

Kathryn S Lilley

List of Publications by Year in descending order

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264
papers

24,828
citations

8755

77
h-index

10955

142
g-index

301
all docs

301
docs citations

301
times ranked

36363
citing authors

#	ARTICLE	IF	CITATIONS
1	A subcellular map of the human proteome. <i>Science</i> , 2017, 356, .	6.0	2,079
2	DIA-NN: neural networks and interference correction enable deep proteome coverage in high throughput. <i>Nature Methods</i> , 2020, 17, 41-44.	9.0	882
3	Mitochondrial dysfunction in schizophrenia: evidence for compromised brain metabolism and oxidative stress. <i>Molecular Psychiatry</i> , 2004, 9, 684-697.	4.1	810
4	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893.	9.4	694
5	Cardioprotection by S-nitrosation of a cysteine switch on mitochondrial complex I. <i>Nature Medicine</i> , 2013, 19, 753-759.	15.2	521
6	Mapping the Arabidopsis organelle proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6518-6523.	3.3	518
7	Circadian Orchestration of the Hepatic Proteome. <i>Current Biology</i> , 2006, 16, 1107-1115.	1.8	506
8	Addressing Accuracy and Precision Issues in iTRAQ Quantitation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1885-1897.	2.5	471
9	Analysis of Detergent-Resistant Membranes in Arabidopsis. Evidence for Plasma Membrane Lipid Rafts. <i>Plant Physiology</i> , 2005, 137, 104-116.	2.3	445
10	The phage abortive infection system, ToxIN, functions as a protein-RNA toxin-antitoxin pair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 894-899.	3.3	445
11	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. <i>Cell Systems</i> , 2020, 11, 11-24.e4.	2.9	439
12	Identification of Glycosylphosphatidylinositol-Anchored Proteins in Arabidopsis. A Proteomic and Genomic Analysis. <i>Plant Physiology</i> , 2003, 132, 568-577.	2.3	364
13	FlyMine: an integrated database for Drosophila and Anopheles genomics. <i>Genome Biology</i> , 2007, 8, R129.	13.9	345
14	Ubiquitination of α -Synuclein in Lewy Bodies Is a Pathological Event Not Associated with Impairment of Proteasome Function. <i>Journal of Biological Chemistry</i> , 2003, 278, 44405-44411.	1.6	325
15	Localization of Organelle Proteins by Isotope Tagging (LOPIT). <i>Molecular and Cellular Proteomics</i> , 2004, 3, 1128-1134.	2.5	305
16	MSnbase-an R/Bioconductor package for isobaric tagged mass spectrometry data visualization, processing and quantitation. <i>Bioinformatics</i> , 2012, 28, 288-289.	1.8	288
17	i-Tracker: For quantitative proteomics using iTRAQ. <i>BMC Genomics</i> , 2005, 6, 145.	1.2	275
18	All about DIGE: quantification technology for differential-display 2D-gel proteomics. <i>Expert Review of Proteomics</i> , 2004, 1, 401-409.	1.3	260

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19	The Tip-Link Antigen, a Protein Associated with the Transduction Complex of Sensory Hair Cells, Is Protocadherin-15. <i>Journal of Neuroscience</i> , 2006, 26, 7022-7034.	1.7	258
20	Two-dimensional gel electrophoresis: recent advances in sample preparation, detection and quantitation. <i>Current Opinion in Chemical Biology</i> , 2002, 6, 46-50.	2.8	248
21	Comprehensive identification of RNA-protein interactions in any organism using orthogonal organic phase separation (OOPS). <i>Nature Biotechnology</i> , 2019, 37, 169-178.	9.4	247
22	A systematic approach to modeling, capturing, and disseminating proteomics experimental data. <i>Nature Biotechnology</i> , 2003, 21, 247-254.	9.4	246
23	Glucocorticoid signaling synchronizes the liver circadian transcriptome. <i>Hepatology</i> , 2007, 45, 1478-1488.	3.6	234
24	Growth control of the eukaryote cell: a systems biology study in yeast. <i>Journal of Biology</i> , 2007, 6, 4.	2.7	234
25	Tracking the embryonic stem cell transition from ground state pluripotency. <i>Development (Cambridge)</i> , 2017, 144, 1221-1234.	1.2	226
26	Toward a Comprehensive Map of the Effectors of Rab GTPases. <i>Developmental Cell</i> , 2014, 31, 358-373.	3.1	224
27	Subunit assembly and active site location in the structure of glutamate dehydrogenase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 12, 75-86.	1.5	221
28	Drosophila Ionotropic Receptor 25a mediates circadian clock resetting by temperature. <i>Nature</i> , 2015, 527, 516-520.	13.7	216
29	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.	5.1	201
30	A draft map of the mouse pluripotent stem cell spatial proteome. <i>Nature Communications</i> , 2016, 7, 8992.	5.8	197
31	Functional Specialization amongst the Arabidopsis Toc159 Family of Chloroplast Protein Import Receptors[W]. <i>Plant Cell</i> , 2004, 16, 2059-2077.	3.1	184
32	Maximising sensitivity for detecting changes in protein expression: Experimental design using minimal CyDyes. <i>Proteomics</i> , 2005, 5, 3105-3115.	1.3	183
33	SETH1 and SETH2, Two Components of the Glycosylphosphatidylinositol Anchor Biosynthetic Pathway, Are Required for Pollen Germination and Tube Growth in Arabidopsis [W]. <i>Plant Cell</i> , 2004, 16, 229-240.	3.1	178
34	Ultra-fast proteomics with Scanning SWATH. <i>Nature Biotechnology</i> , 2021, 39, 846-854.	9.4	173
35	Determining a significant change in protein expression with DeCyderâ„¢ during a pair-wise comparison using two-dimensional difference gel electrophoresis. <i>Proteomics</i> , 2004, 4, 1421-1432.	1.3	163
36	Proteome labeling and protein identification in specific tissues and at specific developmental stages in an animal. <i>Nature Biotechnology</i> , 2014, 32, 465-472.	9.4	161

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37	Analysis of the expression patterns, subcellular localisations and interaction partners of <i>Drosophila</i> proteins using a pigP protein trap library. <i>Development (Cambridge)</i> , 2014, 141, 3994-4005.	1.2	160
38	Subcellular proteomics. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	159
39	The Arabidopsis <i>ppi1</i> Mutant Is Specifically Defective in the Expression, Chloroplast Import, and Accumulation of Photosynthetic Proteins[W]. <i>Plant Cell</i> , 2003, 15, 1859-1871.	3.1	153
40	Experimental and Statistical Considerations to Avoid False Conclusions in Proteomics Studies Using Differential In-gel Electrophoresis. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1354-1364.	2.5	152
41	Putative Glycosyltransferases and Other Plant Golgi Apparatus Proteins Are Revealed by LOPIT Proteomics. <i>Plant Physiology</i> , 2012, 160, 1037-1051.	2.3	149
42	Impact of Replicate Types on Proteomic Expression Analysis. <i>Journal of Proteome Research</i> , 2005, 4, 1867-1871.	1.8	147
43	Design and Analysis Issues in Quantitative Proteomics Studies. <i>Proteomics</i> , 2007, 7, 42-50.	1.3	147
44	Combining LOPIT with differential ultracentrifugation for high-resolution spatial proteomics. <i>Nature Communications</i> , 2019, 10, 331.	5.8	146
45	Comparative proteomics of clathrin-coated vesicles. <i>Journal of Cell Biology</i> , 2006, 175, 571-578.	2.3	145
46	Identification of Putative Stage-Specific Grapevine Berry Biomarkers and Omics Data Integration into Networks. <i>Plant Physiology</i> , 2010, 154, 1439-1459.	2.3	145
47	The RNA-binding protein repertoire of <i>Arabidopsis thaliana</i> . <i>Scientific Reports</i> , 2016, 6, 29766.	1.6	139
48	The <i>Drosophila melanogaster</i> sperm proteome-II (DmSP-II). <i>Journal of Proteomics</i> , 2010, 73, 2171-2185.	1.2	138
49	±Klotho Expression in Human Tissues. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2015, 100, E1308-E1318.	1.8	137
50	Application of partial least squares discriminant analysis to two-dimensional difference gel studies in expression proteomics. <i>Proteomics</i> , 2005, 5, 81-90.	1.3	136
51	A proteomic approach identifies many novel palmitoylated proteins in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2013, 197, 805-814.	3.5	135
52	Detection of Reactive Oxygen Species-sensitive Thiol Proteins by Redox Difference Gel Electrophoresis. <i>Journal of Biological Chemistry</i> , 2007, 282, 22040-22051.	1.6	133
53	Identification of S-nitrosated mitochondrial proteins by S-nitrosothiol difference in gel electrophoresis (SNO-DIGE): implications for the regulation of mitochondrial function by reversible S-nitrosation. <i>Biochemical Journal</i> , 2010, 430, 49-59.	1.7	130
54	Investigating sample pooling strategies for DIGE experiments to address biological variability. <i>Proteomics</i> , 2009, 9, 388-397.	1.3	127

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55	Human Urinary Exosomes as Innate Immune Effectors. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 2017-2027.	3.0	127
56	A time-resolved proteomic and prognostic map of COVID-19. <i>Cell Systems</i> , 2021, 12, 780-794.e7.	2.9	125
57	Independent protein-profiling studies show a decrease in apolipoprotein A1 levels in schizophrenia CSF, brain and peripheral tissues. <i>Molecular Psychiatry</i> , 2008, 13, 1118-1128.	4.1	124
58	Proteomic Analysis Reveals the Role of Synaptic Vesicle Cycling in Sustaining the Suprachiasmatic Circadian Clock. <i>Current Biology</i> , 2009, 19, 2031-2036.	1.8	123
59	dia-PASEF data analysis using FragPipe and DIA-NN for deep proteomics of low sample amounts. <i>Nature Communications</i> , 2022, 13, .	5.8	120
60	Molecular Analysis of Core Kinetochores Composition and Assembly in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2007, 2, e478.	1.1	119
61	Multiple Protein Phosphatases Are Required for Mitosis in <i>Drosophila</i> . <i>Current Biology</i> , 2007, 17, 293-303.	1.8	119
62	Identification of Internal Ribosome Entry Segment (IRES)- <i>trans</i> -Acting Factors for the Myc Family of IRESs. <i>Molecular and Cellular Biology</i> , 2008, 28, 40-49.	1.1	117
63	Specific changes in the <i>Arabidopsis</i> proteome in response to bacterial challenge: differentiating basal and R-gene mediated resistance. <i>Phytochemistry</i> , 2004, 65, 1805-1816.	1.4	114
64	Interrelationships between Colonies, Biofilms, and Planktonic Cells of <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2007, 189, 2411-2416.	1.0	114
65	Using hyperLOPIT to perform high-resolution mapping of the spatial proteome. <i>Nature Protocols</i> , 2017, 12, 1110-1135.	5.5	113
66	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.	1.6	110
67	Interaction between Anillin and RacGAP50C connects the actomyosin contractile ring with spindle microtubules at the cell division site. <i>Journal of Cell Science</i> , 2008, 121, 1151-1158.	1.2	109
68	Global analysis of protein-RNA interactions in SARS-CoV-2-infected cells reveals key regulators of infection. <i>Molecular Cell</i> , 2021, 81, 2851-2867.e7.	4.5	108
69	Proteomic analysis of peach fruit mesocarp softening and chilling injury using difference gel electrophoresis (DIGE). <i>BMC Genomics</i> , 2010, 11, 43.	1.2	107
70	Protein Neighbors and Proximity Proteomics. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2848-2856.	2.5	105
71	2-D DIGE Analysis of Liver and Red Blood Cells Provides Further Evidence for Oxidative Stress in Schizophrenia. <i>Journal of Proteome Research</i> , 2007, 6, 141-149.	1.8	104
72	The Association of Biomolecular Resource Facilities Proteomics Research Group 2006 Study. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1291-1298.	2.5	100

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73	Quantitative proteomic approach to study subcellular localization of membrane proteins. <i>Nature Protocols</i> , 2006, 1, 1778-1789.	5.5	96
74	Deciphering Thylakoid Sub-compartments using a Mass Spectrometry-based Approach. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2147-2167.	2.5	96
75	MRMaid, the Web-based Tool for Designing Multiple Reaction Monitoring (MRM) Transitions. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 696-705.	2.5	95
76	Proteomic approaches to the characterization of protein thiol modification. <i>Current Opinion in Chemical Biology</i> , 2011, 15, 120-128.	2.8	90
77	Nutrient control of eukaryote cell growth: a systems biology study in yeast. <i>BMC Biology</i> , 2010, 8, 68.	1.7	89
78	DNA microarray normalization methods can remove bias from differential protein expression analysis of 2D difference gel electrophoresis results. <i>Bioinformatics</i> , 2004, 20, 2026-2034.	1.8	87
79	Protein profiling of human postmortem brain using 2-dimensional fluorescence difference gel electrophoresis (2-D DIGE). <i>Molecular Psychiatry</i> , 2004, 9, 128-143.	4.1	85
80	Mass-spectrometry-based spatial proteomics data analysis using <tt>pRoloc</tt> and <tt>pRolocdata</tt>. <i>Bioinformatics</i> , 2014, 30, 1322-1324.	1.8	85
81	Precursor ion scanning for detection and structural characterization of heterogeneous glycopeptide mixtures. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 1065-1077.	1.2	83
82	Mutation of <i>nfxB</i> Causes Global Changes in the Physiology and Metabolism of <i>Pseudomonas aeruginosa</i>. <i>Journal of Proteome Research</i> , 2010, 9, 2957-2967.	1.8	83
83	Understudied proteins: opportunities and challenges for functional proteomics. <i>Nature Methods</i> , 2022, 19, 774-779.	9.0	83
84	Guidelines for reporting the use of mass spectrometry in proteomics. <i>Nature Biotechnology</i> , 2008, 26, 860-861.	9.4	82
85	Effects of Traveling Wave Ion Mobility Separation on Data Independent Acquisition in Proteomics Studies. <i>Journal of Proteome Research</i> , 2013, 12, 2323-2339.	1.8	81
86	<i>Trans</i>-acting translational regulatory RNA binding proteins. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1465.	3.2	79
87	Methods of quantitative proteomics and their application to plant organelle characterization. <i>Journal of Experimental Botany</i> , 2006, 57, 1493-1499.	2.4	77
88	Isobaric tagging approaches in quantitative proteomics: the ups and downs. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 1029-1037.	1.9	77
89	Structural and functional characteristics of cGMP-dependent methionine oxidation in <i>Arabidopsis thaliana</i> proteins. <i>Cell Communication and Signaling</i> , 2013, 11, 1.	2.7	77
90	The metabolic background is a global player in <i>Saccharomyces</i> gene expression epistasis. <i>Nature Microbiology</i> , 2016, 1, 15030.	5.9	76

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91	Identification of a New Quorum-Sensing-Controlled Virulence Factor in <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> Secreted via the Type II Targeting Pathway. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 334-342.	1.4	73
92	<i>Drosophila</i> Larp associates with poly(A)-binding protein and is required for male fertility and syncytial embryo development. <i>Developmental Biology</i> , 2009, 334, 186-197.	0.9	73
93	Subcellular localization of membrane proteins. <i>Proteomics</i> , 2008, 8, 3991-4011.	1.3	71
94	Mapping Organelle Proteins and Protein Complexes in <i>Drosophila melanogaster</i> . <i>Journal of Proteome Research</i> , 2009, 8, 2667-2678.	1.8	71
95	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.	2.5	69
96	Sequestration of Polo kinase to microtubules by phosphopriming-independent binding to Map205 is relieved by phosphorylation at a CDK site in mitosis. <i>Genes and Development</i> , 2008, 22, 2707-2720.	2.7	67
97	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.	1.2	67
98	Identification of Trans-Golgi Network Proteins in <i>Arabidopsis thaliana</i> Root Tissue. <i>Journal of Proteome Research</i> , 2014, 13, 763-776.	1.8	65
99	Virulence and Prodigiosin Antibiotic Biosynthesis in <i>Serratia</i> Are Regulated Pleiotropically by the GGDEF/EAL Domain Protein, PigX. <i>Journal of Bacteriology</i> , 2007, 189, 7653-7662.	1.0	64
100	Improving Qualitative and Quantitative Performance for MS ^E -based Label-free Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 2340-2353.	1.8	64
101	Identification by DIGE of apoplastic proteins regulated by oligogalacturonides in <i>Arabidopsis thaliana</i> . <i>Proteomics</i> , 2008, 8, 1042-1054.	1.3	63
102	Comparison of DIGE and post-stained gel electrophoresis with both traditional and SameSpots analysis for quantitative proteomics. <i>Proteomics</i> , 2008, 8, 948-960.	1.3	62
103	The use of isotope-coded affinity tags (ICAT) to study organelle proteomes in <i>Arabidopsis thaliana</i> . <i>Biochemical Society Transactions</i> , 2004, 32, 520-523.	1.6	61
104	Guidelines for reporting the use of gel electrophoresis in proteomics. <i>Nature Biotechnology</i> , 2008, 26, 863-864.	9.4	61
105	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.	1.8	61
106	PEDRo: A database for storing, searching and disseminating experimental proteomics data. <i>BMC Genomics</i> , 2004, 5, 68.	1.2	58
107	Proteome Mapping of a Cyanobacterium Reveals Distinct Compartment Organization and Cell-Dispersed Metabolism. <i>Plant Physiology</i> , 2019, 181, 1721-1738.	2.3	58
108	Genetic and proteomic analysis of the role of luxS in the enteric phytopathogen, <i>Erwinia carotovora</i> . <i>Molecular Plant Pathology</i> , 2006, 7, 31-45.	2.0	57

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109	Genomic tagging reveals a random association of endogenous PtdIns5<i>P</i> 4-kinases IÎ± and IÎ² and a partial nuclear localization of the IÎ± isoform. <i>Biochemical Journal</i> , 2010, 430, 215-221.	1.7	57
110	The beauty of being (label)-free: sample preparation methods for SWATH-MS and next-generation targeted proteomics. <i>F1000Research</i> , 2013, 2, 272.	0.8	57
111	Plant endoplasmic reticulum supports the protein secretory pathway and has a role in proliferating tissues. <i>Plant Journal</i> , 2006, 48, 657-673.	2.8	56
112	N-Terminal sequence similarities between components of the multicatalytic proteinase complex. <i>FEBS Letters</i> , 1990, 262, 327-329.	1.3	55
113	Differential Gel Electrophoresis and Transgenic Mitochondrial Calcium Reporters Demonstrate Spatiotemporal Filtering in Calcium Control of Mitochondria. <i>Journal of Biological Chemistry</i> , 2006, 281, 18849-18858.	1.6	54
114	The Organelle Proteome of the DT40 Lymphocyte Cell Line. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1295-1305.	2.5	54
115	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , 2010, 10, 3957-3969.	1.3	54
116	Ketamine's antidepressant effect is mediated by energy metabolism and antioxidant defense system. <i>Scientific Reports</i> , 2017, 7, 15788.	1.6	54
117	A Bayesian mixture modelling approach for spatial proteomics. <i>PLoS Computational Biology</i> , 2018, 14, e1006516.	1.5	53
118	Changes in the Oligodendrocyte Progenitor Cell Proteome with Ageing. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1281-1302.	2.5	53
119	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.	1.2	50
120	Changes in the Arabidopsis RNA-binding proteome reveal novel stress response mechanisms. <i>BMC Plant Biology</i> , 2019, 19, 139.	1.6	50
121	Plant organelle proteomics. <i>Current Opinion in Plant Biology</i> , 2007, 10, 594-599.	3.5	49
122	In Vivo Analyses of the Roles of Essential Omp85-Related Proteins in the Chloroplast Outer Envelope Membrane. <i>Plant Physiology</i> , 2011, 157, 147-159.	2.3	49
123	A Foundation for Reliable Spatial Proteomics Data Analysis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1937-1952.	2.5	49
124	DsbA Plays a Critical and Multifaceted Role in the Production of Secreted Virulence Factors by the Phytopathogen <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 23739-23753.	1.6	48
125	Label-Free Protein Quantification for Plant Golgi Protein Localization and Abundance. <i>Plant Physiology</i> , 2014, 166, 1033-1043.	2.3	48
126	hiPSC hepatocyte model demonstrates the role of unfolded protein response and inflammatory networks in Î±1-antitrypsin deficiency. <i>Journal of Hepatology</i> , 2018, 69, 851-860.	1.8	48

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127	Learning from Heterogeneous Data Sources: An Application in Spatial Proteomics. <i>PLoS Computational Biology</i> , 2016, 12, e1004920.	1.5	47
128	Gel-Based Proteomics Approach to the Study of Metabolic Changes in Pear Tissue during Storage. <i>Journal of Agricultural and Food Chemistry</i> , 2009, 57, 6997-7004.	2.4	46
129	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.	2.5	46
130	The beauty of being (label)-free: sample preparation methods for SWATH-MS and next-generation targeted proteomics. <i>F1000Research</i> , 0, 2, 272.	0.8	46
131	Recruitment of Polo Kinase to the Spindle Midzone during Cytokinesis Requires the Feo/Klp3A Complex. <i>PLoS ONE</i> , 2007, 2, e572.	1.1	46
132	The essential active-site lysines of clostridial glutamate dehydrogenase. A study with pyridoxal-5'-phosphate. <i>FEBS Journal</i> , 1992, 207, 533-540.	0.2	45
133	Spatial proteomics defines the content of trafficking vesicles captured by golgin tethers. <i>Nature Communications</i> , 2020, 11, 5987.	5.8	45
134	Improved subcellular resolution via simultaneous analysis of organelle proteomics data across varied experimental conditions. <i>Proteomics</i> , 2010, 10, 4213-4219.	1.3	44
135	Evaluation and Properties of the Budding Yeast Phosphoproteome. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.009555.	2.5	44
136	N-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.	3.5	44
137	Optimizing the Difference Gel Electrophoresis (DIGE) Technology. <i>Methods in Molecular Biology</i> , 2008, 428, 93-124.	0.4	43
138	A Combined Metabolomic and Proteomic Investigation of the Effects of a Failure to Express Dystrophin in the Mouse Heart. <i>Journal of Proteome Research</i> , 2008, 7, 2069-2077.	1.8	43
139	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	2.5	42
140	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.	2.8	42
141	Differentiation of Isomeric N-Glycan Structures by Normal-Phase Liquid Chromatography-MALDI-TOF/TOF Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2006, 78, 8491-8498.	3.2	41
142	Isolation and Preparation of Chloroplasts from Arabidopsis thaliana Plants. <i>Methods in Molecular Biology</i> , 2008, 425, 171-186.	0.4	40
143	Proteomics for the Food Industry: Opportunities and Challenges. <i>Critical Reviews in Food Science and Nutrition</i> , 2010, 50, 680-692.	5.4	40
144	Separating Golgi Proteins from Cis to Trans Reveals Underlying Properties of Cisternal Localization. <i>Plant Cell</i> , 2019, 31, 2010-2034.	3.1	40

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145	In-depth characterization of the tomato fruit pericarp proteome. <i>Proteomics</i> , 2017, 17, 1600406.	1.3	39
146	A Quantitative Phosphoproteome Analysis of cGMP-Dependent Cellular Responses in <i>Arabidopsis thaliana</i> . <i>Molecular Plant</i> , 2016, 9, 621-623.	3.9	38
147	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.	1.7	38
148	Drought Stress Causes Specific Changes to the Spliceosome and Stress Granule Components. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 163.	1.6	38
149	Quantitative proteomics analysis of the Arg/N-end rule pathway of targeted degradation in <i>Arabidopsis</i> roots. <i>Proteomics</i> , 2015, 15, 2447-2457.	1.3	37
150	Impact of Azithromycin on the Quorum Sensing-Controlled Proteome of <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2016, 11, e0147698.	1.1	37
151	Antibody-mediated neutralization of myelin-associated EphrinB3 accelerates CNS remyelination. <i>Acta Neuropathologica</i> , 2016, 131, 281-298.	3.9	37
152	Organic phase separation opens up new opportunities to interrogate the RNA-binding proteome. <i>Current Opinion in Chemical Biology</i> , 2020, 54, 70-75.	2.8	35
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154	A Bioconductor workflow for processing and analysing spatial proteomics data. <i>F1000Research</i> , 2016, 5, 2926.	0.8	34
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