Jesper V Olsen

List of Publications by Year
in descending order

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181

papers

45,397

citations

5782

84

h-index

4217

180

g-index

191

all docs

191

docs citations

191

times ranked

62598

citing authors

#	ARTICLE	IF	CITATIONS
1	A deeper look at carrier proteome effects for single-cell proteomics. Communications Biology, 2022, 5, 150.	2.0	31
2	Phosphorylation of SHP2 at Tyr62 Enables Acquired Resistance to SHP2 Allosteric Inhibitors in FLT3-ITDâ€“Driven AML. Cancer Research, 2022, 82, 2141-2155.	0.4	8
3	A Middle Pleistocene Denisovan molar from the Annamite Chain of northern Laos. Nature Communications, 2022, 13, 2557.	5.8	20
4	Brain proteome profiling implicates the complement and coagulation cascade in multiple system atrophy brain pathology. Cellular and Molecular Life Sciences, 2022, 79, .	2.4	6
5	Optimal analytical strategies for sensitive and quantitative phosphoproteomics using TMTâ€based multiplexing. Proteomics, 2022, 22, .	1.3	9
6	Human DDK rescues stalled forks and counteracts checkpoint inhibition at unfired origins to complete DNA replication. Molecular Cell, 2021, 81, 426-441.e8.	4.5	21
7	The methyltransferase METTL9 mediates pervasive 1-methylhistidine modification in mammalian proteomes. Nature Communications, 2021, 12, 891.	5.8	54
8	Human METTL18 is a histidine-specific methyltransferase that targets RPL3 and affects ribosome biogenesis and function. Nucleic Acids Research, 2021, 49, 3185-3203.	6.5	34
9	Proteomic investigation of Cbl and Cbl-b in neuroblastoma cell differentiation highlights roles for SHP-2 and CDK16. IScience, 2021, 24, 102321.	1.9	8
10	Faecal proteomics as a novel method to study mammalian behaviour and physiology. Molecular Ecology Resources, 2021, 21, 1808-1819.	2.2	7
11	Quantitative proteome comparison of human hearts with those of model organisms. PLoS Biology, 2021, 19, e3001144.	2.6	23
12	Proteomics of resistance to Notch1 inhibition in acute lymphoblastic leukemia reveals targetable kinase signatures. Nature Communications, 2021, 12, 2507.	5.8	22
13	GHB analogs confer neuroprotection through specific interaction with the CaMKIIÎ± hub domain. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	31
14	Regulation of the Golgi Apparatus by p38 and JNK Kinases during Cellular Stress Responses. International Journal of Molecular Sciences, 2021, 22, 9595.	1.8	6
15	Causal integration of multiâ€omics data with prior knowledge to generate mechanistic hypotheses. Molecular Systems Biology, 2021, 17, e9730.	3.2	78
16	Spatial-proteomics reveals phospho-signaling dynamics at subcellular resolution. Nature Communications, 2021, 12, 7113.	5.8	38
17	The human methyltransferase ZCCHC4 catalyses N6-methyladenosine modification of 28S ribosomal RNA. Nucleic Acids Research, 2020, 48, 830-846.	6.5	88
18	ProAlanase is an Effective Alternative to Trypsin for Proteomics Applications and Disulfide Bond Mapping. Molecular and Cellular Proteomics, 2020, 19, 2139-2157.	2.5	27

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19	Multi-protease analysis of Pleistocene bone proteomes. Journal of Proteomics, 2020, 228, 103889.	1.2	18
20	Mass-Spectrometry Based Proteome Comparison of Extracellular Vesicle Isolation Methods: Comparison of ME-kit, Size-Exclusion Chromatography, and High-Speed Centrifugation. Biomedicines, 2020, 8, 246.	1.4	43
21	Multi-omic detection of<i>Mycobacterium leprae</i>in archaeological human dental calculus. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190584.	1.8	31
22	Quantitative phosphoproteomics to unravel the cellular response to chemical stressors with different modes of action. Archives of Toxicology, 2020, 94, 1655-1671.	1.9	16
23	Proteome and Phosphoproteome Changes Associated with Prognosis in Acute Myeloid Leukemia. Cancers, 2020, 12, 709.	1.7	33
24	The dental proteome of Homo antecessor. Nature, 2020, 580, 235-238.	13.7	100
25	Rapid and site-specific deep phosphoproteome profiling by data-independent acquisition without the need for spectral libraries. Nature Communications, 2020, 11, 787.	5.8	251
26	Deciphering the human phosphoproteome. Nature Biotechnology, 2020, 38, 285-286.	9.4	6
27	A Compact Quadrupole-Orbitrap Mass Spectrometer with FAIMS Interface Improves Proteome Coverage in Short LC Gradients. Molecular and Cellular Proteomics, 2020, 19, 716-729.	2.5	284
28	Molecular Basis of the Mechanisms Controlling MASTL. Molecular and Cellular Proteomics, 2020, 19, 326-343.	2.5	7
29	Dynamic lineage priming is driven via direct enhancer regulation by ERK. Nature, 2019, 575, 355-360.	13.7	64
30	Palaeoproteomic identification of breast milk protein residues from the archaeological skeletal remains of a neonatal dog. Scientific Reports, 2019, 9, 12841.	1.6	11
31	Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. Nature, 2019, 574, 103-107.	13.7	135
32	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. Cell, 2019, 179, 543-560.e26.	13.5	65
33	Palaeoproteomics resolves sloth relationships. Nature Ecology and Evolution, 2019, 3, 1121-1130.	3.4	91
34	Proteomic characterization of chromosomal common fragile site (CFS)-associated proteins uncovers ATRX as a regulator of CFS stability. Nucleic Acids Research, 2019, 47, 8004-8018.	6.5	25
35	Protein Aggregation Capture on Microparticles Enables Multipurpose Proteomics Sample Preparation*. Molecular and Cellular Proteomics, 2019, 18, 1027a-1035.	2.5	189
36	Enamel proteome shows that Gigantopithecus was an early diverging pongine. Nature, 2019, 576, 262-265.	13.7	82

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37	Large-Scale Phosphoproteomics Reveals Shp-2 Phosphatase-Dependent Regulators of Pdgf Receptor Signaling. Cell Reports, 2018, 22, 2784-2796.	2.9	51
38	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. Angewandte Chemie, 2018, 130, 7491-7496.	1.6	1
39	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. Angewandte Chemie - International Edition, 2018, 57, 7369-7374.	7.2	76
40	Control of endothelial cell tube formation by Notch ligand intracellular domain interactions with activator protein 1 (AP-1). Journal of Biological Chemistry, 2018, 293, 1229-1242.	1.6	12
41	Benchmarking common quantification strategies for large-scale phosphoproteomics. Nature Communications, 2018, 9, 1045.	5.8	232
42	Performance Evaluation of the Q Exactive HF-X for Shotgun Proteomics. Journal of Proteome Research, 2018, 17, 727-738.	1.8	221
43	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. Nature Communications, 2018, 9, 4744.	5.8	63
44	Integrated proximal proteomics reveals IRS2 as a determinant of cell survival in ALK-driven neuroblastoma. Science Signaling, 2018, 11, .	1.6	33
45	Ancient proteins from ceramic vessels at Ã‡atalhÃ¶yÃ¼k West reveal the hidden cuisine of early farmers. Nature Communications, 2018, 9, 4064.	5.8	105
46	Limits for Resolving Isobaric Tandem Mass Tag Reporter Ions Using Phase-Constrained Spectrum Deconvolution. Journal of Proteome Research, 2018, 17, 4008-4016.	1.8	29
47	UbiSite approach for comprehensive mapping of lysine and N-terminal ubiquitination sites. Nature Structural and Molecular Biology, 2018, 25, 631-640.	3.6	341
48	Molecular basis of Tousled-Like Kinase 2 activation. Nature Communications, 2018, 9, 2535.	5.8	24
49	A Novel LC System Embeds Analytes in Pre-formed Gradients for Rapid, Ultra-robust Proteomics. Molecular and Cellular Proteomics, 2018, 17, 2284-2296.	2.5	270
50	The dual methyltransferase METTL13 targets N terminus and Lys55 of eEF1A and modulates codon-specific translation rates. Nature Communications, 2018, 9, 3411.	5.8	81
51	Generic Workflow for Mapping of Complex Disulfide Bonds Using In-Source Reduction and Extracted Ion Chromatograms from Data-Dependent Mass Spectrometry. Analytical Chemistry, 2018, 90, 8202-8210.	3.2	15
52	A comprehensive platform for the analysis of ubiquitin-like protein modifications using in vivo biotinylation. Scientific Reports, 2017, 7, 40756.	1.6	58
53	Complete Mapping of Complex Disulfide Patterns with Closely-Spaced Cysteines by In-Source Reduction and Data-Dependent Mass Spectrometry. Analytical Chemistry, 2017, 89, 5949-5957.	3.2	27
54	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. Cell Systems, 2017, 4, 587-599.e4.	2.9	413

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55	The ubiquitin ligase Cullin5SOCS2 regulates NDR1/STK38 stability and NF-Î°B transactivation. Scientific Reports, 2017, 7, 42800.	1.6	32
56	KITD816V Induces SRC-Mediated Tyrosine Phosphorylation of MITF and Altered Transcription Program in Melanoma. Molecular Cancer Research, 2017, 15, 1265-1274.	1.5	15
57	Cylindromatosis Tumor Suppressor Protein (CYLD) Deubiquitinase is Necessary for Proper Ubiquitination and Degradation of the Epidermal Growth Factor Receptor. Molecular and Cellular Proteomics, 2017, 16, 1433-1446.	2.5	15
58	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. Cell Reports, 2017, 18, 3242-3256.	2.9	81
59	Proteomic profiling of archaeological human bone. Royal Society Open Science, 2017, 4, 161004.	1.1	76
60	Proteomics insights into DNA damage response and translating this knowledge to clinical strategies. Proteomics, 2017, 17, 1600018.	1.3	18
61	Combinatorial Drug Screening Identifies Ewing Sarcomaâ€“specific Sensitivities. Molecular Cancer Therapeutics, 2017, 16, 88-101.	1.9	17
62	Multilayered proteomics reveals molecular switches dictating ligand-dependent EGFR trafficking. Nature Structural and Molecular Biology, 2016, 23, 608-618.	3.6	98
63	Analytic framework for peptidomics applied to large-scale neuropeptide identification. Nature Communications, 2016, 7, 11436.	5.8	92
64	Conformation-specific anti-Mad2 monoclonal antibodies for the dissection of checkpoint signaling. MAbs, 2016, 8, 689-697.	2.6	10
65	Disulfide Linkage Characterization of Disulfide Bond-Containing Proteins and Peptides by Reducing Electrochemistry and Mass Spectrometry. Analytical Chemistry, 2016, 88, 1585-1592.	3.2	35
66	Offline High pH Reversed-Phase Peptide Fractionation for Deep Phosphoproteome Coverage. Methods in Molecular Biology, 2016, 1355, 179-192.	0.4	36
67	Simple and Reproducible Sample Preparation for Single-Shot Phosphoproteomics with High Sensitivity. Methods in Molecular Biology, 2016, 1355, 251-260.	0.4	39
68	From Phosphosites to Kinases. Methods in Molecular Biology, 2016, 1355, 307-321.	0.4	21
69	Protein sequences bound to mineral surfaces persist into deep time. ELife, 2016, 5, .	2.8	176
70	Metaproteomics of saliva identifies human protein markers specific for individuals with periodontitis and dental caries compared to orally healthy controls. PeerJ, 2016, 4, e2433.	0.9	56
71	Temporal proteomics of NGF-TrkA signaling identifies an inhibitory role for the E3 ligase Cbl-b in neuroblastoma cell differentiation. Science Signaling, 2015, 8, ra40.	1.6	64
72	Protein kinase A stimulates Kv7.1 surface expression by regulating Nedd4-2-dependent endocytic trafficking. American Journal of Physiology - Cell Physiology, 2015, 309, C693-C706.	2.1	8

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73	Ubiquitin-specific Protease 11 (USP11) Deubiquitinates Hybrid Small Ubiquitin-like Modifier (SUMO)-Ubiquitin Chains to Counteract RING Finger Protein 4 (RNF4). Journal of Biological Chemistry, 2015, 290, 15526-15537.	1.6	32
74	SUMO-2 Orchestrates Chromatin Modifiers in Response to DNA Damage. Cell Reports, 2015, 10, 1778-1791.	2.9	117
75	Ancient proteins resolve the evolutionary history of Darwinâ€™s South American ungulates. Nature, 2015, 522, 81-84.	13.7	273
76	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. Molecular and Cellular Proteomics, 2015, 14, 1419-1434.	2.5	79
77	Recent findings and technological advances in phosphoproteomics for cells and tissues. Expert Review of Proteomics, 2015, 12, 469-487.	1.3	70
78	Molecular evidence of use of hide glue in 4th millennium BC Europe. Journal of Archaeological Science, 2015, 63, 65-71.	1.2	32
79	Immature truncated O-glycophenotype of cancer directly induces oncogenic features. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4066-75.	3.3	251
80	Analytical Utility of Mass Spectral Binning in Proteomic Experiments by SPectral Immonium Ion Detection (SPIID). Molecular and Cellular Proteomics, 2014, 13, 1914-1924.	2.5	22
81	A direct role of <scp>M</scp> ad1 in the spindle assembly checkpoint beyond <scp>M</scp> ad2 kinetochore recruitment. EMBO Reports, 2014, 15, 282-290.	2.0	38
82	Rapid and Deep Proteomes by Faster Sequencing on a Benchtop Quadrupole Ultra-High-Field Orbitrap Mass Spectrometer. Journal of Proteome Research, 2014, 13, 6187-6195.	1.8	168
83	Off-Line High-pH Reversed-Phase Fractionation for In-Depth Phosphoproteomics. Journal of Proteome Research, 2014, 13, 6176-6186.	1.8	263
84	Pathogens and host immunity in the ancient human oral cavity. Nature Genetics, 2014, 46, 336-344.	9.4	482
85	Uncovering SUMOylation Dynamics during Cell-Cycle Progression Reveals FoxM1 as a Key Mitotic SUMO Target Protein. Molecular Cell, 2014, 53, 1053-1066.	4.5	153
86	Resolution of the type material of the Asian elephant,<i>Elephas maximus</i>Linnaeus, 1758 (Proboscidea, Elephantidae). Zoological Journal of the Linnean Society, 2014, 170, 222-232.	1.0	31
87	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. Nature Methods, 2014, 11, 868-874.	9.0	70
88	Analysis of Changes in SUMO-2/3 Modification during Breast Cancer Progression and Metastasis. Journal of Proteome Research, 2014, 13, 3905-3918.	1.8	25
89	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
90	Resolution of the type material of the Asian elephant, Elephas maximus Linnaeus, 1758 (Proboscidea,) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.0	22

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91	SILAC-Based Temporal Phosphoproteomics. Methods in Molecular Biology, 2014, 1188, 125-148.	0.4	10
92	Predicting Kinase Activity in Angiotensin Receptor Phosphoproteomes Based on Sequence-Motifs and Interactions. PLoS ONE, 2014, 9, e94672.	1.1	7
93	Comprehensive Identification of SUMO2/3 Targets and Their Dynamics during Mitosis. PLoS ONE, 2014, 9, e100692.	1.1	19
94	Species Identification of Archaeological Skin Objects from Danish Bogs: Comparison between Mass Spectrometry-Based Peptide Sequencing and Microscopy-Based Methods. PLoS ONE, 2014, 9, e106875.	1.1	70
95	Structures of Down Syndrome Kinases, DYRKs, Reveal Mechanisms of Kinase Activation and Substrate Recognition. Structure, 2013, 21, 986-996.	1.6	127
96	Functional Proteomics Defines the Molecular Switch Underlying FGF Receptor Trafficking and Cellular Outputs. Molecular Cell, 2013, 51, 707-722.	4.5	145
97	TIMP-1 Increases Expression and Phosphorylation of Proteins Associated with Drug Resistance in Breast Cancer Cells. Journal of Proteome Research, 2013, 12, 4136-4151.	1.8	36
98	The SH2 Domain Interaction Landscape. Cell Reports, 2013, 3, 1293-1305.	2.9	110
99	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
100	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. Nature, 2013, 499, 74-78.	13.7	717
101	Status of Large-scale Analysis of Post-translational Modifications by Mass Spectrometry. Molecular and Cellular Proteomics, 2013, 12, 3444-3452.	2.5	491
102	Systems Biology Approach Identifies the Kinase Csnk1a1 as a Regulator of the DNA Damage Response in Embryonic Stem Cells. Science Signaling, 2013, 6, ra5.	1.6	34
103	In Vivo Phosphoproteomics Analysis Reveals the Cardiac Targets of Î²-Adrenergic Receptor Signaling. Science Signaling, 2013, 6, rs11.	1.6	164
104	Phosphoproteomics taken to heart. Cell Cycle, 2013, 12, 2707-2708.	1.3	4
105	The Ndc80 internal loop is required for recruitment of the Ska complex to establish end-on microtubule attachment to kinetochores.. Journal of Cell Science, 2012, 125, 3243-53.	1.2	62
106	Proteomic Analyses Reveal Divergent Ubiquitylation Site Patterns in Murine Tissues. Molecular and Cellular Proteomics, 2012, 11, 1578-1585.	2.5	244
107	Î±4Î²Î´ GABA _A receptors are high-affinity targets for Î³-hydroxybutyric acid (GHB). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13404-13409.	3.3	87
108	Proteomic Analysis of Lysine Acetylation Sites in Rat Tissues Reveals Organ Specificity and Subcellular Patterns. Cell Reports, 2012, 2, 419-431.	2.9	493

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109	A Major Lineage of Enteroendocrine Cells Coexpress CCK, Secretin, GIP, GLP-1, PYY, and Neurotensin but Not Somatostatin. Endocrinology, 2012, 153, 5782-5795.	1.4	269
110	Correction to Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. Journal of Proteome Research, 2012, 11, 3506-3508.	1.8	11
111	Optimized Fast and Sensitive Acquisition Methods for Shotgun Proteomics on a Quadrupole Orbitrap Mass Spectrometer. Journal of Proteome Research, 2012, 11, 3487-3497.	1.8	270
112	Proteomic Investigations Reveal a Role for RNA Processing Factor THRAP3 in the DNA Damage Response. Molecular Cell, 2012, 46, 212-225.	4.5	298
113	Quantitative maps of protein phosphorylation sites across 14 different rat organs and tissues. Nature Communications, 2012, 3, 876.	5.8	307
114	Proteomic Analysis of a Pleistocene Mammoth Femur Reveals More than One Hundred Ancient Bone Proteins. Journal of Proteome Research, 2012, 11, 917-926.	1.8	196
115	Pinpointing Phosphorylation Sites: Quantitative Filtering and a Novel Site-specific x-Ion Fragment. Journal of Proteome Research, 2011, 10, 2937-2948.	1.8	27
116	Andromeda: A Peptide Search Engine Integrated into the MaxQuant Environment. Journal of Proteome Research, 2011, 10, 1794-1805.	1.8	4,935
117	GeLCMS for In-Depth Protein Characterization and Advanced Analysis of Proteomes. Methods in Molecular Biology, 2011, 753, 143-155.	0.4	36
118	Proteome-Wide Mapping of the <i>Drosophila</i> Acetylome Demonstrates a High Degree of Conservation of Lysine Acetylation. Science Signaling, 2011, 4, ra48.	1.6	243
119	System-Wide Temporal Characterization of the Proteome and Phosphoproteome of Human Embryonic Stem Cell Differentiation. Science Signaling, 2011, 4, rs3.	1.6	389
120	Pre-Clovis Mastodon Hunting 13,800 Years Ago at the Manis Site, Washington. Science, 2011, 334, 351-353.	6.0	148
121	Effective Representation and Storage of Mass Spectrometryâ€“Based Proteomic Data Sets for the Scientific Community. Science Signaling, 2011, 4, pe7.	1.6	17
122	Global Phosphoproteome Profiling Reveals Unanticipated Networks Responsive to Cisplatin Treatment of Embryonic Stem Cells. Molecular and Cellular Biology, 2011, 31, 4964-4977.	1.1	56
123	Phosphorylation of the Yeast Î³-Tubulin Tub4 Regulates Microtubule Function. PLoS ONE, 2011, 6, e19700.	1.1	42
124	The phosphoproteome of tollâ€•like receptorâ€•activated macrophages. Molecular Systems Biology, 2010, 6, 371.	3.2	142
125	Quantitative Phosphoproteomics Dissection of Seven-transmembrane Receptor Signaling Using Full and Biased Agonists. Molecular and Cellular Proteomics, 2010, 9, 1540-1553.	2.5	135
126	MSQuant, an Open Source Platform for Mass Spectrometry-Based Quantitative Proteomics. Journal of Proteome Research, 2010, 9, 393-403.	1.8	237

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127	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. Science Signaling, 2010, 3, ra3.	1.6	1,319
128	Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. Journal of Proteome Research, 2010, 9, 6786-6794.	1.8	149
129	Yeast Expression Proteomics by High-Resolution Mass Spectrometry. Methods in Enzymology, 2010, 470, 259-280.	0.4	8
130	Quantitative Interaction Proteomics and Genome-wide Profiling of Epigenetic Histone Marks and Their Readers. Cell, 2010, 142, 967-980.	13.5	710
131	Phosphorylation of Histone H3 Thr-45 Is Linked to Apoptosis. Journal of Biological Chemistry, 2009, 284, 16575-16583.	1.6	98
132	Global Effects of Kinase Inhibitors on Signaling Networks Revealed by Quantitative Phosphoproteomics. Molecular and Cellular Proteomics, 2009, 8, 2796-2808.	2.5	194
133	A Dual Pressure Linear Ion Trap Orbitrap Instrument with Very High Sequencing Speed. Molecular and Cellular Proteomics, 2009, 8, 2759-2769.	2.5	398
134	Large-scale Proteomics Analysis of the Human Kinome. Molecular and Cellular Proteomics, 2009, 8, 1751-1764.	2.5	257
135	Highâ€accuracy identification and bioinformatic analysis of <i>in vivo</i> protein phosphorylation sites in yeast. Proteomics, 2009, 9, 4642-4652.	1.3	132
136	Proteomics strategy for quantitative protein interaction profiling in cell extracts. Nature Methods, 2009, 6, 741-744.	9.0	141
137	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. Nature Protocols, 2009, 4, 698-705.	5.5	769
138	Lysine Acetylation Targets Protein Complexes and Co-Regulates Major Cellular Functions. Science, 2009, 325, 834-840.	6.0	3,883
139	Mislocalized Activation of Oncogenic RTKs Switches Downstream Signaling Outcomes. Molecular Cell, 2009, 36, 326-339.	4.5	278
140	Global analysis of the yeast osmotic stress response by quantitative proteomics. Molecular BioSystems, 2009, 5, 1337.	2.9	128
141	Global and Site-Specific Quantitative Phosphoproteomics: Principles and Applications. Annual Review of Pharmacology and Toxicology, 2009, 49, 199-221.	4.2	382
142	High Accuracy Mass Spectrometry in Large-Scale Analysis of Protein Phosphorylation. Methods in Molecular Biology, 2009, 492, 131-142.	0.4	54
143	Quantitative phosphoproteome analysis of a mouse liver cell line reveals specificity of phosphatase inhibitors. Proteomics, 2008, 8, 4534-4546.	1.3	93
144	Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast. Nature, 2008, 455, 1251-1254.	13.7	835

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145	Ubc9 Sumoylation Regulates SUMO Target Discrimination. Molecular Cell, 2008, 31, 371-382.	4.5	191
146	Kinase-Selective Enrichment Enables Quantitative Phosphoproteomics of the Kinome across the Cell Cycle. Molecular Cell, 2008, 31, 438-448.	4.5	548
147	Phosphoproteome Analysis of E. coli Reveals Evolutionary Conservation of Bacterial Ser/Thr/Tyr Phosphorylation. Molecular and Cellular Proteomics, 2008, 7, 299-307.	2.5	385
148	Multi-spectra peptide sequencing and its applications to multistage mass spectrometry. Bioinformatics, 2008, 24, i416-i423.	1.8	25
149	Investigation of Protein-tyrosine Phosphatase 1B Function by Quantitative Proteomics. Molecular and Cellular Proteomics, 2008, 7, 1763-1777.	2.5	106
150	Profiling the Phospho-status of the BKCa Channel Î± Subunit in Rat Brain Reveals Unexpected Patterns and Complexity. Molecular and Cellular Proteomics, 2008, 7, 2188-2198.	2.5	79
151	Temporal Dynamics of EGF Receptor Signaling by Quantitative Proteomics. , 2008, , 190-198.		1
152	MAPU: Max-Planck Unified database of organellar, cellular, tissue and body fluid proteomes. Nucleic Acids Research, 2007, 35, D771-D779.	6.5	69
153	The Serine/Threonine/Tyrosine Phosphoproteome of the Model Bacterium Bacillus subtilis. Molecular and Cellular Proteomics, 2007, 6, 697-707.	2.5	359
154	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. Genome Biology, 2007, 8, R250.	13.9	410
155	The Low Molecular Weight Proteome ofHalobacterium salinarum. Journal of Proteome Research, 2007, 6, 1510-1518.	1.8	63
156	Nanoelectrospray peptide mapping revisited: Composite survey spectra allow high dynamic range protein characterization without LCMS on an orbitrap mass spectrometer. International Journal of Mass Spectrometry, 2007, 268, 158-167.	0.7	10
157	Phosphoproteins of the chicken eggshell calcified layer. Proteomics, 2007, 7, 106-115.	1.3	102
158	Quantitative proteomic assessment of very early cellular signaling events. Nature Biotechnology, 2007, 25, 566-568.	9.4	110
159	A mass spectrometryâ€“friendly database for cSNP identification. Nature Methods, 2007, 4, 465-466.	9.0	72
160	Higher-energy C-trap dissociation for peptide modification analysis. Nature Methods, 2007, 4, 709-712.	9.0	844
161	Noncovalent interaction between Ubc9 and SUMO promotes SUMO chain formation. EMBO Journal, 2007, 26, 2797-2807.	3.5	177
162	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. Brain Research, 2007, 1134, 95-106.	1.1	41

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163	The human urinary proteome contains more than 1500 proteins, including a large proportion of membrane proteins. Genome Biology, 2006, 7, R80.	13.9	598
164	Status of complete proteome analysis by mass spectrometry: SILAC labeled yeast as a model system. Genome Biology, 2006, 7, R50.	13.9	244
165	Top-down Protein Sequencing and MS3 on a Hybrid Linear Quadrupole Ion Trap-Orbitrap Mass Spectrometer. Molecular and Cellular Proteomics, 2006, 5, 949-958.	2.5	179
166	Global, In Vivo, and Site-Specific Phosphorylation Dynamics in Signaling Networks. Cell, 2006, 127, 635-648.	13.5	3,201
167	Proteomic analysis of the acid-soluble organic matrix of the chicken calcified eggshell layer. Proteomics, 2006, 6, 3801-3810.	1.3	182
168	In-gel digestion for mass spectrometric characterization of proteins and proteomes. Nature Protocols, 2006, 1, 2856-2860.	5.5	4,265
169	Parts per Million Mass Accuracy on an Orbitrap Mass Spectrometer via Lock Mass Injection into a C-trap. Molecular and Cellular Proteomics, 2005, 4, 2010-2021.	2.5	1,395
170	Quantitative Phosphoproteomics Applied to the Yeast Pheromone Signaling Pathway. Molecular and Cellular Proteomics, 2005, 4, 310-327.	2.5	708
171	Proteomic Mapping of Brain Plasma Membrane Proteins. Molecular and Cellular Proteomics, 2005, 4, 402-408.	2.5	147
172	Improved peptide identification in proteomics by two consecutive stages of mass spectrometric fragmentation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13417-13422.	3.3	317
173	HysTagâ€"A Novel Proteomic Quantification Tool Applied to Differential Display Analysis of Membrane Proteins From Distinct Areas of Mouse Brain. Molecular and Cellular Proteomics, 2004, 3, 82-92.	2.5	88
174	Tyrosine Phosphoproteomics of Fibroblast Growth Factor Signaling. Journal of Biological Chemistry, 2004, 279, 46438-46447.	1.6	90
175	Trypsin Cleaves Exclusively C-terminal to Arginine and Lysine Residues. Molecular and Cellular Proteomics, 2004, 3, 608-614.	2.5	957
176	Integrated Analysis of Protein Composition, Tissue Diversity, and Gene Regulation in Mouse Mitochondria. Cell, 2003, 115, 629-640.	13.5	815
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