Owen A Hoekenga

List of Publications by Year in descending order

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OWEN A HOEKENCA

#	Article	IF	CITATIONS
1	HOW DO CROP PLANTS TOLERATE ACID SOILS? MECHANISMS OF ALUMINUM TOLERANCE AND PHOSPHOROUS EFFICIENCY. Annual Review of Plant Biology, 2004, 55, 459-493.	8.6	1,460
2	A gene in the multidrug and toxic compound extrusion (MATE) family confers aluminum tolerance in sorghum. Nature Genetics, 2007, 39, 1156-1161.	9.4	665
3	The Physiology, Genetics and Molecular Biology of Plant Aluminum Resistance and Toxicity. Plant and Soil, 2005, 274, 175-195.	1.8	597
4	AtALMT1, which encodes a malate transporter, is identified as one of several genes critical for aluminum tolerance in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 9738-9743.	3.3	509
5	Characterization of <i>AtALMT1</i> Expression in Aluminum-Inducible Malate Release and Its Role for Rhizotoxic Stress Tolerance in Arabidopsis. Plant Physiology, 2007, 145, 843-852.	2.3	184
6	Weighted Correlation Network Analysis (WGCNA) Applied to the Tomato Fruit Metabolome. PLoS ONE, 2011, 6, e26683.	1.1	168
7	Identification and Characterization of Aluminum Tolerance Loci in Arabidopsis (Landsberg erecta ×) Tj ETQq1 Z Plant Physiology, 2003, 132, 936-948.	1 0.784314 2.3	ł rgBT /Overla 147
8	Integrating Coexpression Networks with GWAS to Prioritize Causal Genes in Maize. Plant Cell, 2018, 30, 2922-2942.	3.1	137
9	Association and Linkage Analysis of Aluminum Tolerance Genes in Maize. PLoS ONE, 2010, 5, e9958.	1.1	91
10	Natural Genetic Variation in Selected Populations of Arabidopsis thaliana Is Associated with Ionomic Differences. PLoS ONE, 2010, 5, e11081.	1.1	78
11	Genetic and Physiological Analysis of Iron Biofortification in Maize Kernels. PLoS ONE, 2011, 6, e20429.	1.1	77
12	Mechanisms of metal resistance in plants: aluminum and heavy metals. Plant and Soil, 2002, 247, 109-119.	1.8	66
13	The physiology, genetics and molecular biology of plant aluminum resistance and toxicity. Plant Ecophysiology, 2005, , 175-195.	1.5	65
14	Ionomic Characterization of Maize Kernels in the Intermated B73 × Mo17 Population. Crop Science, 2013, 53, 208-220.	0.8	65
15	Single-Kernel Ionomic Profiles Are Highly Heritable Indicators of Genetic and Environmental Influences on Elemental Accumulation in Maize Grain (Zea mays). PLoS ONE, 2014, 9, e87628.	1.1	64
16	Joint genetic and network analyses identify loci associated with root growth under NaCl stress in <i>Arabidopsis thaliana</i> . Plant, Cell and Environment, 2016, 39, 918-934.	2.8	53
17	NLR locus-mediated trade-off between abiotic and biotic stress adaptation in Arabidopsis. Nature Plants, 2017, 3, 17072.	4.7	53
18	Physiological and Genetic Characterization of End-of-Day Far-Red Light Response in Maize Seedlings Â. Plant Physiology, 2010, 154, 173-186.	2.3	47

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19	Developmental Patterns of Chromatin Structure and DNA Methylation Responsible for Epigenetic Expression of a Maize Regulatory Gene. Genetics, 2000, 155, 1889-1902.	1.2	45
20	Multivariate Genome-Wide Association Analyses Reveal the Genetic Basis of Seed Fatty Acid Composition in Oat (<i>Avena sativa</i> L.). G3: Genes, Genomes, Genetics, 2019, 9, 2963-2975.	0.8	44
21	The Interaction of Genotype and Environment Determines Variation in the Maize Kernel Ionome. G3: Genes, Genomes, Genetics, 2016, 6, 4175-4183.	0.8	41
22	A method for cellular localization of gene expression via quantitative in situ hybridization in plants. Plant Journal, 2007, 50, 159-187.	2.8	40
23	Using metabolomics to estimate unintended effects in transgenic crop plants: problems, promises, and opportunities. Journal of Biomolecular Techniques, 2008, 19, 159-66.	0.8	29
24	Iron biofortification of maize grain. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 327-329.	0.4	20
25	Multi-omics prediction of oat agronomic and seed nutritional traits across environments and in distantly related populations. Theoretical and Applied Genetics, 2021, 134, 4043-4054.	1.8	20
26	Heritable temporal gene expression patterns correlate with metabolomic seed content in developing hexaploid oat seed. Plant Biotechnology Journal, 2020, 18, 1211-1222.	4.1	19
27	Genome-Wide Association Study and Genomic Prediction Elucidate the Distinct Genetic Architecture of Aluminum and Proton Tolerance in Arabidopsis thaliana. Frontiers in Plant Science, 2020, 11, 405.	1.7	18
28	Leveraging Non-Targeted Metabolite Profiling via Statistical Genomics. PLoS ONE, 2013, 8, e57667.	1.1	17
29	Compositional Analysis of Genetically Modified (GM) Crops: Key Issues and Future Needs. Journal of Agricultural and Food Chemistry, 2013, 61, 8248-8253.	2.4	11
30	Genetic analysis of potato tuber metabolite composition: Genomeâ€wide association studies applied to a nontargeted metabolome. Crop Science, 2021, 61, 591-603.	0.8	9
31	Genomics of Mineral Nutrient Biofortification: Calcium, Iron and Zinc. , 2014, , 431-454.		9
32	Mechanisms of Aluminum Tolerance. , 2011, , 133-153.		8
33	An Assessment of the Relative Influences of Genetic Background, Functional Diversity at Major Regulatory Genes, and Transgenic Constructs on the Tomato Fruit Metabolome. Plant Genome, 2014, 7, plantgenome2013.06.0021.	1.6	5
34	Mass spectrometry-based analytical developments to link iron speciation to iron bioavailability in maize. Food Chemistry, 2019, 294, 414-422.	4.2	3
35	Chromatographic Methods to Evaluate Nutritional Quality in Oat. Methods in Molecular Biology, 2017, 1536, 115-125.	0.4	3

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#	Article	IF	CITATIONS
37	Iron bioavailability from maizeâ€based diets fed to iron deficient broiler chickens. FASEB Journal, 2010, 24, 208.8.	0.2	1
38	Biofortified maize (Zea mays L.) provides more bioavailable iron than standard maize: Studies in poultry (Gallus gallus) and an in vitro digestion/Cacoâ€2 model. FASEB Journal, 2012, 26, 1019.1.	0.2	0