrometry. <i>Methods in Enzymology</i> , 2010 , 470, 259-80	1.7	8
59	Quantitative interaction proteomics and genome-wide profiling of epigenetic histone marks and their readers. <i>Cell</i> , 2010 , 142, 967-80	56.2	579

58	The phosphoproteome of toll-like receptor-activated macrophages. <i>Molecular Systems Biology</i> , 2010 , 6, 371	12.2	113
57	Phosphorylation of histone H3 Thr-45 is linked to apoptosis. <i>Journal of Biological Chemistry</i> , 2009 , 284, 16575-16583	5.4	85
56	Global effects of kinase inhibitors on signaling networks revealed by quantitative phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 2796-808	7.6	165
55	A dual pressure linear ion trap Orbitrap instrument with very high sequencing speed. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 2759-69	7.6	379
54	Large-scale proteomics analysis of the human kinome. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 1751-646	7.6	236
53	High-accuracy identification and bioinformatic analysis of in vivo protein phosphorylation sites in yeast. <i>Proteomics</i> , 2009 , 9, 4642-52	4.8	103
52	Proteomics strategy for quantitative protein interaction profiling in cell extracts. <i>Nature Methods</i> , 2009 , 6, 741-4	21.6	121
51	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. <i>Nature Protocols</i> , 2009 , 4, 698-705	18.8	637
50	Lysine acetylation targets protein complexes and co-regulates major cellular functions. <i>Science</i> , 2009 , 325, 834-40	33.3	3316
49	Mislocalized activation of oncogenic RTKs switches downstream signaling outcomes. <i>Molecular Cell</i> , 2009 , 36, 326-39	17.6	245
48	Global analysis of the yeast osmotic stress response by quantitative proteomics. <i>Molecular BioSystems</i> , 2009 , 5, 1337-46		108
47	Global and site-specific quantitative phosphoproteomics: principles and applications. <i>Annual Review of Pharmacology and Toxicology</i> , 2009 , 49, 199-221	17.9	350
46	High accuracy mass spectrometry in large-scale analysis of protein phosphorylation. <i>Methods in Molecular Biology</i> , 2009 , 492, 131-42	1.4	43
45	Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast. <i>Nature</i> , 2008 , 455, 1251-4	50.4	745
44	Ubc9 sumoylation regulates SUMO target discrimination. <i>Molecular Cell</i> , 2008 , 31, 371-82	17.6	169
43	Kinase-selective enrichment enables quantitative phosphoproteomics of the kinome across the cell cycle. <i>Molecular Cell</i> , 2008 , 31, 438-48	17.6	495
42	Phosphoproteome analysis of E. coli reveals evolutionary conservation of bacterial Ser/Thr/Tyr phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 299-307	7.6	334
41	Multi-spectra peptide sequencing and its applications to multistage mass spectrometry. <i>Bioinformatics</i> , 2008 , 24, i416-23	7.2	25

40	Investigation of protein-tyrosine phosphatase 1B function by quantitative proteomics. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1763-77	7.6	91
39	Profiling the phospho-status of the BKCa channel alpha subunit in rat brain reveals unexpected patterns and complexity. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 2188-98	7.6	70
38	Quantitative phosphoproteome analysis of a mouse liver cell line reveals specificity of phosphatase inhibitors. <i>Proteomics</i> , 2008 , 8, 4534-46	4.8	89
37	Temporal Dynamics of EGF Receptor Signaling by Quantitative Proteomics 2008 , 190-198		1
36	Nano electrospray peptide mapping revisited: Composite survey spectra allow high dynamic range protein characterization without LCMS on an orbitrap mass spectrometer. <i>International Journal of Mass Spectrometry</i> , 2007 , 268, 158-167	1.9	8
35	Phosphoproteins of the chicken eggshell calcified layer. <i>Proteomics</i> , 2007 , 7, 106-15	4.8	95
34	Quantitative proteomic assessment of very early cellular signaling events. <i>Nature Biotechnology</i> , 2007 , 25, 566-8	44.5	103
33	A mass spectrometry-friendly database for cSNP identification. <i>Nature Methods</i> , 2007 , 4, 465-6	21.6	57
32	Higher-energy C-trap dissociation for peptide modification analysis. <i>Nature Methods</i> , 2007 , 4, 709-12	21.6	727
31	Noncovalent interaction between Ubc9 and SUMO promotes SUMO chain formation. <i>EMBO Journal</i> , 2007 , 26, 2797-807	13	160
30	Quantitative proteomic profiling of membrane proteins from the mouse brain cortex, hippocampus, and cerebellum using the HysTag reagent: mapping of neurotransmitter receptors and ion channels. <i>Brain Research</i> , 2007 , 1134, 95-106	3.7	39
29	MAPU: Max-Planck Unified database of organellar, cellular, tissue and body fluid proteomes. <i>Nucleic Acids Research</i> , 2007 , 35, D771-9	20.1	56
28	The serine/threonine/tyrosine phosphoproteome of the model bacterium <i>Bacillus subtilis</i> . <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 697-707	7.6	309
27	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. <i>Genome Biology</i> , 2007 , 8, R250	18.3	376
26	The low molecular weight proteome of <i>Halobacterium salinarum</i> . <i>Journal of Proteome Research</i> , 2007 , 6, 1510-8	5.6	60
25	The human urinary proteome contains more than 1500 proteins, including a large proportion of membrane proteins. <i>Genome Biology</i> , 2006 , 7, R80	18.3	514
24	Status of complete proteome analysis by mass spectrometry: SILAC labeled yeast as a model system. <i>Genome Biology</i> , 2006 , 7, R50	18.3	224
23	Top-down protein sequencing and MS3 on a hybrid linear quadrupole ion trap-orbitrap mass spectrometer. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 949-58	7.6	163

22	Global, in vivo, and site-specific phosphorylation dynamics in signaling networks. <i>Cell</i> , 2006 , 127, 635-48	56.2	2797
21	Proteomic analysis of the acid-soluble organic matrix of the chicken calcified eggshell layer. <i>Proteomics</i> , 2006 , 6, 3801-10	4.8	162
20	In-gel digestion for mass spectrometric characterization of proteins and proteomes. <i>Nature Protocols</i> , 2006 , 1, 2856-60	18.8	3440
19	Proteomic mapping of brain plasma membrane proteins. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 402-86	7.6	141
18	Parts per million mass accuracy on an Orbitrap mass spectrometer via lock mass injection into a C-trap. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 2010-21	7.6	1233
17	Quantitative phosphoproteomics applied to the yeast pheromone signaling pathway. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 310-27	7.6	665
16	Improved peptide identification in proteomics by two consecutive stages of mass spectrometric fragmentation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 13417-22	11.5	288
15	HysTag--a novel proteomic quantification tool applied to differential display analysis of membrane proteins from distinct areas of mouse brain. <i>Molecular and Cellular Proteomics</i> , 2004 , 3, 82-92	7.6	79
14	Tyrosine phosphoproteomics of fibroblast growth factor signaling: a role for insulin receptor substrate-4. <i>Journal of Biological Chemistry</i> , 2004 , 279, 46438-47	5.4	84
13	Trypsin cleaves exclusively C-terminal to arginine and lysine residues. <i>Molecular and Cellular Proteomics</i> , 2004 , 3, 608-14	7.6	804
12	Integrated analysis of protein composition, tissue diversity, and gene regulation in mouse mitochondria. <i>Cell</i> , 2003 , 115, 629-40	56.2	742
11	Signaling initiated by overexpression of the fibroblast growth factor receptor-1 investigated by mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2003 , 2, 29-36	7.6	67
10	Can relative cleavage frequencies in peptides provide additional sequence information?. <i>International Journal of Mass Spectrometry</i> , 2002 , 219, 283-294	1.9	37
9	Comparison of electron capture dissociation and collisionally activated dissociation of polycations of peptide nucleic acids. <i>Rapid Communications in Mass Spectrometry</i> , 2001 , 15, 969-74	2.2	30
8	Advantages of external accumulation for electron capture dissociation in Fourier transform mass spectrometry. <i>Analytical Chemistry</i> , 2001 , 73, 2998-3005	7.8	101
7	Electron capture dissociation of singly and multiply phosphorylated peptides. <i>Rapid Communications in Mass Spectrometry</i> , 2000 , 14, 1793-800	2.2	325
6	A novel LC system embeds analytes in pre-formed gradients for rapid, ultra-robust proteomics		2
5	Limits for resolving tandem mass tag reporter ions with identical integer mass using phase constrained spectrum deconvolution		1

4	Early Pleistocene enamel proteome sequences from Dmanisi resolve Stephanorhinus 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