

# Kathryn S Lilley

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/7465527/kathryn-s-lilley-publications-by-year.pdf>

**Version:** 2024-04-23

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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 proteomic survival predictor for COVID-19 patients in intensive care <b>2022</b> , 1, e0000007		6
263	Understudied proteins: opportunities and challenges for functional proteomics.. <i>Nature Methods</i> , <b>2022</b> ,	21.6	6
262	An open invitation to the Understudied Proteins Initiative.. <i>Nature Biotechnology</i> , <b>2022</b> ,	44.5	2
261	SUBCELLULAR TRANSCRIPTOMICS & PROTEOMICS: A COMPARATIVE METHODS REVIEW.. <i>Molecular and Cellular Proteomics</i> , <b>2021</b> , 100186	7.6	2
260	Ultra-fast proteomics with Scanning SWATH. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 846-854	44.5	47
259	Subcellular proteomics. <i>Nature Reviews Methods Primers</i> , <b>2021</b> , 1,		13
258	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
257	A Bayesian semi-parametric model for thermal proteome profiling. <i>Communications Biology</i> , <b>2021</b> , 4, 810	6.7	0
256	Localization of Organelle Proteins by Isotope Tagging: Current status and potential applications in drug discovery research.. <i>Drug Discovery Today: Technologies</i> , <b>2021</b> , 39, 57-67	7.1	0
255	A time-resolved proteomic and prognostic map of COVID-19. <i>Cell Systems</i> , <b>2021</b> , 12, 780-794.e7	10.6	32
254	Spatiotemporal proteomic profiling of the pro-inflammatory response to lipopolysaccharide in the THP-1 human leukaemia cell line. <i>Nature Communications</i> , <b>2021</b> , 12, 5773	17.4	5
253	Pan-cancer analysis of transcripts encoding novel open-reading frames (nORFs) and their potential biological functions. <i>Npj Genomic Medicine</i> , <b>2021</b> , 6, 4	6.2	9
252	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
251	Changes in the Oligodendrocyte Progenitor Cell Proteome with Ageing. <i>Molecular and Cellular Proteomics</i> , <b>2020</b> , 19, 1281-1302	7.6	18
250	Proteomics of intracellular freezing survival. <i>PLoS ONE</i> , <b>2020</b> , 15, e0233048	3.7	0
249	Moving Profiling Spatial Proteomics Beyond Discrete Classification. <i>Proteomics</i> , <b>2020</b> , 20, e1900392	4.8	7
248	Organic phase separation opens up new opportunities to interrogate the RNA-binding proteome. <i>Current Opinion in Chemical Biology</i> , <b>2020</b> , 54, 70-75	9.7	15

247	Efficient recovery of the RNA-bound proteome and protein-bound transcriptome using phase separation (OOPS). <i>Nature Protocols</i> , <b>2020</b> , 15, 2568-2588	18.8	4
246	Biotin proximity tagging favours unfolded proteins and enables the study of intrinsically disordered regions. <i>Communications Biology</i> , <b>2020</b> , 3, 38	6.7	14
245	A semi-supervised Bayesian approach for simultaneous protein sub-cellular localisation assignment and novelty detection. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1008288	5	6
244	Identification of the cis-molecular neighbours of the immune checkpoint protein B7-H4 in the breast cancer cell-line SK-BR-3 by proteomic proximity labelling. <i>International Journal of Oncology</i> , <b>2020</b> , 57, 87-99	4.4	0
243	A direct role for SNX9 in the biogenesis of filopodia. <i>Journal of Cell Biology</i> , <b>2020</b> , 219,	7.3	2
242	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
241	A Comprehensive Subcellular Atlas of the Toxoplasma 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
240	Spatial proteomics defines the content of trafficking vesicles captured by golgin tethers. <i>Nature Communications</i> , <b>2020</b> , 11, 5987	17.4	11
239	Characterisation of protein isoforms encoded by the Drosophila Glycogen Synthase Kinase 3 gene shaggy. <i>PLoS ONE</i> , <b>2020</b> , 15, e0236679	3.7	1
238	Characterisation of protein isoforms encoded by the Drosophila Glycogen Synthase Kinase 3 gene shaggy <b>2020</b> , 15, e0236679		
237	Characterisation of protein isoforms encoded by the Drosophila Glycogen Synthase Kinase 3 gene shaggy <b>2020</b> , 15, e0236679		
236	Characterisation of protein isoforms encoded by the Drosophila Glycogen Synthase Kinase 3 gene shaggy <b>2020</b> , 15, e0236679		
235	Characterisation of protein isoforms encoded by the Drosophila Glycogen Synthase Kinase 3 gene shaggy <b>2020</b> , 15, e0236679		
234	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
233	Combining LOPIT with differential ultracentrifugation for high-resolution spatial proteomics. <i>Nature Communications</i> , <b>2019</b> , 10, 331	17.4	74
232	Assessing sub-cellular resolution in spatial proteomics experiments. <i>Current Opinion in Chemical Biology</i> , <b>2019</b> , 48, 123-149	9.7	16
231	Systems Analyses Reveal the Resilience of Escherichia coli Physiology during Accumulation and Export of the Nonnative Organic Acid Citramalate. <i>MSystems</i> , <b>2019</b> , 4,	7.6	5
230	Comparison of Drosophila melanogaster Embryo and Adult Proteome by SWATH-MS Reveals Differential Regulation of Protein Synthesis, Degradation Machinery, and Metabolism Modules. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 2525-2534	5.6	3

229	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
228	A proteomic time course through the differentiation of human induced pluripotent stem cells into hepatocyte-like cells. <i>Scientific Reports</i> , <b>2019</b> , 9, 3270	4.9	9
227	Drought Stress Causes Specific Changes to the Spliceosome and Stress Granule Components. <i>Frontiers in Molecular Biosciences</i> , <b>2019</b> , 6, 163	5.6	7
226	Differential Interactome and Innate Immune Response Activation of Two Structurally Distinct Misfolded Protein Oligomers. <i>ACS Chemical Neuroscience</i> , <b>2019</b> , 10, 3464-3478	5.7	7
225	Separating Golgi Proteins from to Reveals Underlying Properties of Cisternal Localization. <i>Plant Cell</i> , <b>2019</b> , 31, 2010-2034	11.6	21
224	A Bioconductor workflow for the Bayesian analysis of spatial proteomics. <i>F1000Research</i> , <b>2019</b> , 8, 446	3.6	12
223	A Protocol to Map the Spatial Proteome Using HyperLOPIT in. <i>Bio-protocol</i> , <b>2019</b> , 9, e3303	0.9	1
222	Mapping the <i>Saccharomyces cerevisiae</i> Spatial Proteome with High Resolution Using hyperLOPIT. <i>Methods in Molecular Biology</i> , <b>2019</b> , 2049, 165-190	1.4	5
221	Transcriptional regulation of the genes involved in protein metabolism and processing in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , <b>2019</b> , 19,	3.1	1
220	The N-recognin E3 ligase PROTEOLYSIS1 influences the immune response. <i>Plant Direct</i> , <b>2019</b> , 3, e00194	3.3	6
219	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
218	Proteomic responses of HepG2 cell monolayers and 3D spheroids to selected hepatotoxins. <i>Toxicology Letters</i> , <b>2019</b> , 300, 40-50	4.4	14
217	Ketamine's Effects on the Glutamatergic and GABAergic Systems: A Proteomics and Metabolomics Study in Mice. <i>Molecular Neuropsychiatry</i> , <b>2019</b> , 5, 42-51	4.9	13
216	The subcellular organisation of <i>Saccharomyces cerevisiae</i> . <i>Current Opinion in Chemical Biology</i> , <b>2019</b> , 48, 86-95	9.7	15
215	The Parkinson's Disease-Linked Protein DJ-1 Associates with Cytoplasmic mRNP Granules During Stress and Neurodegeneration. <i>Molecular Neurobiology</i> , <b>2019</b> , 56, 61-77	6.2	21
214	Mass spectrometry approaches to study plant endomembrane trafficking. <i>Seminars in Cell and Developmental Biology</i> , <b>2018</b> , 80, 123-132	7.5	6
213	Proteomic Comparison of Various Hepatic Cell Cultures for Preclinical Safety Pharmacology. <i>Toxicological Sciences</i> , <b>2018</b> , 164, 229-239	4.4	4
212	Co-complex protein membership evaluation using Maximum Entropy on GO ontology and InterPro annotation. <i>Bioinformatics</i> , <b>2018</b> , 34, 1884-1892	7.2	9

211	Trans-acting translational regulatory RNA binding proteins. <i>Wiley Interdisciplinary Reviews RNA</i> , <b>2018</b> , 9, e1465	9.3	51
210	Stat3-mediated alterations in lysosomal membrane protein composition. <i>Journal of Biological Chemistry</i> , <b>2018</b> , 293, 4244-4261	5.4	16
209	Negative feedback via RSK modulates Erk-dependent progression from naïve pluripotency. <i>EMBO Reports</i> , <b>2018</b> , 19,	6.5	17
208	hiPSC hepatocyte model demonstrates the role of unfolded protein response and inflammatory networks in trypsin deficiency. <i>Journal of Hepatology</i> , <b>2018</b> , 69, 851-860	13.4	28
207	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
206	A Bayesian mixture modelling approach for spatial proteomics. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1006516	5	32
205	Ethylene Receptors, CTRs and EIN2 Target Protein Identification and Quantification Through Parallel Reaction Monitoring During Tomato Fruit Ripening. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 1626	6.2	25
204	Early Responses to Severe Drought Stress in the Cell Suspension Culture Proteome. <i>Proteomes</i> , <b>2018</b> , 6,	4.6	12
203	Identification of the RNA polymerase I-RNA interactome. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 11002-11013	20.1	11
202	Ciprofloxacin binding to GyrA causes global changes in the proteome of <i>Pseudomonas aeruginosa</i> . <i>FEMS Microbiology Letters</i> , <b>2018</b> , 365,	2.9	7
201	Time, space, and disorder in the expanding proteome universe. <i>Proteomics</i> , <b>2017</b> , 17, 1600399	4.8	16
200	Tracking the embryonic stem cell transition from ground state pluripotency. <i>Development (Cambridge)</i> , <b>2017</b> , 144, 1221-1234	6.6	150
199	A subcellular map of the human proteome. <i>Science</i> , <b>2017</b> , 356,	33.3	1183
198	Using hyperLOPIT to perform high-resolution mapping of the spatial proteome. <i>Nature Protocols</i> , <b>2017</b> , 12, 1110-1135	18.8	67
197	In-depth characterization of the tomato fruit pericarp proteome. <i>Proteomics</i> , <b>2017</b> , 17, 1600406	4.8	17
196	Multiple marker abundance profiling: combining selected reaction monitoring and data-dependent acquisition for rapid estimation of organelle abundance in subcellular samples. <i>Plant Journal</i> , <b>2017</b> , 92, 1202-1217	6.9	11
195	Spectral Libraries for SWATH-MS Assays for <i>Drosophila melanogaster</i> and <i>Solanum lycopersicum</i> . <i>Proteomics</i> , <b>2017</b> , 17, 1700216	4.8	18
194	Glareosin: a novel sexually dimorphic urinary lipocalin in the bank vole,. <i>Open Biology</i> , <b>2017</b> , 7,	7	6

193	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
192	SWATH-MS data of proteome dynamics during embryogenesis. <i>Data in Brief</i> , <b>2016</b> , 9, 771-775	1.2	4
191	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
190	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> , <b>2016</b> , 16, 576-92	4.8	6
189	Analysis of <i>Drosophila melanogaster</i> proteome dynamics during embryonic development by a combination of label-free proteomics approaches. <i>Proteomics</i> , <b>2016</b> , 16, 2068-80	4.8	17
188	Antibody-mediated neutralization of myelin-associated EphrinB3 accelerates CNS remyelination. <i>Acta Neuropathologica</i> , <b>2016</b> , 131, 281-298	14.3	30
187	A draft map of the mouse pluripotent stem cell spatial proteome. <i>Nature Communications</i> , <b>2016</b> , 7, 8992	17.4	135
186	A Quantitative Phosphoproteome Analysis of cGMP-Dependent Cellular Responses in <i>Arabidopsis thaliana</i> . <i>Molecular Plant</i> , <b>2016</b> , 9, 621-3	14.4	28
185	A Bioconductor workflow for processing and analysing spatial proteomics data. <i>F1000Research</i> , <b>2016</b> , 5, 2926	3.6	17
184	A Bioconductor workflow for processing and analysing spatial proteomics data. <i>F1000Research</i> , <b>2016</b> , 5, 2926	3.6	15
183	Learning from Heterogeneous Data Sources: An Application in Spatial Proteomics. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1004920	5	29
182	Impact of Azithromycin on the Quorum Sensing-Controlled Proteome of <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , <b>2016</b> , 11, e0147698	3.7	27
181	Mimicking nature: Phosphopeptide enrichment using combinatorial libraries of affinity ligands. <i>Journal of Chromatography A</i> , <b>2016</b> , 1457, 76-87	4.5	10
180	The RNA-binding protein repertoire of <i>Arabidopsis thaliana</i> . <i>Scientific Reports</i> , <b>2016</b> , 6, 29766	4.9	93
179	Phosphorylation of the dimeric cytoplasmic domain of the phyto-sulfokine receptor, PSKR1. <i>Biochemical Journal</i> , <b>2016</b> , 473, 3081-98	3.8	17
178	SWATH-MS dataset of heat-shock treated embryos. <i>Data in Brief</i> , <b>2016</b> , 9, 991-995	1.2	1
177	SILAC-iPAC: a quantitative method for distinguishing genuine from non-specific components of protein complexes by parallel affinity capture. <i>Journal of Proteomics</i> , <b>2015</b> , 115, 143-56	3.9	8
176	Quantitative proteomics analysis of the Arg/N-end rule pathway of targeted degradation in <i>Arabidopsis</i> roots. <i>Proteomics</i> , <b>2015</b> , 15, 2447-57	4.8	32

175	Analysis of Quality-Related Parameters in Mature Kernels of Polygalacturonase Inhibiting Protein (PGIP) Transgenic Bread Wheat Infected with Fusarium graminearum. <i>Journal of Agricultural and Food Chemistry</i> , <b>2015</b> , 63, 3962-9	5.7	3
174	Protein Neighbors and Proximity Proteomics. <i>Molecular and Cellular Proteomics</i> , <b>2015</b> , 14, 2848-56	7.6	76
173	Mep72, a metzincin protease that is preferentially secreted by biofilms of <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , <b>2015</b> , 197, 762-73	3.5	15
172	EKlotho Expression in Human Tissues. <i>Journal of Clinical Endocrinology and Metabolism</i> , <b>2015</b> , 100, E1308-18	5.18	90
171	Drosophila Ionotropic Receptor 25a mediates circadian clock resetting by temperature. <i>Nature</i> , <b>2015</b> , 527, 516-20	50.4	110
170	Dynamic Proteomic Profiling of Extra-Embryonic Endoderm Differentiation in Mouse Embryonic Stem Cells. <i>Stem Cells</i> , <b>2015</b> , 33, 2712-25	5.8	11
169	The chicken B-cell line DT40 proteome, beadome and interactomes. <i>Data in Brief</i> , <b>2015</b> , 3, 29-33	1.2	1
168	Exploring the Arabidopsis proteome: influence of protein solubilization buffers on proteome coverage. <i>International Journal of Molecular Sciences</i> , <b>2014</b> , 16, 857-70	6.3	9
167	Protein profiling using two-dimensional difference gel electrophoresis (2-D DIGE). <i>Current Protocols in Protein Science</i> , <b>2014</b> , 75, 22.2.1-22.2.17	3.1	5
166	A protocol for the subcellular fractionation of <i>Saccharomyces cerevisiae</i> using nitrogen cavitation and density gradient centrifugation. <i>Yeast</i> , <b>2014</b> , 31, 127-35	3.4	10
165	Remodelling of a polypyrimidine tract-binding protein complex during apoptosis activates cellular IRESs. <i>Cell Death and Differentiation</i> , <b>2014</b> , 21, 161-71	12.7	17
164	Dynamic regulation of the COP9 signalosome in response to DNA damage. <i>Molecular and Cellular Biology</i> , <b>2014</b> , 34, 1066-76	4.8	21
163	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
162	A foundation for reliable spatial proteomics data analysis. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 1937-52	7.6	36
161	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
160	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> , <b>2014</b> , 141, 3994-4005	6.6	93
159	Label-free protein quantification for plant Golgi protein localization and abundance. <i>Plant Physiology</i> , <b>2014</b> , 166, 1033-43	6.6	31
158	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

157	Additional precursor purification in isobaric mass tagging experiments by traveling wave ion mobility separation (TWIMS). <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 3360-9	5.6	10
156	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
155	Determining protein subcellular localization in mammalian cell culture with biochemical fractionation and iTRAQ 8-plex quantification. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1156, 157-74	1.4	11
154	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
153	Toward a comprehensive map of the effectors of rab GTPases. <i>Developmental Cell</i> , <b>2014</b> , 31, 358-373	10.2	148
152	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
151	Mass-spectrometry-based spatial proteomics data analysis using pRoloc and pRolocdata. <i>Bioinformatics</i> , <b>2014</b> , 30, 1322-4	7.2	49
150	CHAPTER 9: Spatial Proteomics: Practical Considerations for Data Acquisition and Analysis in Protein Subcellular Localisation Studies. <i>New Developments in Mass Spectrometry</i> , <b>2014</b> , 185-210	2.3	2
149	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
148	Identification of protein biomarkers in human serum using iTRAQ and shotgun mass spectrometry. <i>Methods in Molecular Biology</i> , <b>2013</b> , 1061, 291-307	1.4	5
147	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> , <b>2013</b> , 14, 822	4.5	25
146	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
145	A proteomic approach identifies many novel palmitoylated proteins in <i>Arabidopsis</i> . <i>New Phytologist</i> , <b>2013</b> , 197, 805-814	9.8	104
144	Interlaboratory studies and initiatives developing standards for proteomics. <i>Proteomics</i> , <b>2013</b> , 13, 904-9	4.8	25
143	Identification and quantitation of signal molecule-dependent protein phosphorylation. <i>Methods in Molecular Biology</i> , <b>2013</b> , 1016, 121-37	1.4	6
142	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
141	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
140	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



139	Palmitoylation in plants: new insights through proteomics. <i>Plant Signaling and Behavior</i> , <b>2013</b> , 8,	2.5	12
138	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
137	Pipeline to assess the greatest source of technical variance in quantitative proteomics using metabolic labelling. <i>Journal of Proteomics</i> , <b>2012</b> , 77, 441-54	3.9	18
136	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
135	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
134	Evaluation and properties of the budding yeast phosphoproteome. <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, M111.009555	7.6	40
133	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
132	MRMaid 2.0: mining PRIDE for evidence-based SRM transitions. <i>OMICS A Journal of Integrative Biology</i> , <b>2012</b> , 16, 483-8	3.8	13
131	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
130	Method for suppressing non-specific protein interactions observed with affinity resins. <i>Methods</i> , <b>2011</b> , 54, 407-12	4.6	13
129	LC-MS/MS methods for absolute quantification and identification of proteins associated with chimeric plant oil bodies. <i>Analytical Chemistry</i> , <b>2011</b> , 83, 9267-72	7.8	7
128	Comparative Proteomic Approaches <b>2011</b> , 121-158		
127	Proteomics of cryoprotective dehydration in <i>Megaphorura arctica</i> Tullberg 1876 (Onychiuridae: Collembola). <i>Insect Molecular Biology</i> , <b>2011</b> , 20, 303-10	3.4	10
126	Challenges for proteomics core facilities. <i>Proteomics</i> , <b>2011</b> , 11, 1017-25	4.8	8
125	The ABRF Proteomics Research Group studies: educational exercises for qualitative and quantitative proteomic analyses. <i>Proteomics</i> , <b>2011</b> , 11, 1371-81	4.8	14
124	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
123	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
122	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

121	ABRF-PRG07: advanced quantitative proteomics study. <i>Journal of Biomolecular Techniques</i> , <b>2011</b> , 22, 21-6	1.1	13
120	Uromodulin exclusion list improves urinary exosomal protein identification. <i>Journal of Biomolecular Techniques</i> , <b>2011</b> , 22, 136-45	1.1	12
119	Enabling technologies for yeast proteome analysis. <i>Methods in Molecular Biology</i> , <b>2011</b> , 759, 149-78	1.4	3
118	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
117	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
116	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
115	Proteomics of total membranes and subcellular membranes. <i>Expert Review of Proteomics</i> , <b>2010</b> , 7, 867-78	4.2	12
114	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
113	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
112	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
111	Addressing accuracy and precision issues in iTRAQ quantitation. <i>Molecular and Cellular Proteomics</i> , <b>2010</b> , 9, 1885-97	7.6	400
110	Proteomic complex detection using sedimentation (ProCoDeS): screening for proteins in stable complexes and their candidate interaction partners. <i>Biochemical Society Transactions</i> , <b>2010</b> , 38, 923-7	5.1	2
109	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
108	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
107	The <i>Drosophila melanogaster</i> sperm proteome-II (DmSP-II). <i>Journal of Proteomics</i> , <b>2010</b> , 73, 2171-85	3.9	106
106	Nutrient control of eukaryote cell growth: a systems biology study in yeast. <i>BMC Biology</i> , <b>2010</b> , 8, 68	7.3	58
105	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , <b>2010</b> , 10, 3957-69	4.8	44
104	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

103	Mutations in rpsL 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> , <b>2010</b> , 156, 1030-1039	2.9	20
102	Chapter 19 Measuring redox changes to mitochondrial protein thiols with redox difference gel electrophoresis (redox-DIGE). <i>Methods in Enzymology</i> , <b>2009</b> , 456, 343-61	1.7	22
101	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
100	The organelle proteome of the DT40 lymphocyte cell line. <i>Molecular and Cellular Proteomics</i> , <b>2009</b> , 8, 1295-305	7.6	50
99	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
98	Investigating sample pooling strategies for DIGE experiments to address biological variability. <i>Proteomics</i> , <b>2009</b> , 9, 388-97	4.8	114
97	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
96	<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
95	Difference Gel Electrophoresis (DIGE). <i>Springer Protocols</i> , <b>2009</b> , 379-408	0.3	
94	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
93	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
92	Guidelines for reporting the use of mass spectrometry in proteomics. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 860-1	44.5	72
91	Guidelines for reporting the use of gel electrophoresis in proteomics. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 863-4	44.5	48
90	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
89	Proteomic analysis of the EhV-86 virion. <i>Proteome Science</i> , <b>2008</b> , 6, 11	2.6	23
88	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
87	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
86	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

85	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> , <b>2008</b> , 22, 2707-20	12.6	57
84	A proteomics approach to membrane trafficking. <i>Plant Physiology</i> , <b>2008</b> , 147, 1584-9	6.6	10
83	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, 23739-54	5.4	40
82	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> , <b>2008</b> , 180, 873-84	4	17
81	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
80	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
79	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
78	Sub-cellular localization of membrane proteins. <i>Proteomics</i> , <b>2008</b> , 8, 3991-4011	4.8	61
77	Optimizing the difference gel electrophoresis (DIGE) technology. <i>Methods in Molecular Biology</i> , <b>2008</b> , 428, 93-124	1.4	40
76	Determination of genuine residents of plant endomembrane organelles using isotope tagging and multivariate statistics. <i>Methods in Molecular Biology</i> , <b>2008</b> , 432, 373-87	1.4	10
75	Proteomic complex detection using sedimentation. <i>Analytical Chemistry</i> , <b>2007</b> , 79, 2078-83	7.8	27
74	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
73	Nuclear phospholipase C gamma: punctate distribution and association with the promyelocytic leukemia protein. <i>Journal of Proteome Research</i> , <b>2007</b> , 6, 2027-32	5.6	7
72	Molecular analysis of core kinetochore composition and assembly in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , <b>2007</b> , 2, e478	3.7	104
71	Glucocorticoid signaling synchronizes the liver circadian transcriptome. <i>Hepatology</i> , <b>2007</b> , 45, 1478-88	11.2	202
70	Growth control of the eukaryote cell: a systems biology study in yeast. <i>Journal of Biology</i> , <b>2007</b> , 6, 4		208
69	Design and analysis issues in quantitative proteomics studies. <i>Proteomics</i> , <b>2007</b> , 7 Suppl 1, 42-50	4.8	128
68	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , <b>2007</b> , 25, 887-93	4.5	583

67	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> , <b>2007</b> , 1773, 147-56	4.9	24
66	Multiple protein phosphatases are required for mitosis in <i>Drosophila</i> . <i>Current Biology</i> , <b>2007</b> , 17, 293-303	6.3	104
65	Plant organelle proteomics. <i>Current Opinion in Plant Biology</i> , <b>2007</b> , 10, 594-9	9.9	48
64	Interrelationships between colonies, biofilms, and planktonic cells of <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , <b>2007</b> , 189, 2411-6	3.5	92
63	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
62	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
61	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
60	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
59	FlyMine: an integrated database for <i>Drosophila</i> and <i>Anopheles</i> genomics. <i>Genome Biology</i> , <b>2007</b> , 8, R129	8.3	260
58	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
57	Big results from small samples: evaluation of amplification protocols for gene expression profiling. <i>Journal of Biomolecular Techniques</i> , <b>2007</b> , 18, 150-61	1.1	22
56	Differences in Protein Profiles in Schizophrenia Prefrontal Cortex Compared to Other Major Brain Disorders. <i>Clinical Schizophrenia and Related Psychoses</i> , <b>2007</b> , 1, 73-91	1.6	7
55	Identification of clock genes using difference gel electrophoresis. <i>Methods in Molecular Biology</i> , <b>2007</b> , 362, 265-87	1.4	1
54	Circadian orchestration of the hepatic proteome. <i>Current Biology</i> , <b>2006</b> , 16, 1107-15	6.3	440
53	Comparative proteomics of clathrin-coated vesicles. <i>Journal of Cell Biology</i> , <b>2006</b> , 175, 571-8	7.3	132
52	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
51	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
50	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

49	Difference gel electrophoresis DIGE. <i>Drug Discovery Today: Technologies</i> , <b>2006</b> , 3, 347-53	7.1	7
48	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
47	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
46	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
45	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
44	Quantitative proteomic approach to study subcellular localization of membrane proteins. <i>Nature Protocols</i> , <b>2006</b> , 1, 1778-89	18.8	70
43	The ABRF MARG microarray survey 2005: taking the pulse of the microarray field. <i>Journal of Biomolecular Techniques</i> , <b>2006</b> , 17, 176-86	1.1	2
42	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
41	Impact of replicate types on proteomic expression analysis. <i>Journal of Proteome Research</i> , <b>2005</b> , 4, 1867-76	7.6	141
40	i-Tracker: for quantitative proteomics using iTRAQ. <i>BMC Genomics</i> , <b>2005</b> , 6, 145	4.5	223
39	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
38	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
37	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> , <b>2005</b> , 19, 3363-8	2.2	23
36	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
35	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
34	Localization of organelle proteins by isotope tagging (LOPIT). <i>Molecular and Cellular Proteomics</i> , <b>2004</b> , 3, 1128-34	7.6	255
33	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
32	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

31	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
30	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
29	PEDRo: a database for storing, searching and disseminating experimental proteomics data. <i>BMC Genomics</i> , <b>2004</b> , 5, 68	4.5	47
28	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
27	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
26	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
25	The use of isotope-coded affinity tags (ICAT) to study organelle proteomes in Arabidopsis thaliana. <i>Biochemical Society Transactions</i> , <b>2004</b> , 32, 520-3	5.1	54
24	Proteomics in Drosophila melanogaster. <i>Briefings in Functional Genomics &amp; Proteomics</i> , <b>2003</b> , 2, 106-13		4
23	A systematic approach to modeling, capturing, and disseminating proteomics experimental data. <i>Nature Biotechnology</i> , <b>2003</b> , 21, 247-54	44.5	220
22	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
21	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
20	The Arabidopsis ppi1 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
19	Characterization of the necrotic protein that regulates the Toll-mediated immune response in Drosophila. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 6175-80	5.4	23
18	Protein profiling using two-dimensional difference gel electrophoresis (2-D DIGE). <i>Current Protocols in Protein Science</i> , <b>2003</b> , Chapter 22, Unit 22.2	3.1	14
17	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
16	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
15	GARNet, the Genomic Arabidopsis Resource Network. <i>Trends in Plant Science</i> , <b>2002</b> , 7, 145-7	13.1	10
14	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

13	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
12	N-terminal sequence similarities between components of the multicatalytic proteinase complex. <i>FEBS Letters</i> , <b>1990</b> , 262, 327-9	3.8	48
11	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
10	A subcellular atlas of <i>Toxoplasma</i> reveals the functional context of the proteome		9
9	Clinical classifiers of COVID-19 infection from novel ultra-high-throughput proteomics		7
8	A time-resolved proteomic and diagnostic map characterizes COVID-19 disease progression and predicts outcome		6
7	Global analysis of protein-RNA interactions in SARS-CoV-2 infected cells reveals key regulators of infection		6
6	Cellular labelling favours unfolded proteins		4
5	Unbiased dynamic characterization of RNA-protein interactions by OOPS		3
4	Scanning SWATH acquisition enables high-throughput proteomics with chromatographic gradients as fast as 30 seconds		7
3	Determining the content of vesicles captured by golgin tethers using LOPIT-DC		4
2	High sensitivity dia-PASEF proteomics with DIA-NN and FragPipe		11
1	A proteomic survival predictor for COVID-19 patients in intensive care		1