

Jesper V. Olsen

List of Publications by Year in descending order

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229
papers

47,969
citations

3731

89
h-index

1857

209
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247
all docs

247
docs citations

247
times ranked

59826
citing authors

#	ARTICLE	IF	CITATIONS
1	A deeper look at carrier proteome effects for single-cell proteomics. <i>Communications Biology</i> , 2022, 5, 150.	4.4	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.	0.9	8
3	SPIN enables high throughput species identification of archaeological bone by proteomics. <i>Nature Communications</i> , 2022, 13, 2458.	12.8	31
4	A Middle Pleistocene Denisovan molar from the Annamite Chain of northern Laos. <i>Nature Communications</i> , 2022, 13, 2557.	12.8	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, .	5.4	6
6	Optimal analytical strategies for sensitive and quantitative phosphoproteomics using TMT-based multiplexing. <i>Proteomics</i> , 2022, 22, .	2.2	9
7	FRMD6 has tumor suppressor functions in prostate cancer. <i>Oncogene</i> , 2021, 40, 763-776.	5.9	24
8	Data Processing and Analysis for DIA-Based Phosphoproteomics Using Spectronaut. <i>Methods in Molecular Biology</i> , 2021, 2361, 95-107.	0.9	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.	9.7	21
10	The methyltransferase METTL9 mediates pervasive 1-methylhistidine modification in mammalian proteomes. <i>Nature Communications</i> , 2021, 12, 891.	12.8	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.	14.5	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.	4.1	8
13	Faecal proteomics as a novel method to study mammalian behaviour and physiology. <i>Molecular Ecology Resources</i> , 2021, 21, 1808-1819.	4.8	7
14	Quantitative proteome comparison of human hearts with those of model organisms. <i>PLoS Biology</i> , 2021, 19, e3001144.	5.6	23
15	Proteomics of resistance to Notch1 inhibition in acute lymphoblastic leukemia reveals targetable kinase signatures. <i>Nature Communications</i> , 2021, 12, 2507.	12.8	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, .	7.1	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.	4.1	6
18	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. <i>Molecular Systems Biology</i> , 2021, 17, e9730.	7.2	78

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19	Spatial-proteomics reveals phospho-signaling dynamics at subcellular resolution. <i>Nature Communications</i> , 2021, 12, 7113.	12.8	38
20	The human methyltransferase ZCCHC4 catalyses N6-methyladenosine modification of 28S ribosomal RNA. <i>Nucleic Acids Research</i> , 2020, 48, 830-846.	14.5	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.	3.8	27
22	Multi-protease analysis of Pleistocene bone proteomes. <i>Journal of Proteomics</i> , 2020, 228, 103889.	2.4	18
23	Effects of active farnesoid X receptor on GLUTag enteroendocrine L cells. <i>Molecular and Cellular Endocrinology</i> , 2020, 517, 110923.	3.2	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.	3.2	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.	4.0	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.	2.4	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.	4.2	16
28	Proteome and Phosphoproteome Changes Associated with Prognosis in Acute Myeloid Leukemia. <i>Cancers</i> , 2020, 12, 709.	3.7	33
29	The dental proteome of Homo antecessor. <i>Nature</i> , 2020, 580, 235-238.	27.8	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.	12.8	251
31	Deciphering the human phosphoproteome. <i>Nature Biotechnology</i> , 2020, 38, 285-286.	17.5	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.	3.8	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.	1.9	9
34	ZAK \pm Recognizes Stalled Ribosomes through Partially Redundant Sensor Domains. <i>Molecular Cell</i> , 2020, 78, 700-713.e7.	9.7	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.	3.8	24
36	Molecular Basis of the Mechanisms Controlling MASTL. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 326-343.	3.8	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.	12.8	84
38	Dynamic lineage priming is driven via direct enhancer regulation by ERK. <i>Nature</i> , 2019, 575, 355-360.	27.8	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.	3.3	11
40	Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , 2019, 574, 103-107.	27.8	135
41	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. <i>Cell</i> , 2019, 179, 543-560.e26.	28.9	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.	0.8	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.	6.4	22
44	Palaeoproteomics resolves sloth relationships. <i>Nature Ecology and Evolution</i> , 2019, 3, 1121-1130.	7.8	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.	14.5	25
46	Protein Aggregation Capture on Microparticles Enables Multipurpose Proteomics Sample Preparation*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1027a-1035.	3.8	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.	6.4	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.	27.8	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.	7.0	55
51	Large-Scale Phosphoproteomics Reveals Shp-2 Phosphatase-Dependent Regulators of Pdgf Receptor Signaling. <i>Cell Reports</i> , 2018, 22, 2784-2796.	6.4	51
52	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. <i>Angewandte Chemie</i> , 2018, 130, 7491-7496.	2.0	1
53	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 7369-7374.	13.8	76
54	Truncated SALL1 Impedes Primary Cilia Function in Townes-Brocks Syndrome. <i>American Journal of Human Genetics</i> , 2018, 102, 249-265.	6.2	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.	3.4	12
56	Benchmarking common quantification strategies for large-scale phosphoproteomics. <i>Nature Communications</i> , 2018, 9, 1045.	12.8	232
57	Performance Evaluation of the Q Exactive HF-X for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 727-738.	3.7	221
58	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. <i>Nature Communications</i> , 2018, 9, 4744.	12.8	63
59	Integrated proximal proteomics reveals IRS2 as a determinant of cell survival in ALK-driven neuroblastoma. <i>Science Signaling</i> , 2018, 11, .	3.6	33
60	Ancient proteins from ceramic vessels at Atlátek West reveal the hidden cuisine of early farmers. <i>Nature Communications</i> , 2018, 9, 4064.	12.8	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.	3.7	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.	8.2	341
63	PKD Phosphorylation as Novel Pathway of KV11.1 Regulation. <i>Cellular Physiology and Biochemistry</i> , 2018, 47, 1742-1750.	1.6	2
64	Molecular basis of Tausled-Like Kinase 2 activation. <i>Nature Communications</i> , 2018, 9, 2535.	12.8	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.	3.8	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.	12.8	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.	14.5	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.	6.5	15
69	A comprehensive platform for the analysis of ubiquitin-like protein modifications using in vivo biotinylation. <i>Scientific Reports</i> , 2017, 7, 40756.	3.3	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.	6.5	27
71	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. <i>Cell Systems</i> , 2017, 4, 587-599.e4.	6.2	413
72	The ubiquitin ligase Cullin5SOCS2 regulates NDR1/STK38 stability and NF- κ B transactivation. <i>Scientific Reports</i> , 2017, 7, 42800.	3.3	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.	3.4	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.	3.8	15
75	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. <i>Cell Reports</i> , 2017, 18, 3242-3256.	6.4	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.	6.4	24
77	Proteomic profiling of archaeological human bone. <i>Royal Society Open Science</i> , 2017, 4, 161004.	2.4	76
78	Proteomics insights into DNA damage response and translating this knowledge to clinical strategies. <i>Proteomics</i> , 2017, 17, 1600018.	2.2	18
79	Combinatorial Drug Screening Identifies Ewing Sarcoma-specific Sensitivities. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 88-101.	4.1	17
80	Multilayered proteomics reveals molecular switches dictating ligand-dependent EGFR trafficking. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 608-618.	8.2	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.	4.1	16
82	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	2.8	113
83	A Conserved Motif Provides Binding Specificity to the PP2A-B56 Phosphatase. <i>Molecular Cell</i> , 2016, 63, 686-695.	9.7	235
84	Analytic framework for peptidomics applied to large-scale neuropeptide identification. <i>Nature Communications</i> , 2016, 7, 11436.	12.8	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.	12.8	82
86	Conformation-specific anti-Mad2 monoclonal antibodies for the dissection of checkpoint signaling. <i>MAbs</i> , 2016, 8, 689-697.	5.2	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.	2.1	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.	6.5	35
89	Offline High pH Reversed-Phase Peptide Fractionation for Deep Phosphoproteome Coverage. <i>Methods in Molecular Biology</i> , 2016, 1355, 179-192.	0.9	36
90	Simple and Reproducible Sample Preparation for Single-Shot Phosphoproteomics with High Sensitivity. <i>Methods in Molecular Biology</i> , 2016, 1355, 251-260.	0.9	39

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91	From Phosphosites to Kinases. Methods in Molecular Biology, 2016, 1355, 307-321.	0.9	21
92	Systems Analysis for Interpretation of Phosphoproteomics Data. Methods in Molecular Biology, 2016, 1355, 341-360.	0.9	15
93	Protein sequences bound to mineral surfaces persist into deep time. ELife, 2016, 5, .	6.0	176
94	Metaproteomics of saliva identifies human protein markers specific for individuals with periodontitis and dental caries compared to orally healthy controls. PeerJ, 2016, 4, e2433.	2.0	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. Science Signaling, 2015, 8, ra40.	3.6	64
98	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.	4.6	8
99	Ubiquitin-SUMO Circuitry Controls Activated Fanconi Anemia ID Complex Dosage in Response to DNA Damage. Molecular Cell, 2015, 57, 150-164.	9.7	106
100	Ctk1 Function Is Necessary for Full Translation Initiation Activity in Saccharomyces cerevisiae. Eukaryotic Cell, 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). Journal of Biological Chemistry, 2015, 290, 15526-15537.	3.4	32
102	SUMO-2 Orchestrates Chromatin Modifiers in Response to DNA Damage. Cell Reports, 2015, 10, 1778-1791.	6.4	117
103	In vivo quantitative phosphoproteomic profiling identifies novel regulators of castration-resistant prostate cancer growth. Oncogene, 2015, 34, 2764-2776.	5.9	63
104	Ancient proteins resolve the evolutionary history of Darwin's South American ungulates. Nature, 2015, 522, 81-84.	27.8	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. Molecular and Cellular Proteomics, 2015, 14, 1419-1434.	3.8	79
106	Recent findings and technological advances in phosphoproteomics for cells and tissues. Expert Review of Proteomics, 2015, 12, 469-487.	3.0	70
107	Molecular evidence of use of hide glue in 4th millennium BC Europe. Journal of Archaeological Science, 2015, 63, 65-71.	2.4	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.	7.1	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.	5.9	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.	7.2	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.	3.8	22
113	A direct role of γ -H2AX in the spindle assembly checkpoint beyond γ -H2AX foci recruitment. EMBO Reports, 2014, 15, 282-290.	4.5	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.	3.7	168
115	Off-Line High-pH Reversed-Phase Fractionation for In-Depth Phosphoproteomics. Journal of Proteome Research, 2014, 13, 6176-6186.	3.7	263
116	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. Molecular and Cellular Proteomics, 2014, 13, 1905-1913.	3.8	42
117	PRIME-XS, a European Infrastructure for Proteomics. Molecular and Cellular Proteomics, 2014, 13, 1901-1904.	3.8	2
118	Pathogens and host immunity in the ancient human oral cavity. Nature Genetics, 2014, 46, 336-344.	21.4	482
119	Uncovering SUMOylation Dynamics during Cell-Cycle Progression Reveals FoxM1 as a Key Mitotic SUMO Target Protein. Molecular Cell, 2014, 53, 1053-1066.	9.7	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.	2.3	31
121	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. Nature Methods, 2014, 11, 868-874.	19.0	70
122	Analysis of Changes in SUMO-2/3 Modification during Breast Cancer Progression and Metastasis. Journal of Proteome Research, 2014, 13, 3905-3918.	3.7	25
123	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
124	The genetic prehistory of the New World Arctic. Science, 2014, 345, 1255832.	12.6	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	2.3	22
126	Direct evidence of milk consumption from ancient human dental calculus. Scientific Reports, 2014, 4, 7104.	3.3	184

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127	SILAC-Based Temporal Phosphoproteomics. <i>Methods in Molecular Biology</i> , 2014, 1188, 125-148.	0.9	10
128	Predicting Kinase Activity in Angiotensin Receptor Phosphoproteomes Based on Sequence-Motifs and Interactions. <i>PLoS ONE</i> , 2014, 9, e94672.	2.5	7
129	Comprehensive Identification of SUMO2/3 Targets and Their Dynamics during Mitosis. <i>PLoS ONE</i> , 2014, 9, e100692.	2.5	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.	2.5	70
131	Structures of Down Syndrome Kinases, DYRKs, Reveal Mechanisms of Kinase Activation and Substrate Recognition. <i>Structure</i> , 2013, 21, 986-996.	3.3	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.	2.3	29
133	Functional Proteomics Defines the Molecular Switch Underlying FGF Receptor Trafficking and Cellular Outputs. <i>Molecular Cell</i> , 2013, 51, 707-722.	9.7	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.	3.7	36
135	The SH2 Domain Interaction Landscape. <i>Cell Reports</i> , 2013, 3, 1293-1305.	6.4	110
136	RNF4 is required for DNA double-strand break repair in vivo. <i>Cell Death and Differentiation</i> , 2013, 20, 490-502.	11.2	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.	21.4	282
138	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.	27.8	717
139	Status of Large-scale Analysis of Post-translational Modifications by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3444-3452.	3.8	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.	3.6	34
141	Phosphorylation Variation during the Cell Cycle Scales with Structural Propensities of Proteins. <i>PLoS Computational Biology</i> , 2013, 9, e1002842.	3.2	54
142	In Vivo Phosphoproteomics Analysis Reveals the Cardiac Targets of β^2 -Adrenergic Receptor Signaling. <i>Science Signaling</i> , 2013, 6, rs11.	3.6	164
143	Phosphoproteomics taken to heart. <i>Cell Cycle</i> , 2013, 12, 2707-2708.	2.6	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.	2.0	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.	3.8	244
146	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, 13404-13409.	7.1	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.	6.4	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.	2.8	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.	3.7	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.	3.7	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.	9.7	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.	5.4	32
153	Quantitative maps of protein phosphorylation sites across 14 different rat organs and tissues. <i>Nature Communications</i> , 2012, 3, 876.	12.8	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.	3.7	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.	3.7	27
156	Andromeda: A Peptide Search Engine Integrated into the MaxQuant Environment. <i>Journal of Proteome Research</i> , 2011, 10, 1794-1805.	3.7	4,935
157	GeLCMS for In-Depth Protein Characterization and Advanced Analysis of Proteomes. <i>Methods in Molecular Biology</i> , 2011, 753, 143-155.	0.9	36
158	Proteome-Wide Mapping of the <i>Drosophila</i> Acetylome Demonstrates a High Degree of Conservation of Lysine Acetylation. <i>Science Signaling</i> , 2011, 4, ra48.	3.6	243
159	System-Wide Temporal Characterization of the Proteome and Phosphoproteome of Human Embryonic Stem Cell Differentiation. <i>Science Signaling</i> , 2011, 4, rs3.	3.6	389
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