

Wolfram Weckwerth

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

244 papers	12,438 citations	58 h-index	104 g-index
271 ext. papers	15,950 ext. citations	6.6 avg, IF	6.62 L-index

#	Paper	IF	Citations
244	GMD@CSB.DB: the Golm Metabolome Database. <i>Bioinformatics</i> , 2005 , 21, 1635-8	7.2	1064
243	1,135 Genomes Reveal the Global Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2016 , 166, 481-491	40.1	620
242	Metabolomics in systems biology. <i>Annual Review of Plant Biology</i> , 2003 , 54, 669-89	30.7	506
241	Epigenomic Diversity in a Global Collection of <i>Arabidopsis thaliana</i> Accessions. <i>Cell</i> , 2016 , 166, 492-505	56.2	353
240	Differential metabolic networks unravel the effects of silent plant phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 7809-14	11.5	335
239	Process for the integrated extraction, identification and quantification of metabolites, proteins and RNA to reveal their co-regulation in biochemical networks. <i>Proteomics</i> , 2004 , 4, 78-83	4.8	308
238	Proteome analysis of <i>Arabidopsis</i> leaf peroxisomes reveals novel targeting peptides, metabolic pathways, and defense mechanisms. <i>Plant Cell</i> , 2007 , 19, 3170-93	11.6	271
237	Enrichment of phosphorylated proteins and peptides from complex mixtures using metal oxide/hydroxide affinity chromatography (MOAC). <i>Proteomics</i> , 2005 , 5, 4389-97	4.8	254
236	PhosPhAt: a database of phosphorylation sites in <i>Arabidopsis thaliana</i> and a plant-specific phosphorylation site predictor. <i>Nucleic Acids Research</i> , 2008 , 36, D1015-21	20.1	249
235	Metabolomics: from pattern recognition to biological interpretation. <i>Drug Discovery Today</i> , 2005 , 10, 1551-8	8.8	237
234	Methylophilic methanogenic <i>Thermoplasma</i> implicated in reduced methane emissions from bovine rumen. <i>Nature Communications</i> , 2013 , 4, 1428	17.4	215
233	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017 , 35, 969-976	44.5	197
232	Metabolite profiling in plant biology: platforms and destinations. <i>Genome Biology</i> , 2004 , 5, 109	18.3	185
231	Quantitative phosphoproteomics reveals the role of the AMPK plant ortholog SnRK1 as a metabolic master regulator under energy deprivation. <i>Scientific Reports</i> , 2016 , 6, 31697	4.9	164
230	A cytosolic pathway for the conversion of hydroxypyruvate to glycerate during photorespiration in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2008 , 20, 2848-59	11.6	160
229	Can we discover novel pathways using metabolomic analysis?. <i>Current Opinion in Biotechnology</i> , 2002 , 13, 156-60	11.4	152
228	<i>Medicago truncatula</i> root nodule proteome analysis reveals differential plant and bacteroid responses to drought stress. <i>Plant Physiology</i> , 2007 , 144, 1495-507	6.6	150

227	Green systems biology - From single genomes, proteomes and metabolomes to ecosystems research and biotechnology. <i>Journal of Proteomics</i> , 2011 , 75, 284-305	3.9	148
226	SnRK1-triggered switch of bZIP63 dimerization mediates the low-energy response in plants. <i>ELife</i> , 2015 , 4,	8.9	132
225	Metabolomics- and proteomics-assisted genome annotation and analysis of the draft metabolic network of <i>Chlamydomonas reinhardtii</i> . <i>Genetics</i> , 2008 , 179, 157-66	4	128
224	The role of mass spectrometry in plant systems biology. <i>Mass Spectrometry Reviews</i> , 2006 , 25, 173-214	11	123
223	Chronic signaling via the metabolic checkpoint kinase mTORC1 induces macrophage granuloma formation and marks sarcoidosis progression. <i>Nature Immunology</i> , 2017 , 18, 293-302	19.1	117
222	Integration of metabolomic and proteomic phenotypes: analysis of data covariance dissects starch and RFO metabolism from low and high temperature compensation response in <i>Arabidopsis thaliana</i> . <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1725-36	7.6	117
221	D-GLYCERATE 3-KINASE, the last unknown enzyme in the photorespiratory cycle in <i>Arabidopsis</i> , belongs to a novel kinase family. <i>Plant Cell</i> , 2005 , 17, 2413-20	11.6	110
220	Deletion of glycine decarboxylase in <i>Arabidopsis</i> is lethal under nonphotorespiratory conditions. <i>Plant Physiology</i> , 2007 , 144, 1328-35	6.6	109
219	Combination of Hypoglycemia and Metformin Impairs Tumor Metabolic Plasticity and Growth by Modulating the PP2A-GSK3 β -MCL-1 Axis. <i>Cancer Cell</i> , 2019 , 35, 798-815.e5	24.3	108
218	Comparative analysis of phytohormone-responsive phosphoproteins in <i>Arabidopsis thaliana</i> using TiO ₂ -phosphopeptide enrichment and mass accuracy precursor alignment. <i>Plant Journal</i> , 2010 , 63, 1-17	6.9	107
217	Proteomics and comparative genomics of <i>Nitrososphaera viennensis</i> reveal the core genome and adaptations of archaeal ammonia oxidizers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E7937-E7946	11.5	103
216	COVAIN: a toolbox for uni- and multivariate statistics, time-series and correlation network analysis and inverse estimation of the differential Jacobian from metabolomics covariance data. <i>Metabolomics</i> , 2012 , 8, 81-93	4.7	98
215	Identification of novel in vivo MAP kinase substrates in <i>Arabidopsis thaliana</i> through use of tandem metal oxide affinity chromatography. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 369-80	7.6	97
214	Comparative quantification and identification of phosphoproteins using stable isotope labeling and liquid chromatography/mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2000 , 14, 1677-81	3.2	95
213	Deciphering metabolic networks. <i>FEBS Journal</i> , 2003 , 270, 579-88		94
212	Carbon metabolism and bacteroid functioning are involved in the regulation of nitrogen fixation in <i>Medicago truncatula</i> under drought and recovery. <i>Molecular Plant-Microbe Interactions</i> , 2009 , 22, 1565-76	3.6	91
211	Systemic cold stress adaptation of <i>Chlamydomonas reinhardtii</i> . <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2032-47	7.6	87
210	MASCP Gator: an aggregation portal for the visualization of <i>Arabidopsis</i> proteomics data. <i>Plant Physiology</i> , 2011 , 155, 259-70	6.6	83

209	Cell-specific protein profiling in <i>Arabidopsis thaliana</i> trichomes: identification of trichome-located proteins involved in sulfur metabolism and detoxification. <i>Phytochemistry</i> , 2004 , 65, 1641-9	4	82
208	Granger causality in integrated GC-MS and LC-MS metabolomics data reveals the interface of primary and secondary metabolism. <i>Metabolomics</i> , 2013 , 9, 564-574	4.7	81
207	Targeted proteomics for <i>Chlamydomonas reinhardtii</i> combined with rapid subcellular protein fractionation, metabolomics and metabolic flux analyses. <i>Molecular BioSystems</i> , 2010 , 6, 1018-31		81
206	Integration of metabolomics and proteomics in molecular plant physiology--coping with the complexity by data-dimensionality reduction. <i>Physiologia Plantarum</i> , 2008 , 132, 176-89	4.6	78
205	Metabolomics unravel contrasting effects of biodiversity on the performance of individual plant species. <i>PLoS ONE</i> , 2010 , 5, e12569	3.7	78
204	The SnRK1 Kinase as Central Mediator of Energy Signaling between Different Organelles. <i>Plant Physiology</i> , 2018 , 176, 1085-1094	6.6	77
203	ProMEX: a mass spectral reference database for proteins and protein phosphorylation sites. <i>BMC Bioinformatics</i> , 2007 , 8, 216	3.6	76
202	Correlative GC-TOF-MS-based metabolite profiling and LC-MS-based protein profiling reveal time-related systemic regulation of metabolite-protein networks and improve pattern recognition for multiple biomarker selection. <i>Metabolomics</i> , 2005 , 1, 109-121	4.7	76
201	A survey of the <i>Arabidopsis thaliana</i> mitochondrial phosphoproteome. <i>Proteomics</i> , 2009 , 9, 4229-40	4.8	75
200	Metabolomics: an integral technique in systems biology. <i>Bioanalysis</i> , 2010 , 2, 829-36	2.1	74
199	Linking protein fractionation with multidimensional monolithic reversed-phase peptide chromatography/mass spectrometry enhances protein identification from complex mixtures even in the presence of abundant proteins. <i>Rapid Communications in Mass Spectrometry</i> , 2004 , 18, 643-50	2.2	73
198	Proteomics and Metabolomics: Two Emerging Areas for Legume Improvement. <i>Frontiers in Plant Science</i> , 2015 , 6, 1116	6.2	72
197	System-level network analysis of nitrogen starvation and recovery in <i>Chlamydomonas reinhardtii</i> reveals potential new targets for increased lipid accumulation. <i>Biotechnology for Biofuels</i> , 2014 , 7, 171	7.8	72
196	Cereal Crop Proteomics: Systemic Analysis of Crop Drought Stress Responses Towards Marker-Assisted Selection Breeding. <i>Frontiers in Plant Science</i> , 2017 , 8, 757	6.2	71
195	Snf1-RELATED KINASE1-Controlled C/S-bZIP Signaling Activates Alternative Mitochondrial Metabolic Pathways to Ensure Plant Survival in Extended Darkness. <i>Plant Cell</i> , 2018 , 30, 495-509	11.6	70
194	Differential multisite phosphorylation of the trehalose-6-phosphate synthase gene family in <i>Arabidopsis thaliana</i> : a mass spectrometry-based process for multiparallel peptide library phosphorylation analysis. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 1614-25	7.6	70
193	A metabolic signature of the beneficial interaction of the endophyte <i>paenibacillus</i> sp. isolate and in vitro-grown poplar plants revealed by metabolomics. <i>Molecular Plant-Microbe Interactions</i> , 2009 , 22, 1032-7	3.6	68
192	A universal protocol for the combined isolation of metabolites, DNA, long RNAs, small RNAs, and proteins from plants and microorganisms. <i>Plant Journal</i> , 2014 , 79, 173-80	6.9	66

191	Subcellular reprogramming of metabolism during cold acclimation in <i>Arabidopsis thaliana</i> . <i>Plant, Cell and Environment</i> , 2017 , 40, 602-610	8.4	66
190	Relative and absolute quantitative shotgun proteomics: targeting low-abundance proteins in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2006 , 57, 1529-35	7	65
189	Cell-specific analysis of the tomato pollen proteome from pollen mother cell to mature pollen provides evidence for developmental priming. <i>Journal of Proteome Research</i> , 2013 , 12, 4892-903	5.6	64
188	Unpredictability of metabolism--the key role of metabolomics science in combination with next-generation genome sequencing. <i>Analytical and Bioanalytical Chemistry</i> , 2011 , 400, 1967-78	4.4	60
187	If the antibody fails--a mass western approach. <i>Plant Journal</i> , 2008 , 55, 1039-46	6.9	59
186	Male Sterility in Maize after Transient Heat Stress during the Tetrad Stage of Pollen Development. <i>Plant Physiology</i> , 2019 , 181, 683-700	6.6	57
185	Detection and characterization of 3D-signature phosphorylation site motifs and their contribution towards improved phosphorylation site prediction in proteins. <i>BMC Bioinformatics</i> , 2009 , 10, 117	3.6	56
184	A rapid approach for phenotype-screening and database independent detection of cSNP/protein polymorphism using mass accuracy precursor alignment. <i>Proteomics</i> , 2008 , 8, 4214-25	4.8	56
183	Phytochemical composition of L. analyzed by an integrative GC-MS and LC-MS metabolomics platform. <i>Metabolomics</i> , 2013 , 9, 599-607	4.7	55
182	An automated GCxGC-TOF-MS protocol for batch-wise extraction and alignment of mass isotopomer matrixes from differential ¹³ C-labelling experiments: a case study for photoautotrophic-mixotrophic grown <i>Chlamydomonas reinhardtii</i> cells. <i>Journal of Basic Microbiology</i> , 2009 , 49, 82-91	2.7	55
181	<i>Arabidopsis thaliana</i> as a model organism for plant proteome research. <i>Journal of Proteomics</i> , 2010 , 73, 2239-48	3.9	55
180	Ectopic overexpression of the cell wall invertase gene CIN1 leads to dehydration avoidance in tomato. <i>Journal of Experimental Botany</i> , 2015 , 66, 863-78	7	53
179	Combining metal oxide affinity chromatography (MOAC) and selective mass spectrometry for robust identification of in vivo protein phosphorylation sites. <i>Plant Methods</i> , 2005 , 1, 9	5.8	53
178	Dynamic adaption of metabolic pathways during germination and growth of lily pollen tubes after inhibition of the electron transport chain. <i>Plant Physiology</i> , 2013 , 162, 1822-33	6.6	50
177	A gentle guide to the analysis of metabolomic data. <i>Methods in Molecular Biology</i> , 2007 , 358, 105-26	1.4	49
176	Different functions of the C3HC4 zinc RING finger peroxins PEX10, PEX2, and PEX12 in peroxisome formation and matrix protein import. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 14915-20	11.5	48
175	Proteome and metabolome profiling of cytokinin action in <i>Arabidopsis</i> identifying both distinct and similar responses to cytokinin down- and up-regulation. <i>Journal of Experimental Botany</i> , 2013 , 64, 4193-206	7	47
174	Biosynthesis of PF1022A and related cyclooctadepsipeptides. <i>Journal of Biological Chemistry</i> , 2000 , 275, 17909-15	5.4	45

173	Comprehensive cell-specific protein analysis in early and late pollen development from diploid microsporocytes to pollen tube growth. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 295-310	7.6	44
172	Neutral loss-based phosphopeptide recognition: a collection of caveats. <i>Journal of Proteome Research</i> , 2007 , 6, 2866-73	5.6	43
171	Stable isotope labeling of phosphopeptides for multiparallel kinase target analysis and identification of phosphorylation sites. <i>Rapid Communications in Mass Spectrometry</i> , 2003 , 17, 1579-84	2.2	43
170	Exploring natural variation of Pinus pinaster Aiton using metabolomics: Is it possible to identify the region of origin of a pine from its metabolites?. <i>Molecular Ecology</i> , 2016 , 25, 959-76	5.7	42
169	An evolutionary perspective of AMPK-TOR signaling in the three domains of life. <i>Journal of Experimental Botany</i> , 2016 , 67, 3897-907	7	41
168	Dynamics of Plant Metabolism during Cold Acclimation. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	41
167	Stable isotope-free quantitative shotgun proteomics combined with sample pattern recognition for rapid diagnostics. <i>Journal of Separation Science</i> , 2006 , 29, 2793-801	3.4	41
166	Evidence for novel tomato seed allergens: IgE-reactive legumin and vicilin proteins identified by multidimensional protein fractionation-mass spectrometry and in silico epitope modeling. <i>Journal of Proteome Research</i> , 2009 , 8, 1111-22	5.6	40
165	Metabolic Consequences of Infection of Grapevine (<i>Vitis vinifera</i> L.) cv. "Modra frankinja" with Flavescence Dorée Phytoplasma. <i>Frontiers in Plant Science</i> , 2016 , 7, 711	6.2	40
164	PANOMICS meets germplasm. <i>Plant Biotechnology Journal</i> , 2020 , 18, 1507-1525	11.6	39
163	Consistency analysis of metabolic correlation networks. <i>BMC Systems Biology</i> , 2007 , 1, 44	3.5	39
162	System level analysis of cacao seed ripening reveals a sequential interplay of primary and secondary metabolism leading to polyphenol accumulation and preparation of stress resistance. <i>Plant Journal</i> , 2016 , 87, 318-32	6.9	39
161	Metabolomics in Plant Stress Physiology. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2018 , 164, 187-236	1.7	38
160	Proteomics of Heat-Stress and Ethylene-Mediated Thermotolerance Mechanisms in Tomato Pollen Grains. <i>Frontiers in Plant Science</i> , 2018 , 9, 1558	6.2	38
159	System-Level and Granger Network Analysis of Integrated Proteomic and Metabolomic Dynamics Identifies Key Points of Grape Berry Development at the Interface of Primary and Secondary Metabolism. <i>Frontiers in Plant Science</i> , 2017 , 8, 1066	6.2	37
158	Absolute quantification of Medicago truncatula sucrose synthase isoforms and N-metabolism enzymes in symbiotic root nodules and the detection of novel nodule phosphoproteins by mass spectrometry. <i>Journal of Experimental Botany</i> , 2008 , 59, 3307-15	7	37
157	A specialized bird pollination system with a bellows mechanism for pollen transfer and staminal food body rewards. <i>Current Biology</i> , 2014 , 24, 1615-1619	6.3	35
156	Bimodal dynamics of primary metabolism-related responses in tolerant potato-Potato virus Y interaction. <i>BMC Genomics</i> , 2015 , 16, 716	4.5	35

155	Quantitative in vivo phosphoproteomics reveals reversible signaling processes during nitrogen starvation and recovery in the biofuel model organism. <i>Biotechnology for Biofuels</i> , 2017 , 10, 280	7.8	34
154	ProMEX - a mass spectral reference database for plant proteomics. <i>Frontiers in Plant Science</i> , 2012 , 3, 125	6.2	34
153	An integrated strategy for identification and relative quantification of site-specific protein phosphorylation using liquid chromatography coupled to MS2/MS3. <i>Rapid Communications in Mass Spectrometry</i> , 2005 , 19, 3626-32	2.2	34
152	Primary Metabolism, Phenylpropanoids and Antioxidant Pathways Are Regulated in Potato as a Response to Potato virus Y Infection. <i>PLoS ONE</i> , 2016 , 11, e0146135	3.7	34
151	Altitudinal patterns of diversity and functional traits of metabolically active microorganisms in stream biofilms. <i>ISME Journal</i> , 2015 , 9, 2454-64	11.9	33
150	Comprehensive tissue-specific proteome analysis of drought stress responses in Pennisetum glaucum (L.) R. Br. (Pearl millet). <i>Journal of Proteomics</i> , 2016 , 143, 122-135	3.9	32
149	Field-omics-understanding large-scale molecular data from field crops. <i>Frontiers in Plant Science</i> , 2014 , 5, 286	6.2	32
148	Metabolism and development - integration of micro computed tomography data and metabolite profiling reveals metabolic reprogramming from floral initiation to silique development. <i>New Phytologist</i> , 2014 , 202, 322-335	9.8	32
147	Integrative profiling of metabolites and proteins: improving pattern recognition and biomarker selection for systems level approaches. <i>Methods in Molecular Biology</i> , 2007 , 358, 57-75	1.4	32
146	Vacuolar sucrose cleavage prevents limitation of cytosolic carbohydrate metabolism and stabilizes photosynthesis under abiotic stress. <i>FEBS Journal</i> , 2018 , 285, 4082-4098	5.7	32
145	Pollen proteomics: from stress physiology to developmental priming. <i>Plant Reproduction</i> , 2016 , 29, 119-32		31
144	Combined Metabolomic Analysis of Plasma and Urine Reveals AHBA, Tryptophan and Serotonin Metabolism as Potential Risk Factors in Gestational Diabetes Mellitus (GDM). <i>Frontiers in Molecular Biosciences</i> , 2017 , 4, 84	5.6	30
143	mzGroupAnalyzer--predicting pathways and novel chemical structures from untargeted high-throughput metabolomics data. <i>PLoS ONE</i> , 2014 , 9, e96188	3.7	30
142	An improved detergent-compatible gel-fractionation LC-LTQ-Orbitrap-MS workflow for plant and microbial proteomics. <i>Methods in Molecular Biology</i> , 2014 , 1072, 347-58	1.4	29
141	Integrated Physiological, Proteomic, and Metabolomic Analysis of Ultra Violet (UV) Stress Responses and Adaptation Mechanisms in. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 485-501	7.6	28
140	Proteomics survey of Solanaceae family: Current status and challenges ahead. <i>Journal of Proteomics</i> , 2017 , 169, 41-57	3.9	28
139	Plant protein phosphorylation monitored by capillary liquid chromatography--element mass spectrometry. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 355, 89-96	3.4	28
138	Metabolomic and Proteomic Profiles Reveal the Dynamics of Primary Metabolism during Seed Development of Lotus (<i>Nelumbo nucifera</i>). <i>Frontiers in Plant Science</i> , 2016 , 7, 750	6.2	28

137	A Benchtop Fractionation Procedure for Subcellular Analysis of the Plant Metabolome. <i>Frontiers in Plant Science</i> , 2016 , 7, 1912	6.2	28
136	Diurnal effects of anoxia on the metabolome of the seagrass <i>Zostera marina</i> . <i>Metabolomics</i> , 2015 , 11, 1208-1218	4.7	27
135	Heat-Treatment-Responsive Proteins in Different Developmental Stages of Tomato Pollen Detected by Targeted Mass Accuracy Precursor Alignment (tMAPA). <i>Journal of Proteome Research</i> , 2015 , 14, 4463-71	5.6	27
134	Redox state-dependent modulation of plant SnRK1 kinase activity differs from AMPK regulation in animals. <i>FEBS Letters</i> , 2017 , 591, 3625-3636	3.8	27
133	Solving the differential biochemical Jacobian from metabolomics covariance data. <i>PLoS ONE</i> , 2014 , 9, e92299	3.7	27
132	The parasitic mechanism of the holostemparasitic plant <i>Cuscuta</i> . <i>Journal of Plant Interactions</i> , 2011 , 6, 207-219	3.8	27
131	Myo-inositol oxygenase is important for the removal of excess myo-inositol from syncytia induced by <i>Heterodera schachtii</i> in <i>Arabidopsis</i> roots. <i>New Phytologist</i> , 2014 , 201, 476-485	9.8	26
130	MAPA distinguishes genotype-specific variability of highly similar regulatory protein isoforms in potato tuber. <i>Journal of Proteome Research</i> , 2011 , 10, 2979-91	5.6	26
129	Comparison between Proteome and Transcriptome Response in Potato (<i>Solanum tuberosum</i> L.) Leaves Following Potato Virus Y (PVY) Infection. <i>Proteomes</i> , 2017 , 5,	4.6	25
128	Pro- and Antioxidant Activity of Three Selected Flavan Type Flavonoids: Catechin, Eriodictyol and Taxifolin. <i>International Journal of Molecular Sciences</i> , 2016 , 17,	6.3	25
127	Quantitative Phosphoproteomic and System-Level Analysis of TOR Inhibition Unravel Distinct Organellar Acclimation in. <i>Frontiers in Plant Science</i> , 2018 , 9, 1590	6.2	25
126	Iron chelation and redox chemistry of anthranilic acid and 3-hydroxyanthranilic acid: A comparison of two structurally related kynurenine pathway metabolites to obtain improved insights into their potential role in neurological disease development. <i>Journal of Organometallic Chemistry</i> , 2015 , 782, 103-110	2.3	24
125	Time to articulate a vision for the future of plant proteomics - A global perspective: An initiative for establishing the International Plant Proteomics Organization (INPPO). <i>Proteomics</i> , 2011 , 11, 1559-68	4.8	24
124	Resolving subcellular plant metabolism. <i>Plant Journal</i> , 2019 , 100, 438-455	6.9	23
123	Mass Spectral Search and Analysis Using the Golm Metabolome Database 2013 , 321-343		23
122	The membrane proteome of male gametophyte in <i>Solanum lycopersicum</i> . <i>Journal of Proteomics</i> , 2016 , 131, 48-60	3.9	22
121	Using ProtMAX to create high-mass-accuracy precursor alignments from label-free quantitative mass spectrometry data generated in shotgun proteomics experiments. <i>Nature Protocols</i> , 2013 , 8, 595-601	18.8	22
120	Integrative molecular profiling indicates a central role of transitory starch breakdown in establishing a stable C/N homeostasis during cold acclimation in two natural accessions of <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2015 , 15, 284	5.3	22

119	Protein sumoylation and phosphorylation intersect in Arabidopsis signaling. <i>Plant Journal</i> , 2017 , 91, 505-517	6.1	21
118	Mathematical modeling reveals that metabolic feedback regulation of SnRK1 and hexokinase is sufficient to control sugar homeostasis from energy depletion to full recovery. <i>Frontiers in Plant Science</i> , 2014 , 5, 365	6.2	21
117	Metabolite changes with induction of Cuscuta haustorium and translocation from host plants. <i>Journal of Plant Interactions</i> , 2012 , 7, 84-93	3.8	21
116	Biological nitrification inhibition in the rhizosphere: determining interactions and impact on microbially mediated processes and potential applications. <i>FEMS Microbiology Reviews</i> , 2020 , 44, 874-908	15.1	21
115	Targeted quantitative analysis of a diurnal RuBisCO subunit expression and translation profile in Chlamydomonas reinhardtii introducing a novel Mass Western approach. <i>Journal of Proteomics</i> , 2015 , 113, 143-53	3.9	20
114	Induction and quantitative proteomic analysis of cell dedifferentiation during callus formation of lotus (Nelumbo nucifera Gaertn.spp. baijiantian). <i>Journal of Proteomics</i> , 2016 , 131, 61-70	3.9	19
113	Eco-Metabolomics and Metabolic Modeling: Making the Leap From Model Systems in the Lab to Native Populations in the Field. <i>Frontiers in Plant Science</i> , 2018 , 9, 1556	6.2	19
112	Adjustment of photosynthetic activity to drought and fluctuating light in wheat. <i>Plant, Cell and Environment</i> , 2020 , 43, 1484-1500	8.4	18
111	Cajanus cajan- a source of PPAR α activators leading to anti-inflammatory and cytotoxic effects. <i>Food and Function</i> , 2016 , 7, 3798-806	6.1	18
110	The High Light Response in Arabidopsis Requires the Calcium Sensor Protein CAS, a Target of STN7- and STN8-Mediated Phosphorylation. <i>Frontiers in Plant Science</i> , 2019 , 10, 974	6.2	17
109	Pepino mosaic virus infection of tomato affects allergen expression, but not the allergenic potential of fruits. <i>PLoS ONE</i> , 2013 , 8, e65116	3.7	17
108	Impact of arbuscular mycorrhizal fungi on the allergenic potential of tomato. <i>Mycorrhiza</i> , 2011 , 21, 341-349	3.9	17
107	Inverse Data-Driven Modeling and Multiomics Analysis Reveals Phgdh as a Metabolic Checkpoint of Macrophage Polarization and Proliferation. <i>Cell Reports</i> , 2020 , 30, 1542-1552.e7	10.6	17
106	Antioxidant Properties and the Formation of Iron Coordination Complexes of 8-Hydroxyquinoline. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	17
105	Proteometabolomic response of Deinococcus radiodurans exposed to UVC and vacuum conditions: Initial studies prior to the Tanpopo space mission. <i>PLoS ONE</i> , 2017 , 12, e0189381	3.7	16
104	Lichen secondary metabolites affect growth of Physcomitrella patens by allelopathy. <i>Protoplasma</i> , 2017 , 254, 1307-1315	3.4	16
103	Expression of root glutamate dehydrogenase genes in tobacco plants subjected to boron deprivation. <i>Plant Physiology and Biochemistry</i> , 2011 , 49, 1350-4	5.4	16
102	Physiological and Proteomic Signatures Reveal Mechanisms of Superior Drought Resilience in Pearl Millet Compared to Wheat. <i>Frontiers in Plant Science</i> , 2020 , 11, 600278	6.2	16

101	Glycolate Induces Redox Tuning Of Photosystem II in Vivo: Study of a Photorespiration Mutant. <i>Plant Physiology</i> , 2018 , 177, 1277-1285	6.6	16
100	Heat stress response mechanisms in pollen development. <i>New Phytologist</i> , 2021 , 231, 571-585	9.8	15
99	Systems biology for crop improvement. <i>Plant Genome</i> , 2021 , 14, e20098	4.4	15
98	Plastic and genetic responses of a common sedge to warming have contrasting effects on carbon cycle processes. <i>Ecology Letters</i> , 2019 , 22, 159-169	10	15
97	Fast-forward breeding for a food-secure world. <i>Trends in Genetics</i> , 2021 , 37, 1124-1136	8.5	15
96	The variations in the nuclear proteome reveal new transcription factors and mechanisms involved in UV stress response in <i>Pinus radiata</i> . <i>Journal of Proteomics</i> , 2016 , 143, 390-400	3.9	14
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