Oliver Berkowitz

List of Publications by Year
in descending order

64 papers	3,208 citations	172457 29 h-index	168389 53 g-index
72 all docs	72 docs citations	72 times ranked	4337 citing authors

#	Article	IF	Citations
1	Root Architecture Responses: In Search of Phosphate. Plant Physiology, 2014, 166, 1713-1723.	4.8	214
2	A Metal-binding Member of the Late Embryogenesis Abundant Protein Family Transports Iron in the Phloem ofRicinus communis L.. Journal of Biological Chemistry, 2002, 277, 25062-25069.	3.4	209
3	The jasmonic acid signaling pathway is linked to auxin homeostasis through the modulation of <scp>YUCCA</scp>8 and <scp>YUCCA</scp>9 gene expression. Plant Journal, 2013, 74, 626-637.	5.7	178
4	Characterization of TCTP, the Translationally Controlled Tumor Protein, fromArabidopsis thalianaÂ. Plant Cell, 2009, 20, 3430-3447.	6.6	155
5	Plant perception of Î²-aminobutyric acid is mediated by an aspartyl-tRNA synthetase. Nature Chemical Biology, 2014, 10, 450-456.	8.0	128
6	Characterization and Expression Analysis of a Serine Acetyltransferase Gene Family Involved in a Key Step of the Sulfur Assimilation Pathway in Arabidopsis. Plant Physiology, 2005, 137, 220-230.	4.8	127
7	Genomic and functional characterization of the oas gene family encoding O-acetylserine (thiol) lyases, enzymes catalyzing the final step in cysteine biosynthesis in Arabidopsis thaliana. Gene, 2000, 253, 237-247.	2.2	125
8	Alternative Splicing Plays a Critical Role in Maintaining Mineral Nutrient Homeostasis in Rice (Oryza sativa). Plant Cell, 2018, 30, 2267-2285.	6.6	121
9	The cysteine synthase complex from plants. FEBS Journal, 2001, 268, 686-693.	0.2	106
10	Molecular and biochemical analysis of the enzymes of cysteine biosynthesis in the plant Arabidopsis thaliana. Amino Acids, 2002, 22, 245-257.	2.7	103
11	Use of Biomolecular Interaction Analysis to Elucidate the Regulatory Mechanism of the Cysteine Synthase Complex fromArabidopsis thaliana. Journal of Biological Chemistry, 2002, 277, 30629-30634.	3.4	97
12	Interaction between hormonal and mitochondrial signalling during growth, development and in plant defence responses. Plant, Cell and Environment, 2016, 39, 1127-1139.	5.7	79
13	Phosphite-induced changes of the transcriptome and secretome in Solanum tuberosum leading to resistance against Phytophthora infestans. BMC Plant Biology, 2014, 14, 254.	3.6	77
14	Phosphorus nutrition of phosphorus-sensitive Australian native plants: threats to plant communities in a global biodiversity hotspot. , 2013, 1, cot010-cot010.		76
15	Identification and characterisation of hypomethylated DNA loci controlling quantitative resistance in Arabidopsis. ELife, 2019, 8, .	6.0	73
16	ANAC017 Coordinates Organellar Functions and Stress Responses by Reprogramming Retrograde Signaling. Plant Physiology, 2019, 180, 634-653.	4.8	72
17	Differentiating phosphate-dependent and phosphate-independent systemic phosphate-starvation response networks in Arabidopsis thaliana through the application of phosphite. Journal of Experimental Botany, 2015, 66, 2501-2514.	4.8	63
18	Subcellular localization and tissue specific expression of amidase 1 from Arabidopsis thaliana. Planta, 2006, 224, 1241-1253.	3.2	60

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19	Applications of hyperspectral imaging in plant phenotyping. Trends in Plant Science, 2022, 27, 301-315.	8.8	60
20	Linking mitochondrial and chloroplast retrograde signalling in plants. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190410.	4.0	55
21	SPX4 Acts on PHR1-Dependent and -Independent Regulation of Shoot Phosphorus Status in Arabidopsis. Plant Physiology, 2019, 181, 332-352.	4.8	54
22	Mitochondrial signalling is critical for acclimation and adaptation to flooding in Arabidopsis thaliana. Plant Journal, 2020, 103, 227-247.	5.7	51
23	Stress responsive mitochondrial proteins in Arabidopsis thaliana. Free Radical Biology and Medicine, 2018, 122, 28-39.	2.9	50
24	RNA-Seq analysis identifies key genes associated with haustorial development in the root hemiparasite Santalum album. Frontiers in Plant Science, 2015, 6, 661.	3.6	49
25	The Transcription Factor MYB29 Is a Regulator of ALTERNATIVE OXIDASE1a. Plant Physiology, 2017, 173, 1824-1843.	4.8	46
26	Stepwise Evolution of a Buried Inhibitor Peptide over 45 My. Molecular Biology and Evolution, 2017, 34, 1505-1516.	8.9	45
27	RNA-seq analysis identifies an intricate regulatory network controlling cluster root development in white lupin. BMC Genomics, 2014, 15, 230.	2.8	43
28	Acclimation responses of Arabidopsis thaliana to sustained phosphite treatments. Journal of Experimental Botany, 2013, 64, 1731-1743.	4.8	42
29	Direct comparison of Arabidopsis gene expression reveals different responses to melatonin versus auxin. BMC Plant Biology, 2019, 19, 567.	3.6	37
30	A family of small, cyclic peptides buried in preproalbumin since the Eocene epoch. Plant Direct, 2018, 2, e00042.	1.9	32
31	Mitochondrial function modulates touch signalling in Arabidopsis thaliana. Plant Journal, 2019, 97, 623-645.	5.7	32
32	Biochemical Characterization of Two Wheat Phosphoethanolamine N-Methyltransferase Isoforms with Different Sensitivities to Inhibition by Phosphatidic Acid. Journal of Biological Chemistry, 2009, 284, 31962-31971.	3.4	31
33	RNAâ€seq analysis of laser microdissected Arabidopsis thaliana leaf epidermis, mesophyll and vasculature defines tissueâ€specific transcriptional responses to multiple stress treatments. Plant Journal, 2021, 107, 938-955.	5.7	31
34	Inactivation of Mitochondrial Complex I Induces the Expression of a Twin Cysteine Protein that Targets and Affects Cytosolic, Chloroplastidic and Mitochondrial Function. Molecular Plant, 2016, 9, 696-710.	8.3	28
35	Isolation of tissues and preservation of <scp>RNA</scp> from intact, germinated barley grain. Plant Journal, 2017, 91, 754-765.	5.7	28
36	Plant-Specific Preprotein and Amino Acid Transporter Proteins Are Required for tRNA Import into Mitochondria. Plant Physiology, 2016, 172, 2471-2490.	4.8	27

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37	Extracellular Vesicles from Fusarium graminearum Contain Protein Effectors Expressed during Infection of Corn. Journal of Fungi (Basel, Switzerland), 2021, 7, 977.	3.5	26
38	Next generation sequencing and de novo transcriptomics to study gene evolution. Plant Methods, 2014, 10, 34.	4.3	23
39	Molecular and physiological responses during thermal acclimation of leaf photosynthesis and respiration in rice. Plant, Cell and Environment, 2020, 43, 594-610.	5.7	23
40	Magnetic quantitative reverse transcription PCR: A high-throughput method for mRNA extraction and quantitative reverse transcription PCR. BioTechniques, 2007, 43, 206-211.	1.8	20
41	NMT1 and NMT3 N-Methyltransferase Activity Is Critical to Lipid Homeostasis, Morphogenesis, and Reproduction. Plant Physiology, 2018, 177, 1605-1628.	4.8	20
42	Characterization of a novel Î²-barrel protein (AtOM47) from the mitochondrial outer membrane ofArabidopsis thaliana. Journal of Experimental Botany, 2016, 67, 6061-6075.	4.8	19
43	Arabidopsis DGD1 SUPPRESSOR1 Is a Subunit of the Mitochondrial Contact Site and Cristae Organizing System and Affects Mitochondrial Biogenesis. Plant Cell, 2019, 31, 1856-1878.	6.6	19
44	Noninvasive imaging technologies in plant phenotyping. Trends in Plant Science, 2022, 27, 316-317.	8.8	19
45	Evidence for Ancient Origins of Bowman-Birk Inhibitors from Selaginella moellendorffii. Plant Cell, 2017, 29, 461-473.	6.6	18
46	Accumulation of endogenous peptides triggers a pathogen stress response in Arabidopsis thaliana. Plant Journal, 2018, 96, 705-715.	5.7	18
47	Temporal tissueâ€specific regulation of transcriptomes during barley (Hordeum vulgare) seed germination. Plant Journal, 2020, 101, 700-715.	5.7	18
48	An Ancient Peptide Family Buried within Vicilin Precursors. ACS Chemical Biology, 2019, 14, 979-993.	3.4	17
49	Transcriptional and biochemical analyses of gibberellin expression and content in germinated barley grain. Journal of Experimental Botany, 2020, 71, 1870-1884.	4.8	17
50	Root Cell-Specific Regulators of Phosphate-Dependent Growth. Plant Physiology, 2017, 174, 1969-1989.	4.8	15
51	The retrograde signaling regulator ANAC017 recruits the MKK9â€“MPK3/6, ethylene, and auxin signaling pathways to balance mitochondrial dysfunction with growth. Plant Cell, 2022, 34, 3460-3481.	6.6	15
52	An enzymatic fluorescent assay for the quantification of phosphite in a microtiter plate format. Analytical Biochemistry, 2011, 412, 74-78.	2.4	14
53	GWAS on multiple traits identifies mitochondrial ACONITASE3 as important for acclimation to submergence stress. Plant Physiology, 2022, 188, 2039-2058.	4.8	13
54	Enhanced reactive oxygen detoxification occurs in saltâ€stressed soybean roots expressing <scp>GmSALT3</scp>. Physiologia Plantarum, 2022, 174, e13709.	5.2	13

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55	Genes That Mediate Starch Metabolism in Developing and Germinated Barley Grain. Frontiers in Plant Science, 2021, 12, 641325.	3.6	12
56	The genetic origin of evolidine, the first cyclopeptide discovered in plants, and related orbitides. Journal of Biological Chemistry, 2020, 295, 14510-14521.	3.4	11
57	Cross-species transcriptomic analyses reveals common and opposite responses in Arabidopsis, rice and barley following oxidative stress and hormone treatment. BMC Plant Biology, 2022, 22, 62.	3.6	11
58	Cyclic Peptides in Seed of Annona muricata Are Ribosomally Synthesized. Journal of Natural Products, 2020, 83, 1167-1173.	3.0	9
59	Knockdown of Succinate Dehydrogenase Assembly Factor 2 Induces Reactive Oxygen Speciesâ€“Mediated Auxin Hypersensitivity Causing pH-Dependent Root Elongation. Plant and Cell Physiology, 2021, 62, 1185-1198.	3.1	9
60	The mitochondrial AAA protease FTSH3 regulates Complex I abundance by promoting its disassembly. Plant Physiology, 2021, 186, 599-610.	4.8	8
61	Conserved and Opposite Transcriptome Patterns during Germination in Hordeum vulgare and Arabidopsis thaliana. International Journal of Molecular Sciences, 2020, 21, 7404.	4.1	6
62	Transcriptional variation is associated with differences in shoot sodium accumulation in distinct barley varieties. Environmental and Experimental Botany, 2019, 166, 103812.	4.2	5
63	Laser-Capture Microdissection RNA-Sequencing for Spatial and Temporal Tissue-Specific Gene Expression Analysis in Plants. Journal of Visualized Experiments, 2020, , .	0.3	3
64	scCloudMine: A cloud-based app for visualization, comparison, and exploration of single-cell transcriptomic data. Plant Communications, 2022, 3, 100302.	7.7	2