

# Kathryn S Lilley

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7465527/publications.pdf>

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 subcellular map of the human proteome. <i>Science</i> , 2017, 356, .	12.6	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.	19.0	882
3	Mitochondrial dysfunction in schizophrenia: evidence for compromised brain metabolism and oxidative stress. <i>Molecular Psychiatry</i> , 2004, 9, 684-697.	7.9	810
4	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893.	17.5	694
5	Cardioprotection by S-nitrosation of a cysteine switch on mitochondrial complex I. <i>Nature Medicine</i> , 2013, 19, 753-759.	30.7	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.	7.1	518
7	Circadian Orchestration of the Hepatic Proteome. <i>Current Biology</i> , 2006, 16, 1107-1115.	3.9	506
8	Addressing Accuracy and Precision Issues in iTRAQ Quantitation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1885-1897.	3.8	471
9	Analysis of Detergent-Resistant Membranes in Arabidopsis. Evidence for Plasma Membrane Lipid Rafts. <i>Plant Physiology</i> , 2005, 137, 104-116.	4.8	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.	7.1	445
11	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. <i>Cell Systems</i> , 2020, 11, 11-24.e4.	6.2	439
12	Identification of Glycosylphosphatidylinositol-Anchored Proteins in Arabidopsis. A Proteomic and Genomic Analysis. <i>Plant Physiology</i> , 2003, 132, 568-577.	4.8	364
13	FlyMine: an integrated database for Drosophila and Anopheles genomics. <i>Genome Biology</i> , 2007, 8, R129.	9.6	345
14	Ubiquitination of $\alpha$ -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.	3.4	325
15	Localization of Organelle Proteins by Isotope Tagging (LOPIT). <i>Molecular and Cellular Proteomics</i> , 2004, 3, 1128-1134.	3.8	305
16	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
17	i-Tracker: For quantitative proteomics using iTRAQ. <i>BMC Genomics</i> , 2005, 6, 145.	2.8	275
18	All about DIGE: quantification technology for differential-display 2D-gel proteomics. <i>Expert Review of Proteomics</i> , 2004, 1, 401-409.	3.0	260

#	ARTICLE	IF	CITATIONS
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.	3.6	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.	6.1	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.	17.5	247
22	A systematic approach to modeling, capturing, and disseminating proteomics experimental data. <i>Nature Biotechnology</i> , 2003, 21, 247-254.	17.5	246
23	Glucocorticoid signaling synchronizes the liver circadian transcriptome. <i>Hepatology</i> , 2007, 45, 1478-1488.	7.3	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.	2.5	226
26	Toward a Comprehensive Map of the Effectors of Rab GTPases. <i>Developmental Cell</i> , 2014, 31, 358-373.	7.0	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.	2.6	221
28	<i>Drosophila</i> Ionotropic Receptor 25a mediates circadian clock resetting by temperature. <i>Nature</i> , 2015, 527, 516-520.	27.8	216
29	A Comprehensive Subcellular Atlas of the <i>Toxoplasma</i> Proteome via hyperLOPIT Provides Spatial Context for Protein Functions. <i>Cell Host and Microbe</i> , 2020, 28, 752-766.e9.	11.0	201
30	A draft map of the mouse pluripotent stem cell spatial proteome. <i>Nature Communications</i> , 2016, 7, 8992.	12.8	197
31	Functional Specialization amongst the <i>Arabidopsis</i> Toc159 Family of Chloroplast Protein Import Receptors[W]. <i>Plant Cell</i> , 2004, 16, 2059-2077.	6.6	184
32	Maximising sensitivity for detecting changes in protein expression: Experimental design using minimal CyDyes. <i>Proteomics</i> , 2005, 5, 3105-3115.	2.2	183
33	SETH1 and SETH2, Two Components of the Glycosylphosphatidylinositol Anchor Biosynthetic Pathway, Are Required for Pollen Germination and Tube Growth in <i>Arabidopsis</i> [W]. <i>Plant Cell</i> , 2004, 16, 229-240.	6.6	178
34	Ultra-fast proteomics with Scanning SWATH. <i>Nature Biotechnology</i> , 2021, 39, 846-854.	17.5	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.	2.2	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.	17.5	161

#	ARTICLE	IF	CITATIONS
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.	2.5	160
38	Subcellular proteomics. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	21.2	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.	6.6	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.	3.8	152
41	Putative Glycosyltransferases and Other Plant Golgi Apparatus Proteins Are Revealed by LOPIT Proteomics A. <i>Plant Physiology</i> , 2012, 160, 1037-1051.	4.8	149
42	Impact of Replicate Types on Proteomic Expression Analysis. <i>Journal of Proteome Research</i> , 2005, 4, 1867-1871.	3.7	147
43	Design and Analysis Issues in Quantitative Proteomics Studies. <i>Proteomics</i> , 2007, 7, 42-50.	2.2	147
44	Combining LOPIT with differential ultracentrifugation for high-resolution spatial proteomics. <i>Nature Communications</i> , 2019, 10, 331.	12.8	146
45	Comparative proteomics of clathrin-coated vesicles. <i>Journal of Cell Biology</i> , 2006, 175, 571-578.	5.2	145
46	Identification of Putative Stage-Specific Grapevine Berry Biomarkers and Omics Data Integration into Networks A A A. <i>Plant Physiology</i> , 2010, 154, 1439-1459.	4.8	145
47	The RNA-binding protein repertoire of Arabidopsis thaliana. <i>Scientific Reports</i> , 2016, 6, 29766.	3.3	139
48	The <i>Drosophila melanogaster</i> sperm proteome-II (DmSP-II). <i>Journal of Proteomics</i> , 2010, 73, 2171-2185.	2.4	138
49	Î±-Klotho Expression in Human Tissues. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2015, 100, E1308-E1318.	3.6	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.	2.2	136
51	A proteomic approach identifies many novel palmitoylated proteins in Arabidopsis. <i>New Phytologist</i> , 2013, 197, 805-814.	7.3	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.	3.4	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.	3.7	130
54	Investigating sample pooling strategies for DIGE experiments to address biological variability. <i>Proteomics</i> , 2009, 9, 388-397.	2.2	127

#	ARTICLE	IF	CITATIONS
55	Human Urinary Exosomes as Innate Immune Effectors. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 2017-2027.	6.1	127
56	A time-resolved proteomic and prognostic map of COVID-19. <i>Cell Systems</i> , 2021, 12, 780-794.e7.	6.2	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.	7.9	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.	3.9	123
59	dia-PASEF data analysis using FragPipe and DIA-NN for deep proteomics of low sample amounts. <i>Nature Communications</i> , 2022, 13, .	12.8	120
60	Molecular Analysis of Core Kinetochores Composition and Assembly in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2007, 2, e478.	2.5	119
61	Multiple Protein Phosphatases Are Required for Mitosis in <i>Drosophila</i> . <i>Current Biology</i> , 2007, 17, 293-303.	3.9	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.	2.3	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.	2.9	114
64	Interrelationships between Colonies, Biofilms, and Planktonic Cells of <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2007, 189, 2411-2416.	2.2	114
65	Using hyperLOPIT to perform high-resolution mapping of the spatial proteome. <i>Nature Protocols</i> , 2017, 12, 1110-1135.	12.0	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.	3.4	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.	2.0	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.	9.7	108
69	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
70	Protein Neighbors and Proximity Proteomics. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2848-2856.	3.8	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.	3.7	104
72	The Association of Biomolecular Resource Facilities Proteomics Research Group 2006 Study. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1291-1298.	3.8	100

#	ARTICLE	IF	CITATIONS
73	Quantitative proteomic approach to study subcellular localization of membrane proteins. <i>Nature Protocols</i> , 2006, 1, 1778-1789.	12.0	96
74	Deciphering Thylakoid Sub-compartments using a Mass Spectrometry-based Approach. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2147-2167.	3.8	96
75	MRMaid, the Web-based Tool for Designing Multiple Reaction Monitoring (MRM) Transitions. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 696-705.	3.8	95
76	Proteomic approaches to the characterization of protein thiol modification. <i>Current Opinion in Chemical Biology</i> , 2011, 15, 120-128.	6.1	90
77	Nutrient control of eukaryote cell growth: a systems biology study in yeast. <i>BMC Biology</i> , 2010, 8, 68.	3.8	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.	4.1	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.	7.9	85
80	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
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.	2.8	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.	3.7	83
83	Understudied proteins: opportunities and challenges for functional proteomics. <i>Nature Methods</i> , 2022, 19, 774-779.	19.0	83
84	Guidelines for reporting the use of mass spectrometry in proteomics. <i>Nature Biotechnology</i> , 2008, 26, 860-861.	17.5	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.	3.7	81
86	<i>Trans</i>-acting translational regulatory RNA binding proteins. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1465.	6.4	79
87	Methods of quantitative proteomics and their application to plant organelle characterization. <i>Journal of Experimental Botany</i> , 2006, 57, 1493-1499.	4.8	77
88	Isobaric tagging approaches in quantitative proteomics: the ups and downs. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 1029-1037.	3.7	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.	6.5	77
90	The metabolic background is a global player in <i>Saccharomyces</i> gene expression epistasis. <i>Nature Microbiology</i> , 2016, 1, 15030.	13.3	76

#	ARTICLE	IF	CITATIONS
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.	2.6	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.	2.0	73
93	Subcellular localization of membrane proteins. <i>Proteomics</i> , 2008, 8, 3991-4011.	2.2	71
94	Mapping Organelle Proteins and Protein Complexes in <i>Drosophila melanogaster</i> . <i>Journal of Proteome Research</i> , 2009, 8, 2667-2678.	3.7	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.	3.8	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.	5.9	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.	2.8	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.	3.7	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.	2.2	64
100	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
101	Identification by DIGE of apoplastic proteins regulated by oligogalacturonides in <i>Arabidopsis thaliana</i> . <i>Proteomics</i> , 2008, 8, 1042-1054.	2.2	63
102	Comparison of DIGE and poststained gel electrophoresis with both traditional and SameSpots analysis for quantitative proteomics. <i>Proteomics</i> , 2008, 8, 948-960.	2.2	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.	3.4	61
104	Guidelines for reporting the use of gel electrophoresis in proteomics. <i>Nature Biotechnology</i> , 2008, 26, 863-864.	17.5	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.	3.7	61
106	PEDRo: A database for storing, searching and disseminating experimental proteomics data. <i>BMC Genomics</i> , 2004, 5, 68.	2.8	58
107	Proteome Mapping of a Cyanobacterium Reveals Distinct Compartment Organization and Cell-Dispersed Metabolism. <i>Plant Physiology</i> , 2019, 181, 1721-1738.	4.8	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.	4.2	57

#	ARTICLE	IF	CITATIONS
109	Genomic tagging reveals a random association of endogenous PtdIns5<i>P</i> 4-kinases II $\pm$ and II $\hat{2}$ and a partial nuclear localization of the II $\pm$ isoform. <i>Biochemical Journal</i> , 2010, 430, 215-221.	3.7	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.	1.6	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.	5.7	56
112	N-Terminal sequence similarities between components of the multicatalytic proteinase complex. <i>FEBS Letters</i> , 1990, 262, 327-329.	2.8	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.	3.4	54
114	The Organelle Proteome of the DT40 Lymphocyte Cell Line. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1295-1305.	3.8	54
115	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , 2010, 10, 3957-3969.	2.2	54
116	Ketamine $\hat{e}$ ™s antidepressant effect is mediated by energy metabolism and antioxidant defense system. <i>Scientific Reports</i> , 2017, 7, 15788.	3.3	54
117	A Bayesian mixture modelling approach for spatial proteomics. <i>PLoS Computational Biology</i> , 2018, 14, e1006516.	3.2	53
118	Changes in the Oligodendrocyte Progenitor Cell Proteome with Ageing. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1281-1302.	3.8	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.	2.8	50
120	Changes in the Arabidopsis RNA-binding proteome reveal novel stress response mechanisms. <i>BMC Plant Biology</i> , 2019, 19, 139.	3.6	50
121	Plant organelle proteomics. <i>Current Opinion in Plant Biology</i> , 2007, 10, 594-599.	7.1	49
122	In Vivo Analyses of the Roles of Essential Omp85-Related Proteins in the Chloroplast Outer Envelope Membrane $\hat{A}$ . <i>Plant Physiology</i> , 2011, 157, 147-159.	4.8	49
123	A Foundation for Reliable Spatial Proteomics Data Analysis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1937-1952.	3.8	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.	3.4	48
125	Label-Free Protein Quantification for Plant Golgi Protein Localization and Abundance. <i>Plant Physiology</i> , 2014, 166, 1033-1043.	4.8	48
126	hiPSC hepatocyte model demonstrates the role of unfolded protein response and inflammatory networks in $\hat{1}$ -antitrypsin deficiency. <i>Journal of Hepatology</i> , 2018, 69, 851-860.	3.7	48



#	ARTICLE	IF	CITATIONS
127	Learning from Heterogeneous Data Sources: An Application in Spatial Proteomics. <i>PLoS Computational Biology</i> , 2016, 12, e1004920.	3.2	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.	5.2	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.	3.8	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.	1.6	46
131	Recruitment of Polo Kinase to the Spindle Midzone during Cytokinesis Requires the Feo/Klp3A Complex. <i>PLoS ONE</i> , 2007, 2, e572.	2.5	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.	12.8	45
134	Improved subcellular resolution via simultaneous analysis of organelle proteomics data across varied experimental conditions. <i>Proteomics</i> , 2010, 10, 4213-4219.	2.2	44
135	Evaluation and Properties of the Budding Yeast Phosphoproteome. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.009555.	3.8	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.	7.3	44
137	Optimizing the Difference Gel Electrophoresis (DIGE) Technology. <i>Methods in Molecular Biology</i> , 2008, 428, 93-124.	0.9	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.	3.7	43
139	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
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.	5.7	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.	6.5	41
142	Isolation and Preparation of Chloroplasts from Arabidopsis thaliana Plants. <i>Methods in Molecular Biology</i> , 2008, 425, 171-186.	0.9	40
143	Proteomics for the Food Industry: Opportunities and Challenges. <i>Critical Reviews in Food Science and Nutrition</i> , 2010, 50, 680-692.	10.3	40
144	Separating Golgi Proteins from Cis to Trans Reveals Underlying Properties of Cisternal Localization. <i>Plant Cell</i> , 2019, 31, 2010-2034.	6.6	40

#	ARTICLE	IF	CITATIONS
145	In-depth characterization of the tomato fruit pericarp proteome. <i>Proteomics</i> , 2017, 17, 1600406.	2.2	39
146	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
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.	3.6	38
148	Drought Stress Causes Specific Changes to the Spliceosome and Stress Granule Components. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 163.	3.5	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.	2.2	37
150	Impact of Azithromycin on the Quorum Sensing-Controlled Proteome of <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2016, 11, e0147698.	2.5	37
151	Antibody-mediated neutralization of myelin-associated EphrinB3 accelerates CNS remyelination. <i>Acta Neuropathologica</i> , 2016, 131, 281-298.	7.7	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.	6.1	35
153	Mutations in <i>rpsL</i> that confer streptomycin resistance show pleiotropic effects on virulence and the production of a carbapenem antibiotic in <i>Erwinia carotovora</i> . <i>Microbiology (United Kingdom)</i> , 2010, 156, 1030-1039.	1.8	34
154	A Bioconductor workflow for processing and analysing spatial proteomics data. <i>F1000Research</i> , 2016, 5, 2926.	1.6	34
155	Proteomic analysis of the EhV-86 virion. <i>Proteome Science</i> , 2008, 6, 11.	1.7	33
156	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
157	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
158	Assessing sub-cellular resolution in spatial proteomics experiments. <i>Current Opinion in Chemical Biology</i> , 2019, 48, 123-149.	6.1	31
159	Unresolved stalled ribosome complexes restrict cell-cycle progression after genotoxic stress. <i>Molecular Cell</i> , 2022, 82, 1557-1572.e7.	9.7	30
160	Characterization of the Necrotic Protein That Regulates the Toll-mediated Immune Response in <i>Drosophila</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 6175-6180.	3.4	29
161	Confident protein identification using the average peptide score method coupled with search-specific, <i>ab initio</i> thresholds. <i>Rapid Communications in Mass Spectrometry</i> , 2005, 19, 3363-3368.	1.5	29
162	Quantification and identification of mitochondrial proteins containing vicinal dithiols. <i>Archives of Biochemistry and Biophysics</i> , 2010, 504, 228-235.	3.0	29

#	ARTICLE	IF	CITATIONS
163	Interlaboratory studies and initiatives developing standards for proteomics. <i>Proteomics</i> , 2013, 13, 904-909.	2.2	29
164	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
165	Proteomic Complex Detection Using Sedimentation. <i>Analytical Chemistry</i> , 2007, 79, 2078-2083.	6.5	28
166	Negative feedback via RSK modulates Erk-dependent progression from naïve pluripotency. <i>EMBO Reports</i> , 2018, 19, .	4.5	28
167	A proteomic survival predictor for COVID-19 patients in intensive care. , 2022, 1, e0000007.		28
168	Phosphorylation of the dimeric cytoplasmic domain of the phytosulfokine receptor, PSKR1. <i>Biochemical Journal</i> , 2016, 473, 3081-3098.	3.7	27
169	A Bioconductor workflow for the Bayesian analysis of spatial proteomics. <i>F1000Research</i> , 2019, 8, 446.	1.6	27
170	Comparative proteomic analysis reveals differential expression of Hsp25 following the directed differentiation of mouse embryonic stem cells. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2007, 1773, 147-156.	4.1	26
171	Stat3-mediated alterations in lysosomal membrane protein composition. <i>Journal of Biological Chemistry</i> , 2018, 293, 4244-4261.	3.4	26
172	The subcellular organisation of <i>Saccharomyces cerevisiae</i> . <i>Current Opinion in Chemical Biology</i> , 2019, 48, 86-95.	6.1	26
173	Biotin proximity tagging favours unfolded proteins and enables the study of intrinsically disordered regions. <i>Communications Biology</i> , 2020, 3, 38.	4.4	26
174	A Bioconductor workflow for processing and analysing spatial proteomics data. <i>F1000Research</i> , 2016, 5, 2926.	1.6	26
175	An open invitation to the Understudied Proteins Initiative. <i>Nature Biotechnology</i> , 2022, 40, 815-817.	17.5	25
176	Taming the isobaric tagging elephant in the room in quantitative proteomics. <i>Nature Methods</i> , 2011, 8, 911-913.	19.0	24
177	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
178	Dynamic Regulation of the COP9 Signalosome in Response to DNA Damage. <i>Molecular and Cellular Biology</i> , 2014, 34, 1066-1076.	2.3	24
179	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
180	Early Responses to Severe Drought Stress in the <i>Arabidopsis thaliana</i> Cell Suspension Culture Proteome. <i>Proteomes</i> , 2018, 6, 38.	3.5	24

#	ARTICLE	IF	CITATIONS
181	Subcellular Transcriptomics and Proteomics: A Comparative Methods Review. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100186.	3.8	23
182	Chapter 19 Measuring Redox Changes to Mitochondrial Protein Thiols With Redox Difference Gel Electrophoresis (Redoxâ€Dige). <i>Methods in Enzymology</i> , 2009, 456, 343-361.	1.0	22
183	Big results from small samples: evaluation of amplification protocols for gene expression profiling. <i>Journal of Biomolecular Techniques</i> , 2007, 18, 150-61.	1.5	22
184	Spectral Libraries for SWATHâ€CMS Assays for <i>Drosophila melanogaster</i> and <i>Solanum lycopersicum</i> . <i>Proteomics</i> , 2017, 17, 1700216.	2.2	21
185	The Dominant Cold-Sensitive Out-Cold Mutants of <i>Drosophila melanogaster</i> Have Novel Missense Mutations in the Voltage-Gated Sodium Channel Gene <i>paralytic</i> . <i>Genetics</i> , 2008, 180, 873-884.	2.9	20
186	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
187	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
188	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
189	Time, space, and disorder in the expanding proteome universe. <i>Proteomics</i> , 2017, 17, 1600399.	2.2	19
190	Identification of the RNA polymerase I-RNA interactome. <i>Nucleic Acids Research</i> , 2018, 46, 11002-11013.	14.5	19
191	Proteomic responses of HepG2 cell monolayers and 3D spheroids to selected hepatotoxins. <i>Toxicology Letters</i> , 2019, 300, 40-50.	0.8	19
192	Moving Profiling Spatial Proteomics Beyond Discrete Classification. <i>Proteomics</i> , 2020, 20, e1900392.	2.2	19
193	The ABRF Proteomics Research Group Studies: Educational exercises for qualitative and quantitative proteomic analyses. <i>Proteomics</i> , 2011, 11, 1371-1381.	2.2	18
194	Co-complex protein membership evaluation using Maximum Entropy on GO ontology and InterPro annotation. <i>Bioinformatics</i> , 2018, 34, 1884-1892.	4.1	18
195	A Proteomics Approach to Membrane Trafficking. <i>Plant Physiology</i> , 2008, 147, 1584-1589.	4.8	17
196	Method for suppressing non-specific protein interactions observed with affinity resins. <i>Methods</i> , 2011, 54, 407-412.	3.8	16
197	Dynamic Proteomic Profiling of Extra-Embryonic Endoderm Differentiation in Mouse Embryonic Stem Cells. <i>Stem Cells</i> , 2015, 33, 2712-2725.	3.2	16
198	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

#	ARTICLE	IF	CITATIONS
199	Protein Profiling Using Two-Dimensional Difference Gel Electrophoresis (2D-DIGE). <i>Current Protocols in Protein Science</i> , 2002, 30, Unit 22.2.	2.8	15
200	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
201	Palmitoylation in plants. <i>Plant Signaling and Behavior</i> , 2013, 8, e25209.	2.4	15
202	A proteomic time course through the differentiation of human induced pluripotent stem cells into hepatocyte-like cells. <i>Scientific Reports</i> , 2019, 9, 3270.	3.3	15
203	Ketamine's Effects on the Glutamatergic and GABAergic Systems: A Proteomics and Metabolomics Study in Mice. <i>Molecular Neuropsychiatry</i> , 2019, 5, 42-51.	2.9	15
204	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
205	Proteomics of total membranes and subcellular membranes. <i>Expert Review of Proteomics</i> , 2010, 7, 867-878.	3.0	14
206	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
207	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
208	ABRF-PRG07: advanced quantitative proteomics study. <i>Journal of Biomolecular Techniques</i> , 2011, 22, 21-6.	1.5	13
209	Uromodulin exclusion list improves urinary exosomal protein identification. <i>Journal of Biomolecular Techniques</i> , 2011, 22, 136-45.	1.5	13
210	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
211	The <i>Arabidopsis thaliana</i> N-recognin E3 ligase PROTEOLYSIS1 influences the immune response. <i>Plant Direct</i> , 2019, 3, e00194.	1.9	12
212	Determination of Genuine Residents of Plant Endomembrane Organelles using Isotope Tagging and Multivariate Statistics. <i>Methods in Molecular Biology</i> , 2008, 432, 373-387.	0.9	12
213	GARNet, the Genomic <i>Arabidopsis</i> Resource Network. <i>Trends in Plant Science</i> , 2002, 7, 145-147.	8.8	10
214	Proteomics of cryoprotective dehydration in <i>Megaphorura arctica</i> Tullberg 1876 (Onychiuridae). <i>Journal of Proteome Research</i> , 2010, 9, 1070-1078.	2.0	10
215	Mimicking nature: Phosphopeptide enrichment using combinatorial libraries of affinity ligands. <i>Journal of Chromatography A</i> , 2016, 1457, 76-87.	3.7	10
216	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

#	ARTICLE	IF	CITATIONS
217	Difference gel electrophoresis DIGE. <i>Drug Discovery Today: Technologies</i> , 2006, 3, 347-353.	4.0	9
218	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
219	Systems Analyses Reveal the Resilience of <i>Escherichia coli</i> Physiology during Accumulation and Export of the Nonnative Organic Acid Citramalate. <i>MSystems</i> , 2019, 4, .	3.8	9
220	A direct role for SNX9 in the biogenesis of filopodia. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	9
221	Nuclear Phospholipase C Gamma: Punctate Distribution and Association with the Promyelocytic Leukemia Protein. <i>Journal of Proteome Research</i> , 2007, 6, 2027-2032.	3.7	8
222	Challenges for proteomics core facilities. <i>Proteomics</i> , 2011, 11, 1017-1025.	2.2	8
223	Identification and Quantitation of Signal Molecule-Dependent Protein Phosphorylation. <i>Methods in Molecular Biology</i> , 2013, 1016, 121-137.	0.9	8
224	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
225	Mass spectrometry approaches to study plant endomembrane trafficking. <i>Seminars in Cell and Developmental Biology</i> , 2018, 80, 123-132.	5.0	8
226	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
227	Differences in Protein Profiles in Schizophrenia Prefrontal Cortex Compared to Other Major Brain Disorders. <i>Clinical Schizophrenia and Related Psychoses</i> , 2007, 1, 73-91.	1.4	8
228	Protein Profiling Using Two-Dimensional Difference Gel Electrophoresis (2D DIGE). <i>Current Protocols in Protein Science</i> , 2014, 75, 22.2.1-22.2.17.	2.8	7
229	SWATH-MS data of <i>Drosophila melanogaster</i> proteome dynamics during embryogenesis. <i>Data in Brief</i> , 2016, 9, 771-775.	1.0	7
230	Analysis of temperature-mediated changes in the wine yeast <i>Saccharomyces bayanus</i> var <i>uvarum</i> . An oenological study of how the protein content influences wine quality. <i>Proteomics</i> , 2016, 16, 576-592.	2.2	7
231	Glareosin: a novel sexually dimorphic urinary lipocalin in the bank vole, <i>Myodes glareolus</i> . <i>Open Biology</i> , 2017, 7, 170135.	3.6	7
232	Differential Interactome and Innate Immune Response Activation of Two Structurally Distinct Misfolded Protein Oligomers. <i>ACS Chemical Neuroscience</i> , 2019, 10, 3464-3478.	3.5	7
233	Comparison of <i>Drosophila melanogaster</i> Embryo and Adult Proteome by SWATH-MS Reveals Differential Regulation of Protein Synthesis, Degradation Machinery, and Metabolism Modules. <i>Journal of Proteome Research</i> , 2019, 18, 2525-2534.	3.7	7
234	Editorial overview: Untangling proteome organization in space and time. <i>Current Opinion in Chemical Biology</i> , 2019, 48, A1-A4.	6.1	6

#	ARTICLE	IF	CITATIONS
235	A Bayesian semi-parametric model for thermal proteome profiling. <i>Communications Biology</i> , 2021, 4, 810.	4.4	6
236	Multi-omic based production strain improvement (MOBpsi) for bio-manufacturing of toxic chemicals. <i>Metabolic Engineering</i> , 2022, 72, 133-149.	7.0	6
237	In Depth Exploration of the Alternative Proteome of <i>Drosophila melanogaster</i> . <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	3.7	6
238	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
239	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
240	Proteomic Comparison of Various Hepatic Cell Cultures for Preclinical Safety Pharmacology. <i>Toxicological Sciences</i> , 2018, 164, 229-239.	3.1	5
241	Characterisation of protein isoforms encoded by the <i>Drosophila</i> Glycogen Synthase Kinase 3 gene shaggy. <i>PLoS ONE</i> , 2020, 15, e0236679.	2.5	5
242	Localization of Organelle Proteins by Isotope Tagging: Current status and potential applications in drug discovery research. <i>Drug Discovery Today: Technologies</i> , 2021, 39, 57-67.	4.0	5
243	<i>Drosophila</i> nicotinic acetylcholine receptor subunits and their native interactions with insecticidal peptide toxins. <i>ELife</i> , 2022, 11, .	6.0	5
244	Proteomics in <i>Drosophila melanogaster</i> . <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2003, 2, 106-113.	3.8	4
245	Enabling Technologies for Yeast Proteome Analysis. <i>Methods in Molecular Biology</i> , 2011, 759, 149-178.	0.9	4
246	CFTR Rescue by Lumacaftor (VX-809) Induces an Extensive Reorganization of Mitochondria in the Cystic Fibrosis Bronchial Epithelium. <i>Cells</i> , 2022, 11, 1938.	4.1	4
247	SWATH-MS dataset of heat-shock treated <i>Drosophila melanogaster</i> embryos. <i>Data in Brief</i> , 2016, 9, 991-995.	1.0	3
248	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
249	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
250	Focus on Quantitative Proteomics. <i>Proteomics</i> , 2015, 15, 3101-3103.	2.2	2
251	A Protocol to Map the Spatial Proteome Using HyperLOPIT in <i>Saccharomyces cerevisiae</i> . <i>Bio-protocol</i> , 2019, 9, e3303.	0.4	2
252	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

#	ARTICLE	IF	CITATIONS
253	The ABRF MARG microarray survey 2005: taking the pulse of the microarray field. <i>Journal of Biomolecular Techniques</i> , 2006, 17, 176-86.	1.5	2
254	The chicken B-cell line DT40 proteome, beadome and interactomes. <i>Data in Brief</i> , 2015, 3, 29-33.	1.0	1
255	Transcriptional regulation of the genes involved in protein metabolism and processing in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2019, 19, .	2.3	1
256	Proteomics of intracellular freezing survival. <i>PLoS ONE</i> , 2020, 15, e0233048.	2.5	1
257	Identification of Clock Genes Using Difference Gel Electrophoresis. <i>Methods in Molecular Biology</i> , 2007, 362, 265-287.	0.9	1
258	Difference Gel Electrophoresis (DIGE). <i>Springer Protocols</i> , 2009, , 379-408.	0.3	0
259	Proteomic analysis in primary T cells reveals IL-7 alters T cell receptor thresholding via CYTIP/cytohesin/LFA-1 localisation and activation. <i>Biochemical Journal</i> , 2022, 479, 225-243.	3.7	0
260	Prior Signal Acquisition Software Versions for Orbitrap Underestimate Low Isobaric Mass Tag Intensities, Without Detriment to Differential Abundance Experiments. <i>ACS Measurement Science Au</i> , 2022, 2, 233-240.	4.4	0
261	Title is missing!. , 2020, 15, e0236679.		0
262	Title is missing!. , 2020, 15, e0236679.		0
263	Title is missing!. , 2020, 15, e0236679.		0
264	Title is missing!. , 2020, 15, e0236679.		0