

# Kathryn S Lilley

## List of Publications by Year in descending order

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Version: 2024-02-01

264  
papers

24,828  
citations

7568

77  
h-index

9589

142  
g-index

301  
all docs

301  
docs citations

301  
times ranked

32918  
citing authors

#	ARTICLE	IF	CITATIONS
1	A proteomic survival predictor for COVID-19 patients in intensive care. , 2022, 1, e0000007.		28
2	Proteomic analysis in primary T cells reveals IL-7 alters T cell receptor thresholding via CYTIP/cytohesin/LFA-1 localisation and activation. Biochemical Journal, 2022, 479, 225-243.	3.7	0
3	Subcellular Transcriptomics and Proteomics: A Comparative Methods Review. Molecular and Cellular Proteomics, 2022, 21, 100186.	3.8	23
4	Unresolved stalled ribosome complexes restrict cell-cycle progression after genotoxic stress. Molecular Cell, 2022, 82, 1557-1572.e7.	9.7	30
5	Prior Signal Acquisition Software Versions for Orbitrap Underestimate Low Isobaric Mass Tag Intensities, Without Detriment to Differential Abundance Experiments. ACS Measurement Science Au, 2022, 2, 233-240.	4.4	0
6	Multi-omic based production strain improvement (MOBpsi) for bio-manufacturing of toxic chemicals. Metabolic Engineering, 2022, 72, 133-149.	7.0	6
7	Understudied proteins: opportunities and challenges for functional proteomics. Nature Methods, 2022, 19, 774-779.	19.0	83
8	An open invitation to the Understudied Proteins Initiative. Nature Biotechnology, 2022, 40, 815-817.	17.5	25
9	Drosophila nicotinic acetylcholine receptor subunits and their native interactions with insecticidal peptide toxins. ELife, 2022, 11, .	6.0	5
10	In Depth Exploration of the Alternative Proteome of Drosophila melanogaster. Frontiers in Cell and Developmental Biology, 2022, 10, .	3.7	6
11	CFTR Rescue by Lumacaftor (VX-809) Induces an Extensive Reorganization of Mitochondria in the Cystic Fibrosis Bronchial Epithelium. Cells, 2022, 11, 1938.	4.1	4
12	dia-PASEF data analysis using FragPipe and DIA-NN for deep proteomics of low sample amounts. Nature Communications, 2022, 13, .	12.8	120
13	Ultra-fast proteomics with Scanning SWATH. Nature Biotechnology, 2021, 39, 846-854.	17.5	173
14	Subcellular proteomics. Nature Reviews Methods Primers, 2021, 1, .	21.2	159
15	Global analysis of protein-RNA interactions in SARS-CoV-2-infected cells reveals key regulators of infection. Molecular Cell, 2021, 81, 2851-2867.e7.	9.7	108
16	A Bayesian semi-parametric model for thermal proteome profiling. Communications Biology, 2021, 4, 810.	4.4	6
17	Localization of Organelle Proteins by Isotope Tagging: Current status and potential applications in drug discovery research. Drug Discovery Today: Technologies, 2021, 39, 57-67.	4.0	5
18	A time-resolved proteomic and prognostic map of COVID-19. Cell Systems, 2021, 12, 780-794.e7.	6.2	125

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19	Spatiotemporal proteomic profiling of the pro-inflammatory response to lipopolysaccharide in the THP-1 human leukaemia cell line. <i>Nature Communications</i> , 2021, 12, 5773.	12.8	29
20	Pan-cancer analysis of transcripts encoding novel open-reading frames (nORFs) and their potential biological functions. <i>Npj Genomic Medicine</i> , 2021, 6, 4.	3.8	20
21	DIA-NN: neural networks and interference correction enable deep proteome coverage in high throughput. <i>Nature Methods</i> , 2020, 17, 41-44.	19.0	882
22	A Comprehensive Subcellular Atlas of the Toxoplasma Proteome via hyperLOPIT Provides Spatial Context for Protein Functions. <i>Cell Host and Microbe</i> , 2020, 28, 752-766.e9.	11.0	201
23	Spatial proteomics defines the content of trafficking vesicles captured by golgin tethers. <i>Nature Communications</i> , 2020, 11, 5987.	12.8	45
24	Characterisation of protein isoforms encoded by the Drosophila Glycogen Synthase Kinase 3 gene shaggy. <i>PLoS ONE</i> , 2020, 15, e0236679.	2.5	5
25	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. <i>Cell Systems</i> , 2020, 11, 11-24.e4.	6.2	439
26	Changes in the Oligodendrocyte Progenitor Cell Proteome with Ageing. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1281-1302.	3.8	53
27	Proteomics of intracellular freezing survival. <i>PLoS ONE</i> , 2020, 15, e0233048.	2.5	1
28	Moving Profiling Spatial Proteomics Beyond Discrete Classification. <i>Proteomics</i> , 2020, 20, e1900392.	2.2	19
29	Organic phase separation opens up new opportunities to interrogate the RNA-binding proteome. <i>Current Opinion in Chemical Biology</i> , 2020, 54, 70-75.	6.1	35
30	Efficient recovery of the RNA-bound proteome and protein-bound transcriptome using phase separation (OOPS). <i>Nature Protocols</i> , 2020, 15, 2568-2588.	12.0	15
31	Biotin proximity tagging favours unfolded proteins and enables the study of intrinsically disordered regions. <i>Communications Biology</i> , 2020, 3, 38.	4.4	26
32	A direct role for SNX9 in the biogenesis of filopodia. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	9
33	A semi-supervised Bayesian approach for simultaneous protein sub-cellular localisation assignment and novelty detection. <i>PLoS Computational Biology</i> , 2020, 16, e1008288.	3.2	16
34	Identification of the cis-molecular neighbours of the immune checkpoint protein <i>CTLA4</i> in the breast cancer cell line SKBR3 by proteomic proximity labelling. <i>International Journal of Oncology</i> , 2020, 57, 87-99.	3.3	2
35	Title is missing!. , 2020, 15, e0236679.		0
36	Title is missing!. , 2020, 15, e0236679.		0

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37	Title is missing!. , 2020, 15, e0236679.		0
38	Title is missing!. , 2020, 15, e0236679.		0
39	Differential Interactome and Innate Immune Response Activation of Two Structurally Distinct Misfolded Protein Oligomers. ACS Chemical Neuroscience, 2019, 10, 3464-3478.	3.5	7
40	Separating Golgi Proteins from <i>Cis</i> to <i>Trans</i> Reveals Underlying Properties of Cisternal Localization. Plant Cell, 2019, 31, 2010-2034.	6.6	40
41	Proteome Mapping of a Cyanobacterium Reveals Distinct Compartment Organization and Cell-Dispersed Metabolism. Plant Physiology, 2019, 181, 1721-1738.	4.8	58
42	Combining LOPIT with differential ultracentrifugation for high-resolution spatial proteomics. Nature Communications, 2019, 10, 331.	12.8	146
43	Assessing sub-cellular resolution in spatial proteomics experiments. Current Opinion in Chemical Biology, 2019, 48, 123-149.	6.1	31
44	Systems Analyses Reveal the Resilience of Escherichia coli Physiology during Accumulation and Export of the Nonnative Organic Acid Citramalate. MSystems, 2019, 4, .	3.8	9
45	Comparison of <i>Drosophila melanogaster</i> Embryo and Adult Proteome by SWATH-MS Reveals Differential Regulation of Protein Synthesis, Degradation Machinery, and Metabolism Modules. Journal of Proteome Research, 2019, 18, 2525-2534.	3.7	7
46	Changes in the Arabidopsis RNA-binding proteome reveal novel stress response mechanisms. BMC Plant Biology, 2019, 19, 139.	3.6	50
47	A proteomic time course through the differentiation of human induced pluripotent stem cells into hepatocyte-like cells. Scientific Reports, 2019, 9, 3270.	3.3	15
48	Editorial overview: Untangling proteome organization in space and time. Current Opinion in Chemical Biology, 2019, 48, A1-A4.	6.1	6
49	Transcriptional regulation of the genes involved in protein metabolism and processing in <i>Saccharomyces cerevisiae</i> . FEMS Yeast Research, 2019, 19, .	2.3	1
50	The Arabidopsis thaliana Æcognin E3 ligase PROTEOLYSIS1 influences the immune response. Plant Direct, 2019, 3, e00194.	1.9	12
51	Comprehensive identification of RNAÆ protein interactions in any organism using orthogonal organic phase separation (OOPS). Nature Biotechnology, 2019, 37, 169-178.	17.5	247
52	Proteomic responses of HepG2 cell monolayers and 3D spheroids to selected hepatotoxins. Toxicology Letters, 2019, 300, 40-50.	0.8	19
53	KetamineÆ™s Effects on the Glutamatergic and GABAergic Systems: A Proteomics and Metabolomics Study in Mice. Molecular Neuropsychiatry, 2019, 5, 42-51.	2.9	15
54	The subcellular organisation of Saccharomyces cerevisiae. Current Opinion in Chemical Biology, 2019, 48, 86-95.	6.1	26

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55	The Parkinson's Disease-Linked Protein DJ-1 Associates with Cytoplasmic mRNP Granules During Stress and Neurodegeneration. <i>Molecular Neurobiology</i> , 2019, 56, 61-77.	4.0	33
56	Drought Stress Causes Specific Changes to the Spliceosome and Stress Granule Components. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 163.	3.5	38
57	Mapping the <i>Saccharomyces cerevisiae</i> Spatial Proteome with High Resolution Using hyperLOPIT. <i>Methods in Molecular Biology</i> , 2019, 2049, 165-190.	0.9	8
58	A Bioconductor workflow for the Bayesian analysis of spatial proteomics. <i>F1000Research</i> , 2019, 8, 446.	1.6	27
59	A Protocol to Map the Spatial Proteome Using HyperLOPIT in <i>Saccharomyces cerevisiae</i> . <i>Bio-protocol</i> , 2019, 9, e3303.	0.4	2
60	Mass spectrometry approaches to study plant endomembrane trafficking. <i>Seminars in Cell and Developmental Biology</i> , 2018, 80, 123-132.	5.0	8
61	Proteomic Comparison of Various Hepatic Cell Cultures for Preclinical Safety Pharmacology. <i>Toxicological Sciences</i> , 2018, 164, 229-239.	3.1	5
62	Co-complex protein membership evaluation using Maximum Entropy on GO ontology and InterPro annotation. <i>Bioinformatics</i> , 2018, 34, 1884-1892.	4.1	18
63	Transacting translational regulatory RNA binding proteins. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1465.	6.4	79
64	Stat3-mediated alterations in lysosomal membrane protein composition. <i>Journal of Biological Chemistry</i> , 2018, 293, 4244-4261.	3.4	26
65	Terminomics reveals control of Arabidopsis seed storage proteins and proteases by the Arg/N-end rule pathway. <i>New Phytologist</i> , 2018, 218, 1106-1126.	7.3	44
66	A Bayesian mixture modelling approach for spatial proteomics. <i>PLoS Computational Biology</i> , 2018, 14, e1006516.	3.2	53
67	Ethylene Receptors, CTRs and EIN2 Target Protein Identification and Quantification Through Parallel Reaction Monitoring During Tomato Fruit Ripening. <i>Frontiers in Plant Science</i> , 2018, 9, 1626.	3.6	38
68	Early Responses to Severe Drought Stress in the Arabidopsis thaliana Cell Suspension Culture Proteome. <i>Proteomes</i> , 2018, 6, 38.	3.5	24
69	Identification of the RNA polymerase I-RNA interactome. <i>Nucleic Acids Research</i> , 2018, 46, 11002-11013.	14.5	19
70	Ciprofloxacin binding to GyrA causes global changes in the proteome of <i>Pseudomonas aeruginosa</i> . <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	10
71	Negative feedback via RSK modulates Erk-dependent progression from naïve pluripotency. <i>EMBO Reports</i> , 2018, 19, .	4.5	28
72	hiPSC hepatocyte model demonstrates the role of unfolded protein response and inflammatory networks in $\alpha$ 1-antitrypsin deficiency. <i>Journal of Hepatology</i> , 2018, 69, 851-860.	3.7	48

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73	Time, space, and disorder in the expanding proteome universe. <i>Proteomics</i> , 2017, 17, 1600399.	2.2	19
74	Tracking the embryonic stem cell transition from ground state pluripotency. <i>Development (Cambridge)</i> , 2017, 144, 1221-1234.	2.5	226
75	A subcellular map of the human proteome. <i>Science</i> , 2017, 356, .	12.6	2,079
76	Using hyperLOPIT to perform high-resolution mapping of the spatial proteome. <i>Nature Protocols</i> , 2017, 12, 1110-1135.	12.0	113
77	In-depth characterization of the tomato fruit pericarp proteome. <i>Proteomics</i> , 2017, 17, 1600406.	2.2	39
78	Multiple marker abundance profiling: combining selected reaction monitoring and data-independent acquisition for rapid estimation of organelle abundance in subcellular samples. <i>Plant Journal</i> , 2017, 92, 1202-1217.	5.7	42
79	Spectral Libraries for SWATH-MS Assays for <i>Drosophila melanogaster</i> and <i>Solanum lycopersicum</i> . <i>Proteomics</i> , 2017, 17, 1700216.	2.2	21
80	Clareosin: a novel sexually dimorphic urinary lipocalin in the bank vole, <i>Myodes glareolus</i> . <i>Open Biology</i> , 2017, 7, 170135.	3.6	7
81	Ketamine's antidepressant effect is mediated by energy metabolism and antioxidant defense system. <i>Scientific Reports</i> , 2017, 7, 15788.	3.3	54
82	Impact of Azithromycin on the Quorum Sensing-Controlled Proteome of <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2016, 11, e0147698.	2.5	37
83	Mimicking nature: Phosphopeptide enrichment using combinatorial libraries of affinity ligands. <i>Journal of Chromatography A</i> , 2016, 1457, 76-87.	3.7	10
84	The RNA-binding protein repertoire of <i>Arabidopsis thaliana</i> . <i>Scientific Reports</i> , 2016, 6, 29766.	3.3	139
85	Phosphorylation of the dimeric cytoplasmic domain of the phytosulfoligand receptor, PSKR1. <i>Biochemical Journal</i> , 2016, 473, 3081-3098.	3.7	27
86	SWATH-MS dataset of heat-shock treated <i>Drosophila melanogaster</i> embryos. <i>Data in Brief</i> , 2016, 9, 991-995.	1.0	3
87	SWATH-MS data of <i>Drosophila melanogaster</i> proteome dynamics during embryogenesis. <i>Data in Brief</i> , 2016, 9, 771-775.	1.0	7
88	The metabolic background is a global player in <i>Saccharomyces</i> gene expression epistasis. <i>Nature Microbiology</i> , 2016, 1, 15030.	13.3	76
89	Analysis of temperature-mediated changes in the wine yeast <i>Saccharomyces bayanus var uvarum</i> . An oenological study of how the protein content influences wine quality. <i>Proteomics</i> , 2016, 16, 576-592.	2.2	7
90	Analysis of <i>Drosophila melanogaster</i> proteome dynamics during embryonic development by a combination of label-free proteomics approaches. <i>Proteomics</i> , 2016, 16, 2068-2080.	2.2	24

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91	Antibody-mediated neutralization of myelin-associated EphrinB3 accelerates CNS remyelination. <i>Acta Neuropathologica</i> , 2016, 131, 281-298.	7.7	37
92	A draft map of the mouse pluripotent stem cell spatial proteome. <i>Nature Communications</i> , 2016, 7, 8992.	12.8	197
93	A Quantitative Phosphoproteome Analysis of cGMP-Dependent Cellular Responses in <i>Arabidopsis thaliana</i> . <i>Molecular Plant</i> , 2016, 9, 621-623.	8.3	38
94	A Bioconductor workflow for processing and analysing spatial proteomics data. <i>F1000Research</i> , 2016, 5, 2926.	1.6	34
95	A Bioconductor workflow for processing and analysing spatial proteomics data. <i>F1000Research</i> , 2016, 5, 2926.	1.6	26
96	Learning from Heterogeneous Data Sources: An Application in Spatial Proteomics. <i>PLoS Computational Biology</i> , 2016, 12, e1004920.	3.2	47
97	Focus on Quantitative Proteomics. <i>Proteomics</i> , 2015, 15, 3101-3103.	2.2	2
98	Dynamic Proteomic Profiling of Extra-Embryonic Endoderm Differentiation in Mouse Embryonic Stem Cells. <i>Stem Cells</i> , 2015, 33, 2712-2725.	3.2	16
99	The chicken B-cell line DT40 proteome, beadome and interactomes. <i>Data in Brief</i> , 2015, 3, 29-33.	1.0	1
100	SILAC-iPAC: A quantitative method for distinguishing genuine from non-specific components of protein complexes by parallel affinity capture. <i>Journal of Proteomics</i> , 2015, 115, 143-156.	2.4	8
101	Exploring the Arabidopsis Proteome: Influence of Protein Solubilization Buffers on Proteome Coverage. <i>International Journal of Molecular Sciences</i> , 2015, 16, 857-870.	4.1	19
102	Quantitative proteomics analysis of the Arg/N $\epsilon$ rule pathway of targeted degradation in Arabidopsis roots. <i>Proteomics</i> , 2015, 15, 2447-2457.	2.2	37
103	Analysis of Quality-Related Parameters in Mature Kernels of Polygalacturonase Inhibiting Protein (PGIP) Transgenic Bread Wheat Infected with <i>Fusarium graminearum</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 3962-3969.	5.2	5
104	Protein Neighbors and Proximity Proteomics. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2848-2856.	3.8	105
105	Mep72, a Metzincin Protease That Is Preferentially Secreted by Biofilms of <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2015, 197, 762-773.	2.2	32
106	$\hat{\pm}$ -Klotho Expression in Human Tissues. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2015, 100, E1308-E1318.	3.6	137
107	<i>Drosophila</i> Ionotropic Receptor 25a mediates circadian clock resetting by temperature. <i>Nature</i> , 2015, 527, 516-520.	27.8	216
108	New Insights into the DT40 B Cell Receptor Cluster Using a Proteomic Proximity Labeling Assay. <i>Journal of Biological Chemistry</i> , 2014, 289, 14434-14447.	3.4	110

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109	Toward a Comprehensive Map of the Effectors of Rab GTPases. <i>Developmental Cell</i> , 2014, 31, 358-373.	7.0	224
110	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	3.8	42
111	Mass-spectrometry-based spatial proteomics data analysis using <tt>pRoloc</tt> and <tt>pRolocdata</tt>. <i>Bioinformatics</i> , 2014, 30, 1322-1324.	4.1	85
112	Protein Profiling Using Twoâ€²Dimensional Difference Gel Electrophoresis (2â€²DIGE). <i>Current Protocols in Protein Science</i> , 2014, 75, 22.2.1-22.2.17.	2.8	7
113	A protocol for the subcellular fractionation of <i>Saccharomyces cerevisiae</i> using nitrogen cavitation and density gradient centrifugation. <i>Yeast</i> , 2014, 31, 127-135.	1.7	12
114	Remodelling of a polypyrimidine tract-binding protein complex during apoptosis activates cellular IRESs. <i>Cell Death and Differentiation</i> , 2014, 21, 161-171.	11.2	24
115	Dynamic Regulation of the COP9 Signalosome in Response to DNA Damage. <i>Molecular and Cellular Biology</i> , 2014, 34, 1066-1076.	2.3	24
116	Human Urinary Exosomes as Innate Immune Effectors. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 2017-2027.	6.1	127
117	A Foundation for Reliable Spatial Proteomics Data Analysis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1937-1952.	3.8	49
118	Identification of Trans-Golgi Network Proteins in <i>Arabidopsis thaliana</i> Root Tissue. <i>Journal of Proteome Research</i> , 2014, 13, 763-776.	3.7	65
119	Analysis of the expression patterns, subcellular localisations and interaction partners of <i>Drosophila</i> proteins using a <i>pigP</i> protein trap library. <i>Development (Cambridge)</i> , 2014, 141, 3994-4005.	2.5	160
120	Label-Free Protein Quantification for Plant Golgi Protein Localization and Abundance. <i>Plant Physiology</i> , 2014, 166, 1033-1043.	4.8	48
121	Deciphering Thylakoid Sub-compartments using a Mass Spectrometry-based Approach. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2147-2167.	3.8	96
122	Additional Precursor Purification in Isobaric Mass Tagging Experiments by Traveling Wave Ion Mobility Separation (TWIMS). <i>Journal of Proteome Research</i> , 2014, 13, 3360-3369.	3.7	13
123	Proteome labeling and protein identification in specific tissues and at specific developmental stages in an animal. <i>Nature Biotechnology</i> , 2014, 32, 465-472.	17.5	161
124	Determining Protein Subcellular Localization in Mammalian Cell Culture with Biochemical Fractionation and iTRAQ 8-Plex Quantification. <i>Methods in Molecular Biology</i> , 2014, 1156, 157-174.	0.9	13
125	Spatial Proteomics: Practical Considerations for Data Acquisition and Analysis in Protein Subcellular Localisation Studies. <i>New Developments in Mass Spectrometry</i> , 2014, , 185-210.	0.2	3
126	Improving Qualitative and Quantitative Performance for MS <sup>E</sup> -based Label-free Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 2340-2353.	3.7	64



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127	Identification of Protein Biomarkers in Human Serum Using iTRAQ and Shotgun Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2013, 1061, 291-307.	0.9	5
128	RNA-seq reveals the RNA binding proteins, Hfq and RsmA, play various roles in virulence, antibiotic production and genomic flux in <i>Serratia</i> sp. ATCC 39006. <i>BMC Genomics</i> , 2013, 14, 822.	2.8	50
129	Structural and functional characteristics of cGMP-dependent methionine oxidation in <i>Arabidopsis thaliana</i> proteins. <i>Cell Communication and Signaling</i> , 2013, 11, 1.	6.5	77
130	A proteomic approach identifies many novel palmitoylated proteins in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2013, 197, 805-814.	7.3	135
131	Interlaboratory studies and initiatives developing standards for proteomics. <i>Proteomics</i> , 2013, 13, 904-909.	2.2	29
132	Identification and Quantitation of Signal Molecule-Dependent Protein Phosphorylation. <i>Methods in Molecular Biology</i> , 2013, 1016, 121-137.	0.9	8
133	Cardioprotection by S-nitrosation of a cysteine switch on mitochondrial complex I. <i>Nature Medicine</i> , 2013, 19, 753-759.	30.7	521
134	Effects of Traveling Wave Ion Mobility Separation on Data Independent Acquisition in Proteomics Studies. <i>Journal of Proteome Research</i> , 2013, 12, 2323-2339.	3.7	81
135	Popular Computational Methods to Assess Multiprotein Complexes Derived From Label-Free Affinity Purification and Mass Spectrometry (AP-MS) Experiments. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1-13.	3.8	46
136	Palmitoylation in plants. <i>Plant Signaling and Behavior</i> , 2013, 8, e25209.	2.4	15
137	The beauty of being (label)-free: sample preparation methods for SWATH-MS and next-generation targeted proteomics. <i>F1000Research</i> , 2013, 2, 272.	1.6	57
138	MSnbase-an R/Bioconductor package for isobaric tagged mass spectrometry data visualization, processing and quantitation. <i>Bioinformatics</i> , 2012, 28, 288-289.	4.1	288
139	Evaluation and Properties of the Budding Yeast Phosphoproteome. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.009555.	3.8	44
140	Putative Glycosyltransferases and Other Plant Golgi Apparatus Proteins Are Revealed by LOPIT Proteomics. <i>Plant Physiology</i> , 2012, 160, 1037-1051.	4.8	149
141	MRMaid 2.0: Mining PRIDE for Evidence-Based SRM Transitions. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 483-488.	2.0	15
142	Pipeline to assess the greatest source of technical variance in quantitative proteomics using metabolic labelling. <i>Journal of Proteomics</i> , 2012, 77, 441-454.	2.4	20
143	Isobaric tagging approaches in quantitative proteomics: the ups and downs. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 1029-1037.	3.7	77
144	Two-Dimensional Differential in Gel Electrophoresis (2D-DIGE) Analysis of Grape Berry Proteome during Postharvest Withering. <i>Journal of Proteome Research</i> , 2011, 10, 429-446.	3.7	61

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145	Method for suppressing non-specific protein interactions observed with affinity resins. <i>Methods</i> , 2011, 54, 407-412.	3.8	16
146	LC-MS/MS Methods for Absolute Quantification and Identification of Proteins Associated with Chimeric Plant Oil Bodies. <i>Analytical Chemistry</i> , 2011, 83, 9267-9272.	6.5	9
147	Proteomics of cryoprotective dehydration in <i>Megaphorura arctica</i> Tullberg 1876 (Onychiuridae: Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.0	10
148	Challenges for proteomics core facilities. <i>Proteomics</i> , 2011, 11, 1017-1025.	2.2	8
149	The ABRF Proteomics Research Group Studies: Educational exercises for qualitative and quantitative proteomic analyses. <i>Proteomics</i> , 2011, 11, 1371-1381.	2.2	18
150	Proteomic approaches to the characterization of protein thiol modification. <i>Current Opinion in Chemical Biology</i> , 2011, 15, 120-128.	6.1	90
151	In Vivo Analysis of Proteomes and Interactomes Using Parallel Affinity Capture (iPAC) Coupled to Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.002386.	3.8	69
152	In Vivo Analyses of the Roles of Essential Omp85-Related Proteins in the Chloroplast Outer Envelope Membrane $\bar{A} \bar{A}$ . <i>Plant Physiology</i> , 2011, 157, 147-159.	4.8	49
153	Taming the isobaric tagging elephant in the room in quantitative proteomics. <i>Nature Methods</i> , 2011, 8, 911-913.	19.0	24
154	Enabling Technologies for Yeast Proteome Analysis. <i>Methods in Molecular Biology</i> , 2011, 759, 149-178.	0.9	4
155	ABRF-PRG07: advanced quantitative proteomics study. <i>Journal of Biomolecular Techniques</i> , 2011, 22, 21-6.	1.5	13
156	Uromodulin exclusion list improves urinary exosomal protein identification. <i>Journal of Biomolecular Techniques</i> , 2011, 22, 136-45.	1.5	13
157	Proteomic Complex Detection using Sedimentation (ProCoDeS): screening for proteins in stable complexes and their candidate interaction partners. <i>Biochemical Society Transactions</i> , 2010, 38, 923-927.	3.4	2
158	Proteomic analysis of peach fruit mesocarp softening and chilling injury using difference gel electrophoresis (DIGE). <i>BMC Genomics</i> , 2010, 11, 43.	2.8	107
159	Expression proteomics of UPF1 knockdown in HeLa cells reveals autoregulation of hnRNP A2/B1 mediated by alternative splicing resulting in nonsense-mediated mRNA decay. <i>BMC Genomics</i> , 2010, 11, 565.	2.8	67
160	The <i>Drosophila melanogaster</i> sperm proteome-II (DmSP-II). <i>Journal of Proteomics</i> , 2010, 73, 2171-2185.	2.4	138
161	Nutrient control of eukaryote cell growth: a systems biology study in yeast. <i>BMC Biology</i> , 2010, 8, 68.	3.8	89
162	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , 2010, 10, 3957-3969.	2.2	54

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