

# Kathryn S Lilley

## List of Publications by Citations

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264  
papers

18,034  
citations

71  
h-index

128  
g-index

301  
ext. papers

21,981  
ext. citations

8.1  
avg. IF

6.55  
L-index

#	Paper	IF	Citations
264	A subcellular map of the human proteome. <i>Science</i> , <b>2017</b> , 356,	33.3	1183
263	Mitochondrial dysfunction in schizophrenia: evidence for compromised brain metabolism and oxidative stress. <i>Molecular Psychiatry</i> , <b>2004</b> , 9, 684-97, 643	15.1	703
262	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , <b>2007</b> , 25, 887-915	24.5	583
261	Mapping the Arabidopsis organelle proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 6518-23	11.5	464
260	Circadian orchestration of the hepatic proteome. <i>Current Biology</i> , <b>2006</b> , 16, 1107-15	6.3	440
259	Cardioprotection by S-nitrosation of a cysteine switch on mitochondrial complex I. <i>Nature Medicine</i> , <b>2013</b> , 19, 753-9	50.5	437
258	Addressing accuracy and precision issues in iTRAQ quantitation. <i>Molecular and Cellular Proteomics</i> , <b>2010</b> , 9, 1885-97	7.6	400
257	Analysis of detergent-resistant membranes in Arabidopsis. Evidence for plasma membrane lipid rafts. <i>Plant Physiology</i> , <b>2005</b> , 137, 104-16	6.6	395
256	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> , <b>2009</b> , 106, 894-9	11.5	357
255	Identification of glycosylphosphatidylinositol-anchored proteins in Arabidopsis. A proteomic and genomic analysis. <i>Plant Physiology</i> , <b>2003</b> , 132, 568-77	6.6	322
254	Ubiquitination of alpha-synuclein in Lewy bodies is a pathological event not associated with impairment of proteasome function. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 44405-11	5.4	265
253	FlyMine: an integrated database for Drosophila and Anopheles genomics. <i>Genome Biology</i> , <b>2007</b> , 8, R12918.3	18.3	260
252	Localization of organelle proteins by isotope tagging (LOPIT). <i>Molecular and Cellular Proteomics</i> , <b>2004</b> , 3, 1128-34	7.6	255
251	All about DIGE: quantification technology for differential-display 2D-gel proteomics. <i>Expert Review of Proteomics</i> , <b>2004</b> , 1, 401-9	4.2	229
250	Two-dimensional gel electrophoresis: recent advances in sample preparation, detection and quantitation. <i>Current Opinion in Chemical Biology</i> , <b>2002</b> , 6, 46-50	9.7	223
249	i-Tracker: for quantitative proteomics using iTRAQ. <i>BMC Genomics</i> , <b>2005</b> , 6, 145	4.5	223
248	A systematic approach to modeling, capturing, and disseminating proteomics experimental data. <i>Nature Biotechnology</i> , <b>2003</b> , 21, 247-54	44.5	220

247	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. <i>Cell Systems</i> , <b>2020</b> , 11, 11-24.e4	10.6	219
246	The tip-link antigen, a protein associated with the transduction complex of sensory hair cells, is protocadherin-15. <i>Journal of Neuroscience</i> , <b>2006</b> , 26, 7022-34	6.6	213
245	Growth control of the eukaryote cell: a systems biology study in yeast. <i>Journal of Biology</i> , <b>2007</b> , 6, 4		208
244	Subunit assembly and active site location in the structure of glutamate dehydrogenase. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1992</b> , 12, 75-86	4.2	206
243	Glucocorticoid signaling synchronizes the liver circadian transcriptome. <i>Hepatology</i> , <b>2007</b> , 45, 1478-88	11.2	202
242	MSnbase-an R/Bioconductor package for isobaric tagged mass spectrometry data visualization, processing and quantitation. <i>Bioinformatics</i> , <b>2012</b> , 28, 288-9	7.2	180
241	DIA-NN: neural networks and interference correction enable deep proteome coverage in high throughput. <i>Nature Methods</i> , <b>2020</b> , 17, 41-44	21.6	179
240	Maximising sensitivity for detecting changes in protein expression: experimental design using minimal CyDyes. <i>Proteomics</i> , <b>2005</b> , 5, 3105-15	4.8	175
239	Functional specialization amongst the Arabidopsis Toc159 family of chloroplast protein import receptors. <i>Plant Cell</i> , <b>2004</b> , 16, 2059-77	11.6	154
238	Determining a significant change in protein expression with DeCyder during a pair-wise comparison using two-dimensional difference gel electrophoresis. <i>Proteomics</i> , <b>2004</b> , 4, 1421-32	4.8	154
237	Tracking the embryonic stem cell transition from ground state pluripotency. <i>Development (Cambridge)</i> , <b>2017</b> , 144, 1221-1234	6.6	150
236	SETH1 and SETH2, two components of the glycosylphosphatidylinositol anchor biosynthetic pathway, are required for pollen germination and tube growth in Arabidopsis. <i>Plant Cell</i> , <b>2004</b> , 16, 229-40	11.6	150
235	Toward a comprehensive map of the effectors of rab GTPases. <i>Developmental Cell</i> , <b>2014</b> , 31, 358-373	10.2	148
234	Experimental and statistical considerations to avoid false conclusions in proteomics studies using differential in-gel electrophoresis. <i>Molecular and Cellular Proteomics</i> , <b>2007</b> , 6, 1354-64	7.6	142
233	Impact of replicate types on proteomic expression analysis. <i>Journal of Proteome Research</i> , <b>2005</b> , 4, 1867-76	7.6	141
232	The Arabidopsis <i>ppi1</i> mutant is specifically defective in the expression, chloroplast import, and accumulation of photosynthetic proteins. <i>Plant Cell</i> , <b>2003</b> , 15, 1859-71	11.6	136
231	A draft map of the mouse pluripotent stem cell spatial proteome. <i>Nature Communications</i> , <b>2016</b> , 7, 8992	17.4	135
230	Proteome labeling and protein identification in specific tissues and at specific developmental stages in an animal. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 465-72	44.5	134

229	Comparative proteomics of clathrin-coated vesicles. <i>Journal of Cell Biology</i> , <b>2006</b> , 175, 571-8	7.3	132
228	Comprehensive identification of RNA-protein interactions in any organism using orthogonal organic phase separation (OOPS). <i>Nature Biotechnology</i> , <b>2019</b> , 37, 169-178	44.5	132
227	Design and analysis issues in quantitative proteomics studies. <i>Proteomics</i> , <b>2007</b> , 7 Suppl 1, 42-50	4.8	128
226	Application of partial least squares discriminant analysis to two-dimensional difference gel studies in expression proteomics. <i>Proteomics</i> , <b>2005</b> , 5, 81-90	4.8	127
225	Identification of putative stage-specific grapevine berry biomarkers and omics data integration into networks. <i>Plant Physiology</i> , <b>2010</b> , 154, 1439-59	6.6	123
224	Detection of reactive oxygen species-sensitive thiol proteins by redox difference gel electrophoresis: implications for mitochondrial redox signaling. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 22040-51	5.4	121
223	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> , <b>2010</b> , 430, 49-59	3.8	119
222	Putative glycosyltransferases and other plant Golgi apparatus proteins are revealed by LOPIT proteomics. <i>Plant Physiology</i> , <b>2012</b> , 160, 1037-51	6.6	119
221	Investigating sample pooling strategies for DIGE experiments to address biological variability. <i>Proteomics</i> , <b>2009</b> , 9, 388-97	4.8	114
220	Drosophila Ionotropic Receptor 25a mediates circadian clock resetting by temperature. <i>Nature</i> , <b>2015</b> , 527, 516-20	50.4	110
219	Identification of internal ribosome entry segment (IRES)-trans-acting factors for the Myc family of IRESs. <i>Molecular and Cellular Biology</i> , <b>2008</b> , 28, 40-9	4.8	109
218	Independent protein-profiling studies show a decrease in apolipoprotein A1 levels in schizophrenia CSF, brain and peripheral tissues. <i>Molecular Psychiatry</i> , <b>2008</b> , 13, 1118-28	15.1	108
217	Specific changes in the Arabidopsis proteome in response to bacterial challenge: differentiating basal and R-gene mediated resistance. <i>Phytochemistry</i> , <b>2004</b> , 65, 1805-16	4	108
216	The Drosophila melanogaster sperm proteome-II (DmSP-II). <i>Journal of Proteomics</i> , <b>2010</b> , 73, 2171-85	3.9	106
215	A proteomic approach identifies many novel palmitoylated proteins in Arabidopsis. <i>New Phytologist</i> , <b>2013</b> , 197, 805-814	9.8	104
214	Molecular analysis of core kinetochore composition and assembly in Drosophila melanogaster. <i>PLoS ONE</i> , <b>2007</b> , 2, e478	3.7	104
213	Multiple protein phosphatases are required for mitosis in Drosophila. <i>Current Biology</i> , <b>2007</b> , 17, 293-303	6.3	104
212	Proteomic analysis reveals the role of synaptic vesicle cycling in sustaining the suprachiasmatic circadian clock. <i>Current Biology</i> , <b>2009</b> , 19, 2031-6	6.3	102

211	Interaction between Anillin and RacGAP50C connects the actomyosin contractile ring with spindle microtubules at the cell division site. <i>Journal of Cell Science</i> , <b>2008</b> , 121, 1151-8	5.3	100
210	2-D DIGE analysis of liver and red blood cells provides further evidence for oxidative stress in schizophrenia. <i>Journal of Proteome Research</i> , <b>2007</b> , 6, 141-9	5.6	98
209	Proteomic analysis of peach fruit mesocarp softening and chilling injury using difference gel electrophoresis (DIGE). <i>BMC Genomics</i> , <b>2010</b> , 11, 43	4.5	97
208	Human urinary exosomes as innate immune effectors. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2014</b> , 25, 2017-27	12.7	93
207	Analysis of the expression patterns, subcellular localisations and interaction partners of Drosophila proteins using a pigP protein trap library. <i>Development (Cambridge)</i> , <b>2014</b> , 141, 3994-4005	6.6	93
206	The RNA-binding protein repertoire of Arabidopsis thaliana. <i>Scientific Reports</i> , <b>2016</b> , 6, 29766	4.9	93
205	Interrelationships between colonies, biofilms, and planktonic cells of Pseudomonas aeruginosa. <i>Journal of Bacteriology</i> , <b>2007</b> , 189, 2411-6	3.5	92
204	Eklotho Expression in Human Tissues. <i>Journal of Clinical Endocrinology and Metabolism</i> , <b>2015</b> , 100, E1308-18	5.18	90
203	MRMaid, the web-based tool for designing multiple reaction monitoring (MRM) transitions. <i>Molecular and Cellular Proteomics</i> , <b>2009</b> , 8, 696-705	7.6	88
202	The Association of Biomolecular Resource Facilities Proteomics Research Group 2006 study: relative protein quantitation. <i>Molecular and Cellular Proteomics</i> , <b>2007</b> , 6, 1291-8	7.6	87
201	DNA microarray normalization methods can remove bias from differential protein expression analysis of 2D difference gel electrophoresis results. <i>Bioinformatics</i> , <b>2004</b> , 20, 2026-34	7.2	81
200	Proteomic approaches to the characterization of protein thiol modification. <i>Current Opinion in Chemical Biology</i> , <b>2011</b> , 15, 120-8	9.7	78
199	New insights into the DT40 B cell receptor cluster using a proteomic proximity labeling assay. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 14434-47	5.4	77
198	Protein profiling of human postmortem brain using 2-dimensional fluorescence difference gel electrophoresis (2-D DIGE). <i>Molecular Psychiatry</i> , <b>2004</b> , 9, 128-43	15.1	77
197	Protein Neighbors and Proximity Proteomics. <i>Molecular and Cellular Proteomics</i> , <b>2015</b> , 14, 2848-56	7.6	76
196	Precursor ion scanning for detection and structural characterization of heterogeneous glycopeptide mixtures. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2002</b> , 13, 1065-77	3.5	76
195	Combining LOPIT with differential ultracentrifugation for high-resolution spatial proteomics. <i>Nature Communications</i> , <b>2019</b> , 10, 331	17.4	74
194	Guidelines for reporting the use of mass spectrometry in proteomics. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 860-1	44.5	72

193	Effects of traveling wave ion mobility separation on data independent acquisition in proteomics studies. <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 2323-39	5.6	70
192	Methods of quantitative proteomics and their application to plant organelle characterization. <i>Journal of Experimental Botany</i> , <b>2006</b> , 57, 1493-9	7	70
191	Quantitative proteomic approach to study subcellular localization of membrane proteins. <i>Nature Protocols</i> , <b>2006</b> , 1, 1778-89	18.8	70
190	Isobaric tagging approaches in quantitative proteomics: the ups and downs. <i>Analytical and Bioanalytical Chemistry</i> , <b>2012</b> , 404, 1029-37	4.4	68
189	Using hyperLOPIT to perform high-resolution mapping of the spatial proteome. <i>Nature Protocols</i> , <b>2017</b> , 12, 1110-1135	18.8	67
188	Mutation of nfxB causes global changes in the physiology and metabolism of <i>Pseudomonas aeruginosa</i> . <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 2957-67	5.6	67
187	Deciphering thylakoid sub-compartments using a mass spectrometry-based approach. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 2147-67	7.6	65
186	In vivo analysis of proteomes and interactomes using Parallel Affinity Capture (iPAC) coupled to mass spectrometry. <i>Molecular and Cellular Proteomics</i> , <b>2011</b> , 10, M110.002386	7.6	64
185	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> , <b>2005</b> , 18, 334-42	3.6	64
184	<i>Drosophila</i> Larp associates with poly(A)-binding protein and is required for male fertility and syncytial embryo development. <i>Developmental Biology</i> , <b>2009</b> , 334, 186-97	3.1	63
183	Virulence and prodigiosin antibiotic biosynthesis in <i>Serratia</i> are regulated pleiotropically by the GGDEF/EAL domain protein, PigX. <i>Journal of Bacteriology</i> , <b>2007</b> , 189, 7653-62	3.5	62
182	Sub-cellular localization of membrane proteins. <i>Proteomics</i> , <b>2008</b> , 8, 3991-4011	4.8	61
181	A Comprehensive Subcellular Atlas of the <i>Toxoplasma</i> Proteome via hyperLOPIT Provides Spatial Context for Protein Functions. <i>Cell Host and Microbe</i> , <b>2020</b> , 28, 752-766.e9	23.4	61
180	Comparison of DIGE and post-stained gel electrophoresis with both traditional and SameSpots analysis for quantitative proteomics. <i>Proteomics</i> , <b>2008</b> , 8, 948-60	4.8	60
179	Nutrient control of eukaryote cell growth: a systems biology study in yeast. <i>BMC Biology</i> , <b>2010</b> , 8, 68	7.3	58
178	Improving qualitative and quantitative performance for MS(E)-based label-free proteomics. <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 2340-53	5.6	57
177	Sequestration of Polo kinase to microtubules by phosphoprime-independent binding to Map205 is relieved by phosphorylation at a CDK site in mitosis. <i>Genes and Development</i> , <b>2008</b> , 22, 2707-20	12.6	57
176	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> , <b>2010</b> , 11, 565	4.5	55

175	Identification by 2-D DIGE of apoplastic proteins regulated by oligogalacturonides in <i>Arabidopsis thaliana</i> . <i>Proteomics</i> , <b>2008</b> , 8, 1042-54	4.8	55
174	Structural and functional characteristics of cGMP-dependent methionine oxidation in <i>Arabidopsis thaliana</i> proteins. <i>Cell Communication and Signaling</i> , <b>2013</b> , 11, 1	7.5	54
173	Mapping organelle proteins and protein complexes in <i>Drosophila melanogaster</i> . <i>Journal of Proteome Research</i> , <b>2009</b> , 8, 2667-78	5.6	54
172	The use of isotope-coded affinity tags (ICAT) to study organelle proteomes in <i>Arabidopsis thaliana</i> . <i>Biochemical Society Transactions</i> , <b>2004</b> , 32, 520-3	5.1	54
171	The metabolic background is a global player in <i>Saccharomyces</i> gene expression epistasis. <i>Nature Microbiology</i> , <b>2016</b> , 1, 15030	26.6	53
170	Genetic and proteomic analysis of the role of luxS in the enteric phytopathogen, <i>Erwinia carotovora</i> . <i>Molecular Plant Pathology</i> , <b>2006</b> , 7, 31-45	5.7	53
169	Trans-acting translational regulatory RNA binding proteins. <i>Wiley Interdisciplinary Reviews RNA</i> , <b>2018</b> , 9, e1465	9.3	51
168	The organelle proteome of the DT40 lymphocyte cell line. <i>Molecular and Cellular Proteomics</i> , <b>2009</b> , 8, 1295-305	7.6	50
167	Identification of trans-golgi network proteins in <i>Arabidopsis thaliana</i> root tissue. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 763-76	5.6	49
166	Mass-spectrometry-based spatial proteomics data analysis using pRoloc and pRolocdata. <i>Bioinformatics</i> , <b>2014</b> , 30, 1322-4	7.2	49
165	The beauty of being (label)-free: sample preparation methods for SWATH-MS and next-generation targeted proteomics. <i>F1000Research</i> , <b>2013</b> , 2, 272	3.6	49
164	Guidelines for reporting the use of gel electrophoresis in proteomics. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 863-4	44.5	48
163	Plant organelle proteomics. <i>Current Opinion in Plant Biology</i> , <b>2007</b> , 10, 594-9	9.9	48
162	N-terminal sequence similarities between components of the multicatalytic proteinase complex. <i>FEBS Letters</i> , <b>1990</b> , 262, 327-9	3.8	48
161	PEDRo: a database for storing, searching and disseminating experimental proteomics data. <i>BMC Genomics</i> , <b>2004</b> , 5, 68	4.5	47
160	Ultra-fast proteomics with Scanning SWATH. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 846-854	44.5	47
159	Two-dimensional differential in gel electrophoresis (2D-DIGE) analysis of grape berry proteome during postharvest withering. <i>Journal of Proteome Research</i> , <b>2011</b> , 10, 429-46	5.6	46
158	Differential gel electrophoresis and transgenic mitochondrial calcium reporters demonstrate spatiotemporal filtering in calcium control of mitochondria. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 18849-58	5.4	46

157	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , <b>2010</b> , 10, 3957-69	4.8	44
156	Plant endoplasmic reticulum supports the protein secretory pathway and has a role in proliferating tissues. <i>Plant Journal</i> , <b>2006</b> , 48, 657-73	6.9	43
155	Recruitment of Polo kinase to the spindle midzone during cytokinesis requires the Feo/Klp3A complex. <i>PLoS ONE</i> , <b>2007</b> , 2, e572	3.7	42
154	In vivo analyses of the roles of essential Omp85-related proteins in the chloroplast outer envelope membrane. <i>Plant Physiology</i> , <b>2011</b> , 157, 147-59	6.6	40
153	Evaluation and properties of the budding yeast phosphoproteome. <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, M111.009555	7.6	40
152	Gel-based proteomics approach to the study of metabolic changes in pear tissue during storage. <i>Journal of Agricultural and Food Chemistry</i> , <b>2009</b> , 57, 6997-7004	5.7	40
151	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> , <b>2008</b> , 283, 23739-53	5.4	40
150	Optimizing the difference gel electrophoresis (DIGE) technology. <i>Methods in Molecular Biology</i> , <b>2008</b> , 428, 93-124	1.4	40
149	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> , <b>2013</b> , 12, 1-13	7.6	39
148	The essential active-site lysines of clostridial glutamate dehydrogenase. A study with pyridoxal-5-phosphate. <i>FEBS Journal</i> , <b>1992</b> , 207, 533-40		39
147	Differentiation of isomeric N-glycan structures by normal-phase liquid chromatography-MALDI-TOF/TOF tandem mass spectrometry. <i>Analytical Chemistry</i> , <b>2006</b> , 78, 8491-8	7.8	38
146	The beauty of being (label)-free: sample preparation methods for SWATH-MS and next-generation targeted proteomics. <i>F1000Research</i> , <b>2</b> , 272	3.6	38
145	A foundation for reliable spatial proteomics data analysis. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 1937-52	7.6	36
144	qcML: an exchange format for quality control metrics from mass spectrometry experiments. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 1905-13	7.6	36
143	Improved sub-cellular resolution via simultaneous analysis of organelle proteomics data across varied experimental conditions. <i>Proteomics</i> , <b>2010</b> , 10, 4213-9	4.8	36
142	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> , <b>2008</b> , 7, 2069-77	5.6	36
141	Genomic tagging reveals a random association of endogenous PtdIns5P 4-kinases IIalpha and IIbeta and a partial nuclear localization of the IIalpha isoform. <i>Biochemical Journal</i> , <b>2010</b> , 430, 215-21	3.8	35
140	Isolation and preparation of chloroplasts from <i>Arabidopsis thaliana</i> plants. <i>Methods in Molecular Biology</i> , <b>2008</b> , 425, 171-86	1.4	34



139	Quantitative proteomics analysis of the Arg/N-end rule pathway of targeted degradation in Arabidopsis roots. <i>Proteomics</i> , <b>2015</b> , 15, 2447-57	4.8	32
138	A Bayesian mixture modelling approach for spatial proteomics. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1006516	5	32
137	A time-resolved proteomic and prognostic map of COVID-19. <i>Cell Systems</i> , <b>2021</b> , 12, 780-794.e7	10.6	32
136	Proteome Mapping of a Cyanobacterium Reveals Distinct Compartment Organization and Cell-Dispersed Metabolism. <i>Plant Physiology</i> , <b>2019</b> , 181, 1721-1738	6.6	31
135	Label-free protein quantification for plant Golgi protein localization and abundance. <i>Plant Physiology</i> , <b>2014</b> , 166, 1033-43	6.6	31
134	Ketamine's antidepressant effect is mediated by energy metabolism and antioxidant defense system. <i>Scientific Reports</i> , <b>2017</b> , 7, 15788	4.9	31
133	Proteomics for the food industry: opportunities and challenges. <i>Critical Reviews in Food Science and Nutrition</i> , <b>2010</b> , 50, 680-92	11.5	31
132	Antibody-mediated neutralization of myelin-associated EphrinB3 accelerates CNS remyelination. <i>Acta Neuropathologica</i> , <b>2016</b> , 131, 281-298	14.3	30
131	N-terminomics reveals control of Arabidopsis seed storage proteins and proteases by the Arg/N-end rule pathway. <i>New Phytologist</i> , <b>2018</b> , 218, 1106-1126	9.8	30
130	Learning from Heterogeneous Data Sources: An Application in Spatial Proteomics. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1004920	5	29
129	A Quantitative Phosphoproteome Analysis of cGMP-Dependent Cellular Responses in Arabidopsis thaliana. <i>Molecular Plant</i> , <b>2016</b> , 9, 621-3	14.4	28
128	hiPSC hepatocyte model demonstrates the role of unfolded protein response and inflammatory networks in Entitrypsin deficiency. <i>Journal of Hepatology</i> , <b>2018</b> , 69, 851-860	13.4	28
127	Changes in the Arabidopsis RNA-binding proteome reveal novel stress response mechanisms. <i>BMC Plant Biology</i> , <b>2019</b> , 19, 139	5.3	27
126	Proteomic complex detection using sedimentation. <i>Analytical Chemistry</i> , <b>2007</b> , 79, 2078-83	7.8	27
125	Global analysis of protein-RNA interactions in SARS-CoV-2-infected cells reveals key regulators of infection. <i>Molecular Cell</i> , <b>2021</b> , 81, 2851-2867.e7	17.6	27
124	Impact of Azithromycin on the Quorum Sensing-Controlled Proteome of Pseudomonas aeruginosa. <i>PLoS ONE</i> , <b>2016</b> , 11, e0147698	3.7	27
123	Quantification and identification of mitochondrial proteins containing vicinal dithiols. <i>Archives of Biochemistry and Biophysics</i> , <b>2010</b> , 504, 228-35	4.1	26
122	RNA-seq reveals the RNA binding proteins, Hfq and RsmA, play various roles in virulence, antibiotic production and genomic flux in Serratia sp. ATCC 39006. <i>BMC Genomics</i> , <b>2013</b> , 14, 822	4.5	25

121	Interlaboratory studies and initiatives developing standards for proteomics. <i>Proteomics</i> , <b>2013</b> , 13, 904-948	4.8	25
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