

# Justin W. Walley

## List of Publications by Year in descending order

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Version: 2024-02-01

48  
papers

3,400  
citations

218677

26  
h-index

197818

49  
g-index

67  
all docs

67  
docs citations

67  
times ranked

5432  
citing authors

#	ARTICLE	IF	CITATIONS
1	To the proteome and beyond: advances in single-cell omics profiling for plant systems. <i>Plant Physiology</i> , 2022, 188, 726-737.	4.8	31
2	SCT1-Specific Domain Mutations Impair Interactions with the Barley MLA6 Immune Receptor in Association with Loss of NLR Protein. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 274-289.	2.6	4
3	Integrated omics reveal novel functions and underlying mechanisms of the receptor kinase FERONIA in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2022, 34, 2594-2614.	6.6	18
4	<i>slim shady</i> is a novel allele of <i>PHYTOCHROME B</i> present in the Tâ€DNA line SALK_015201. <i>Plant Direct</i> , 2021, 5, e00326.	1.9	6
5	qTeller: a tool for comparative multi-genomic gene expression analysis. <i>Bioinformatics</i> , 2021, 38, 236-242.	4.1	15
6	The F-box E3 ubiquitin ligase BAF1 mediates the degradation of the brassinosteroid-activated transcription factor BES1 through selective autophagy in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2021, 33, 3532-3554.	6.6	27
7	Robotic Assay for Drought (RoAD): an automated phenotyping system for brassinosteroid and drought responses. <i>Plant Journal</i> , 2021, 107, 1837-1853.	5.7	4
8	Vision, challenges and opportunities for a Plant Cell Atlas. <i>ELife</i> , 2021, 10, .	6.0	31
9	Advances in functional proteomics to study plant-pathogen interactions. <i>Current Opinion in Plant Biology</i> , 2021, 63, 102061.	7.1	15
10	Integrated omics networks reveal the temporal signaling events of brassinosteroid response in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2021, 12, 5858.	12.8	54
11	Post-Synthetic Reduction of Pectin Methylesterification Causes Morphological Abnormalities and Alterations to Stress Response in <i>Arabidopsis thaliana</i> . <i>Plants</i> , 2020, 9, 1558.	3.5	10
12	Current status of the multinational <i>Arabidopsis</i> community. <i>Plant Direct</i> , 2020, 4, e00248.	1.9	13
13	Integrated multi-omics framework of the plant response to jasmonic acid. <i>Nature Plants</i> , 2020, 6, 290-302.	9.3	145
14	Quantitative Profiling of Protein Abundance and Phosphorylation State in Plant Tissues Using Tandem Mass Tags. <i>Methods in Molecular Biology</i> , 2020, 2139, 147-156.	0.9	13
15	Auxin Induces Widespread Proteome Remodeling in <i>Arabidopsis</i> Seedlings. <i>Proteomics</i> , 2019, 19, 1900199.	2.2	10
16	TurboID-based proximity labeling reveals that UBR7 is a regulator of N NLR immune receptor-mediated immunity. <i>Nature Communications</i> , 2019, 10, 3252.	12.8	159
17	<i>GSK</i> -like kinase <i>BIN</i> 2 phosphorylates <i>RD</i> 26 to potentiate drought signaling in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2019, 100, 923-937.	5.7	87
18	The Tomato Translational Landscape Revealed by Transcriptome Assembly and Ribosome Profiling. <i>Plant Physiology</i> , 2019, 181, 367-380.	4.8	66

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19	Receptor-Like Kinase Phosphorylation of Arabidopsis Heterotrimeric G-Protein $\alpha$ -Subunit AtGPA1. <i>Proteomics</i> , 2019, 19, e1900265.	2.2	8
20	Maize <i>defective kernel5</i> is a bacterial TamB homologue required for chloroplast envelope biogenesis. <i>Journal of Cell Biology</i> , 2019, 218, 2638-2658.	5.2	19
21	Directions for research and training in plant omics: Big Questions and Big Data. <i>Plant Direct</i> , 2019, 3, e00133.	1.9	47
22	Comparative Analysis of the Transcriptome and Proteome during Mouse Placental Development. <i>Journal of Proteome Research</i> , 2019, 18, 2088-2099.	3.7	21
23	Quantitative Early Auxin Root Proteomics Identifies GAUT10, a Galacturonosyltransferase, as a Novel Regulator of Root Meristem Maintenance. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1157-1170.	3.8	29
24	Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. <i>Plant Direct</i> , 2019, 3, e00109.	1.9	14
25	The Receptor-like Cytoplasmic Kinase BIK1 Localizes to the Nucleus and Regulates Defense Hormone Expression during Plant Innate Immunity. <i>Cell Host and Microbe</i> , 2018, 23, 485-497.e5.	11.0	92
26	Fungal-induced protein hyperacetylation in maize identified by acetylome profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 210-215.	7.1	71
27	Heterotrimeric G-Protein-Dependent Proteome and Phosphoproteome in Unstimulated Arabidopsis Roots. <i>Proteomics</i> , 2018, 18, e1800323.	2.2	26
28	FERONIA Receptor Kinase Contributes to Plant Immunity by Suppressing Jasmonic Acid Signaling in Arabidopsis thaliana. <i>Current Biology</i> , 2018, 28, 3316-3324.e6.	3.9	154
29	Assessment and Refinement of Sample Preparation Methods for Deep and Quantitative Plant Proteome Profiling. <i>Proteomics</i> , 2018, 18, e1800220.	2.2	37
30	Selective Autophagy of BES1 Mediated by DSK2 Balances Plant Growth and Survival. <i>Developmental Cell</i> , 2017, 41, 33-46.e7.	7.0	262
31	Sample Preparation Protocols for Protein Abundance, Acetylome, and Phosphoproteome Profiling of Plant Tissues. <i>Methods in Molecular Biology</i> , 2017, 1610, 123-133.	0.9	6
32	Dynamic Protein Acetylation in Plant-Pathogen Interactions. <i>Frontiers in Plant Science</i> , 2016, 7, 421.	3.6	33
33	Integration of omic networks in a developmental atlas of maize. <i>Science</i> , 2016, 353, 814-818.	12.6	411
34	Dual use of peptide mass spectra: Protein atlas and genome annotation. <i>Current Plant Biology</i> , 2015, 2, 21-24.	4.7	15
35	A High-Resolution Tissue-Specific Proteome and Phosphoproteome Atlas of Maize Primary Roots Reveals Functional Gradients along the Root Axes. <i>Plant Physiology</i> , 2015, 168, 233-246.	4.8	64
36	Plastid-produced interorgannellar stress signal MEcPP potentiates induction of the unfolded protein response in endoplasmic reticulum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6212-6217.	7.1	82

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37	An Automated Proteogenomic Method Uses Mass Spectrometry to Reveal Novel Genes in Zea mays. Molecular and Cellular Proteomics, 2014, 13, 157-167.	3.8	79
38	Fatty acids and early detection of pathogens. Current Opinion in Plant Biology, 2013, 16, 520-526.	7.1	137
39	Reconstruction of protein networks from an atlas of maize seed proteotypes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4808-17.	7.1	174
40	Molecular Mechanisms Regulating Rapid Stress Signaling Networks in Arabidopsis. Journal of Integrative Plant Biology, 2010, 52, 354-359.	8.5	73
41	Deficiencies in Jasmonate-Mediated Plant Defense Reveal Quantitative Variation in Botrytis cinerea Pathogenesis. PLoS Pathogens, 2010, 6, e1000861.	4.7	141
42	EXPOSURE TO ENVIRONMENTALLY RELEVANT LEVELS OF CADMIUM PRIMARILY IMPACTS TRANSPIRATION IN FIELD-GROWN SOYBEAN. Journal of Plant Nutrition, 2010, 33, 1519-1530.	1.9	10
43	Investigating the function of CAF1 deadenylases during plant stress responses. Plant Signaling and Behavior, 2010, 5, 802-805.	2.4	19
44	Arachidonic Acid: An Evolutionarily Conserved Signaling Molecule Modulates Plant Stress Signaling Networks. Plant Cell, 2010, 22, 3193-3205.	6.6	152
45	Arabidopsis Deadenylases AtCAF1a and AtCAF1b Play Overlapping and Distinct Roles in Mediating Environmental Stress Responses. Plant Physiology, 2010, 152, 866-875.	4.8	98
46	The Chromatin Remodeler SPLAYED Regulates Specific Stress Signaling Pathways. PLoS Pathogens, 2008, 4, e1000237.	4.7	129
47	Mechanical Stress Induces Biotic and Abiotic Stress Responses via a Novel cis-Element. PLoS Genetics, 2007, 3, e172.	3.5	205
48	Rice HYDROPEROXIDE LYASES with Unique Expression Patterns Generate Distinct Aldehyde Signatures in Arabidopsis. Plant Physiology, 2006, 141, 121-134.	4.8	61