

Jesper V. Olsen

List of Publications by Year in descending order

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Version: 2024-02-01

229
papers

47,969
citations

4345

89
h-index

2142

209
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247
all docs

247
docs citations

247
times ranked

66062
citing authors

#	ARTICLE	IF	CITATIONS
1	A deeper look at carrier proteome effects for single-cell proteomics. <i>Communications Biology</i> , 2022, 5, 150.	2.0	31
2	Phosphorylation of SHP2 at Tyr62 Enables Acquired Resistance to SHP2 Allosteric Inhibitors in FLT3-ITD-Driven AML. <i>Cancer Research</i> , 2022, 82, 2141-2155.	0.4	8
3	SPIN enables high throughput species identification of archaeological bone by proteomics. <i>Nature Communications</i> , 2022, 13, 2458.	5.8	31
4	A Middle Pleistocene Denisovan molar from the Annamite Chain of northern Laos. <i>Nature Communications</i> , 2022, 13, 2557.	5.8	20
5	Brain proteome profiling implicates the complement and coagulation cascade in multiple system atrophy brain pathology. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	6
6	Optimal analytical strategies for sensitive and quantitative phosphoproteomics using TMT-based multiplexing. <i>Proteomics</i> , 2022, 22, .	1.3	9
7	FRMD6 has tumor suppressor functions in prostate cancer. <i>Oncogene</i> , 2021, 40, 763-776.	2.6	24
8	Data Processing and Analysis for DIA-Based Phosphoproteomics Using Spectronaut. <i>Methods in Molecular Biology</i> , 2021, 2361, 95-107.	0.4	21
9	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.	4.5	21
10	The methyltransferase METTL9 mediates pervasive 1-methylhistidine modification in mammalian proteomes. <i>Nature Communications</i> , 2021, 12, 891.	5.8	54
11	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.	6.5	34
12	Proteomic investigation of Cbl and Cbl-b in neuroblastoma cell differentiation highlights roles for SHP-2 and CDK16. <i>IScience</i> , 2021, 24, 102321.	1.9	8
13	Faecal proteomics as a novel method to study mammalian behaviour and physiology. <i>Molecular Ecology Resources</i> , 2021, 21, 1808-1819.	2.2	7
14	Quantitative proteome comparison of human hearts with those of model organisms. <i>PLoS Biology</i> , 2021, 19, e3001144.	2.6	23
15	Proteomics of resistance to Notch1 inhibition in acute lymphoblastic leukemia reveals targetable kinase signatures. <i>Nature Communications</i> , 2021, 12, 2507.	5.8	22
16	GHB analogs confer neuroprotection through specific interaction with the CaMKII β hub domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	31
17	Regulation of the Golgi Apparatus by p38 and JNK Kinases during Cellular Stress Responses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9595.	1.8	6
18	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. <i>Molecular Systems Biology</i> , 2021, 17, e9730.	3.2	78

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19	Spatial-proteomics reveals phospho-signaling dynamics at subcellular resolution. <i>Nature Communications</i> , 2021, 12, 7113.	5.8	38
20	The human methyltransferase ZCCHC4 catalyses N6-methyladenosine modification of 28S ribosomal RNA. <i>Nucleic Acids Research</i> , 2020, 48, 830-846.	6.5	88
21	ProAlanase is an Effective Alternative to Trypsin for Proteomics Applications and Disulfide Bond Mapping. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 2139-2157.	2.5	27
22	Multi-protease analysis of Pleistocene bone proteomes. <i>Journal of Proteomics</i> , 2020, 228, 103889.	1.2	18
23	Effects of active farnesoid X receptor on GLUTag enteroendocrine L cells. <i>Molecular and Cellular Endocrinology</i> , 2020, 517, 110923.	1.6	5
24	Mass-Spectrometry Based Proteome Comparison of Extracellular Vesicle Isolation Methods: Comparison of ME-kit, Size-Exclusion Chromatography, and High-Speed Centrifugation. <i>Biomedicines</i> , 2020, 8, 246.	1.4	43
25	Multi-omic detection of <i>Mycobacterium leprae</i> in archaeological human dental calculus. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190584.	1.8	31
26	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.	1.1	6
27	Quantitative phosphoproteomics to unravel the cellular response to chemical stressors with different modes of action. <i>Archives of Toxicology</i> , 2020, 94, 1655-1671.	1.9	16
28	Proteome and Phosphoproteome Changes Associated with Prognosis in Acute Myeloid Leukemia. <i>Cancers</i> , 2020, 12, 709.	1.7	33
29	The dental proteome of <i>Homo antecessor</i> . <i>Nature</i> , 2020, 580, 235-238.	13.7	100
30	Rapid and site-specific deep phosphoproteome profiling by data-independent acquisition without the need for spectral libraries. <i>Nature Communications</i> , 2020, 11, 787.	5.8	251
31	Deciphering the human phosphoproteome. <i>Nature Biotechnology</i> , 2020, 38, 285-286.	9.4	6
32	A Compact Quadrupole-Orbitrap Mass Spectrometer with FAIMS Interface Improves Proteome Coverage in Short LC Gradients. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 716-729.	2.5	284
33	Quantitative proteomics characterization of acutely isolated primary adult rat cardiomyocytes and fibroblasts. <i>Journal of Molecular and Cellular Cardiology</i> , 2020, 143, 63-70.	0.9	9
34	ZAK1± Recognizes Stalled Ribosomes through Partially Redundant Sensor Domains. <i>Molecular Cell</i> , 2020, 78, 700-713.e7.	4.5	90
35	Quantitative Proteomics of Human Heart Samples Collected In Vivo Reveal the Remodeled Protein Landscape of Dilated Left Atrium Without Atrial Fibrillation. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1132-1144.	2.5	24
36	Molecular Basis of the Mechanisms Controlling MASTL. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 326-343.	2.5	7

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37	Quantitative proteomics and single-nucleus transcriptomics of the sinus node elucidates the foundation of cardiac pacemaking. <i>Nature Communications</i> , 2019, 10, 2889.	5.8	84
38	Dynamic lineage priming is driven via direct enhancer regulation by ERK. <i>Nature</i> , 2019, 575, 355-360.	13.7	64
39	Palaeoproteomic identification of breast milk protein residues from the archaeological skeletal remains of a neonatal dog. <i>Scientific Reports</i> , 2019, 9, 12841.	1.6	11
40	Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , 2019, 574, 103-107.	13.7	135
41	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. <i>Cell</i> , 2019, 179, 543-560.e26.	13.5	65
42	The Role of TTP Phosphorylation in the Regulation of Inflammatory Cytokine Production by MK2/3. <i>Journal of Immunology</i> , 2019, 203, 2291-2300.	0.4	28
43	Alternative Translation Initiation Generates a Functionally Distinct Isoform of the Stress-Activated Protein Kinase MK2. <i>Cell Reports</i> , 2019, 27, 2859-2870.e6.	2.9	22
44	Palaeoproteomics resolves sloth relationships. <i>Nature Ecology and Evolution</i> , 2019, 3, 1121-1130.	3.4	91
45	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.	6.5	25
46	Protein Aggregation Capture on Microparticles Enables Multipurpose Proteomics Sample Preparation*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1027a-1035.	2.5	189
47	GIGYF1/2-Driven Cooperation between ZNF598 and TTP in Posttranscriptional Regulation of Inflammatory Signaling. <i>Cell Reports</i> , 2019, 26, 3511-3521.e4.	2.9	44
48	Expression and secretion of a lytic polysaccharide monooxygenase by a fast-growing cyanobacterium. <i>Biotechnology for Biofuels</i> , 2019, 12, 74.	6.2	23
49	Enamel proteome shows that <i>Gigantopithecus</i> was an early diverging pongine. <i>Nature</i> , 2019, 576, 262-265.	13.7	82
50	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.	3.2	55
51	Large-Scale Phosphoproteomics Reveals Shp-2 Phosphatase-Dependent Regulators of Pdgf Receptor Signaling. <i>Cell Reports</i> , 2018, 22, 2784-2796.	2.9	51
52	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. <i>Angewandte Chemie</i> , 2018, 130, 7491-7496.	1.6	1
53	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 7369-7374.	7.2	76
54	Truncated SALL1 Impedes Primary Cilia Function in Townes-Brocks Syndrome. <i>American Journal of Human Genetics</i> , 2018, 102, 249-265.	2.6	27

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55	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.	1.6	12
56	Benchmarking common quantification strategies for large-scale phosphoproteomics. <i>Nature Communications</i> , 2018, 9, 1045.	5.8	232
57	Performance Evaluation of the Q Exactive HF-X for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 727-738.	1.8	221
58	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. <i>Nature Communications</i> , 2018, 9, 4744.	5.8	63
59	Integrated proximal proteomics reveals IRS2 as a determinant of cell survival in ALK-driven neuroblastoma. <i>Science Signaling</i> , 2018, 11, .	1.6	33
60	Ancient proteins from ceramic vessels at Neolithic West reveal the hidden cuisine of early farmers. <i>Nature Communications</i> , 2018, 9, 4064.	5.8	105
61	Limits for Resolving Isobaric Tandem Mass Tag Reporter Ions Using Phase-Constrained Spectrum Deconvolution. <i>Journal of Proteome Research</i> , 2018, 17, 4008-4016.	1.8	29
62	UbiSite approach for comprehensive mapping of lysine and N-terminal ubiquitination sites. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 631-640.	3.6	341
63	PKD Phosphorylation as Novel Pathway of KV11.1 Regulation. <i>Cellular Physiology and Biochemistry</i> , 2018, 47, 1742-1750.	1.1	2
64	Molecular basis of Tausled-Like Kinase 2 activation. <i>Nature Communications</i> , 2018, 9, 2535.	5.8	24
65	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.	2.5	270
66	The dual methyltransferase METTL13 targets N terminus and Lys55 of eEF1A and modulates codon-specific translation rates. <i>Nature Communications</i> , 2018, 9, 3411.	5.8	81
67	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.	6.5	39
68	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.	3.2	15
69	A comprehensive platform for the analysis of ubiquitin-like protein modifications using in vivo biotinylation. <i>Scientific Reports</i> , 2017, 7, 40756.	1.6	58
70	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.	3.2	27
71	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. <i>Cell Systems</i> , 2017, 4, 587-599.e4.	2.9	413
72	The ubiquitin ligase Cullin5SOCS2 regulates NDR1/STK38 stability and NF- κ B transactivation. <i>Scientific Reports</i> , 2017, 7, 42800.	1.6	32

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73	KITD816V Induces SRC-Mediated Tyrosine Phosphorylation of MITF and Altered Transcription Program in Melanoma. <i>Molecular Cancer Research</i> , 2017, 15, 1265-1274.	1.5	15
74	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.	2.5	15
75	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. <i>Cell Reports</i> , 2017, 18, 3242-3256.	2.9	81
76	Proteomics Reveals Global Regulation of Protein SUMOylation by ATM and ATR Kinases during Replication Stress. <i>Cell Reports</i> , 2017, 21, 546-558.	2.9	24
77	Proteomic profiling of archaeological human bone. <i>Royal Society Open Science</i> , 2017, 4, 161004.	1.1	76
78	Proteomics insights into DNA damage response and translating this knowledge to clinical strategies. <i>Proteomics</i> , 2017, 17, 1600018.	1.3	18
79	Combinatorial Drug Screening Identifies Ewing Sarcoma-specific Sensitivities. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 88-101.	1.9	17
80	Multilayered proteomics reveals molecular switches dictating ligand-dependent EGFR trafficking. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 608-618.	3.6	98
81	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, 1614-1626.	1.9	16
82	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	1.2	113
83	A Conserved Motif Provides Binding Specificity to the PP2A-B56 Phosphatase. <i>Molecular Cell</i> , 2016, 63, 686-695.	4.5	235
84	Analytic framework for peptidomics applied to large-scale neuropeptide identification. <i>Nature Communications</i> , 2016, 7, 11436.	5.8	92
85	miR-625-3p regulates oxaliplatin resistance by targeting MAP2K6-p38 signalling in human colorectal adenocarcinoma cells. <i>Nature Communications</i> , 2016, 7, 12436.	5.8	82
86	Conformation-specific anti-Mad2 monoclonal antibodies for the dissection of checkpoint signaling. <i>MAbs</i> , 2016, 8, 689-697.	2.6	10
87	CDX2 downregulation is associated with poor differentiation and MMR deficiency in colon cancer. <i>Experimental and Molecular Pathology</i> , 2016, 100, 59-66.	0.9	46
88	Disulfide Linkage Characterization of Disulfide Bond-Containing Proteins and Peptides by Reducing Electrochemistry and Mass Spectrometry. <i>Analytical Chemistry</i> , 2016, 88, 1585-1592.	3.2	35
89	Offline High pH Reversed-Phase Peptide Fractionation for Deep Phosphoproteome Coverage. <i>Methods in Molecular Biology</i> , 2016, 1355, 179-192.	0.4	36
90	Simple and Reproducible Sample Preparation for Single-Shot Phosphoproteomics with High Sensitivity. <i>Methods in Molecular Biology</i> , 2016, 1355, 251-260.	0.4	39

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91	From Phosphosites to Kinases. <i>Methods in Molecular Biology</i> , 2016, 1355, 307-321.	0.4	21
92	Systems Analysis for Interpretation of Phosphoproteomics Data. <i>Methods in Molecular Biology</i> , 2016, 1355, 341-360.	0.4	15
93	Protein sequences bound to mineral surfaces persist into deep time. <i>ELife</i> , 2016, 5, .	2.8	176
94	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.	0.9	56
95	Abstract 1127: KIT/D816V induces SRC-mediated tyrosine phosphorylation of MITF and altered transcription program in melanoma. , 2016, , .		1
96	Abstract 2927: miR-625-3p regulates oxaliplatin resistance by targeting MAP2K6-p38 signalling in human colorectal adenocarcinoma cell. , 2016, , .		0
97	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.	1.6	64
98	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-C706.	2.1	8
99	Ubiquitin-SUMO Circuitry Controls Activated Fanconi Anemia ID Complex Dosage in Response to DNA Damage. <i>Molecular Cell</i> , 2015, 57, 150-164.	4.5	106
100	Ctk1 Function Is Necessary for Full Translation Initiation Activity in <i>Saccharomyces cerevisiae</i> . <i>Eukaryotic Cell</i> , 2015, 14, 86-95.	3.4	17
101	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.	1.6	32
102	SUMO-2 Orchestrates Chromatin Modifiers in Response to DNA Damage. <i>Cell Reports</i> , 2015, 10, 1778-1791.	2.9	117
103	In vivo quantitative phosphoproteomic profiling identifies novel regulators of castration-resistant prostate cancer growth. <i>Oncogene</i> , 2015, 34, 2764-2776.	2.6	63
104	Ancient proteins resolve the evolutionary history of Darwin's South American ungulates. <i>Nature</i> , 2015, 522, 81-84.	13.7	273
105	System-wide Analysis of SUMOylation Dynamics in Response to Replication Stress Reveals Novel Small Ubiquitin-like Modified Target Proteins and Acceptor Lysines Relevant for Genome Stability. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1419-1434.	2.5	79
106	Recent findings and technological advances in phosphoproteomics for cells and tissues. <i>Expert Review of Proteomics</i> , 2015, 12, 469-487.	1.3	70
107	Molecular evidence of use of hide glue in 4th millennium BC Europe. <i>Journal of Archaeological Science</i> , 2015, 63, 65-71.	1.2	32
108	Abstract 3585: HER3 and IGF1R are major mediators of both acquired and intrinsic cetuximab resistance in head and neck squamous cell carcinomas. , 2015, , .		0

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109	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
110	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. Oncogene, 2014, 33, 5360-5369.	2.6	15
111	B-lymphoid tyrosine kinase (Blk) is an oncogene and a potential target for therapy with dasatinib in cutaneous T-cell lymphoma (CTCL). Leukemia, 2014, 28, 2109-2112.	3.3	39
112	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
113	A direct role of $\text{M}^{\text{ad}1}$ in the spindle assembly checkpoint beyond $\text{M}^{\text{ad}2}$ kinetochore recruitment. EMBO Reports, 2014, 15, 282-290.	2.0	38
114	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
115	Off-Line High-pH Reversed-Phase Fractionation for In-Depth Phosphoproteomics. Journal of Proteome Research, 2014, 13, 6176-6186.	1.8	263
116	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. Molecular and Cellular Proteomics, 2014, 13, 1905-1913.	2.5	42
117	PRIME-XS, a European Infrastructure for Proteomics. Molecular and Cellular Proteomics, 2014, 13, 1901-1904.	2.5	2
118	Pathogens and host immunity in the ancient human oral cavity. Nature Genetics, 2014, 46, 336-344.	9.4	482
119	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
120	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
121	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. Nature Methods, 2014, 11, 868-874.	9.0	70
122	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
123	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
124	The genetic prehistory of the New World Arctic. Science, 2014, 345, 1255832.	6.0	264
125	Resolution of the type material of the Asian elephant, <i>Elephas maximus</i> Linnaeus, 1758 (Proboscidea,) Tj ETQq1 1 0,784314 rgBT /Overl	1.0	22
126	Direct evidence of milk consumption from ancient human dental calculus. Scientific Reports, 2014, 4, 7104.	1.6	184

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127	SILAC-Based Temporal Phosphoproteomics. <i>Methods in Molecular Biology</i> , 2014, 1188, 125-148.	0.4	10
128	Predicting Kinase Activity in Angiotensin Receptor Phosphoproteomes Based on Sequence-Motifs and Interactions. <i>PLoS ONE</i> , 2014, 9, e94672.	1.1	7
129	Comprehensive Identification of SUMO2/3 Targets and Their Dynamics during Mitosis. <i>PLoS ONE</i> , 2014, 9, e100692.	1.1	19
130	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.	1.1	70
131	Structures of Down Syndrome Kinases, DYRKs, Reveal Mechanisms of Kinase Activation and Substrate Recognition. <i>Structure</i> , 2013, 21, 986-996.	1.6	127
132	Genomic and Proteomic Analyses of Prdm5 Reveal Interactions with Insulator Binding Proteins in Embryonic Stem Cells. <i>Molecular and Cellular Biology</i> , 2013, 33, 4504-4516.	1.1	29
133	Functional Proteomics Defines the Molecular Switch Underlying FGF Receptor Trafficking and Cellular Outputs. <i>Molecular Cell</i> , 2013, 51, 707-722.	4.5	145
134	TIMP-1 Increases Expression and Phosphorylation of Proteins Associated with Drug Resistance in Breast Cancer Cells. <i>Journal of Proteome Research</i> , 2013, 12, 4136-4151.	1.8	36
135	The SH2 Domain Interaction Landscape. <i>Cell Reports</i> , 2013, 3, 1293-1305.	2.9	110
136	RNF4 is required for DNA double-strand break repair in vivo. <i>Cell Death and Differentiation</i> , 2013, 20, 490-502.	5.0	102
137	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	9.4	282
138	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.	13.7	717
139	Status of Large-scale Analysis of Post-translational Modifications by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3444-3452.	2.5	491
140	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.	1.6	34
141	Phosphorylation Variation during the Cell Cycle Scales with Structural Propensities of Proteins. <i>PLoS Computational Biology</i> , 2013, 9, e1002842.	1.5	54
142	In Vivo Phosphoproteomics Analysis Reveals the Cardiac Targets of β^2 -Adrenergic Receptor Signaling. <i>Science Signaling</i> , 2013, 6, rs11.	1.6	164
143	Phosphoproteomics taken to heart. <i>Cell Cycle</i> , 2013, 12, 2707-2708.	1.3	4
144	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.	1.2	62

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145	Proteomic Analyses Reveal Divergent Ubiquitylation Site Patterns in Murine Tissues. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1578-1585.	2.5	244
146	δ -GABA receptors are high-affinity targets for γ -hydroxybutyric acid (GHB). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13404-13409.	3.3	87
147	Proteomic Analysis of Lysine Acetylation Sites in Rat Tissues Reveals Organ Specificity and Subcellular Patterns. <i>Cell Reports</i> , 2012, 2, 419-431.	2.9	493
148	A Major Lineage of Enteroendocrine Cells Coexpress CCK, Secretin, GIP, GLP-1, PYY, and Neurotensin but Not Somatostatin. <i>Endocrinology</i> , 2012, 153, 5782-5795.	1.4	269
149	Correction to Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. <i>Journal of Proteome Research</i> , 2012, 11, 3506-3508.	1.8	11
150	Optimized Fast and Sensitive Acquisition Methods for Shotgun Proteomics on a Quadrupole Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2012, 11, 3487-3497.	1.8	270
151	Proteomic Investigations Reveal a Role for RNA Processing Factor THRAP3 in the DNA Damage Response. <i>Molecular Cell</i> , 2012, 46, 212-225.	4.5	298
152	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.	2.6	32
153	Quantitative maps of protein phosphorylation sites across 14 different rat organs and tissues. <i>Nature Communications</i> , 2012, 3, 876.	5.8	307
154	Proteomic Analysis of a Pleistocene Mammoth Femur Reveals More than One Hundred Ancient Bone Proteins. <i>Journal of Proteome Research</i> , 2012, 11, 917-926.	1.8	196
155	Pinpointing Phosphorylation Sites: Quantitative Filtering and a Novel Site-specific x-Ion Fragment. <i>Journal of Proteome Research</i> , 2011, 10, 2937-2948.	1.8	27
156	Andromeda: A Peptide Search Engine Integrated into the MaxQuant Environment. <i>Journal of Proteome Research</i> , 2011, 10, 1794-1805.	1.8	4,935
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