Owen A Hoekenga

List of Publications by Year
in descending order

38 papers	4,933 citations	257450 24 h-index	345221 36 g-index
45 all docs	45 docs citations	45 times ranked	4789 citing authors

#	Article	IF	Citations
1	Genetic analysis of potato tuber metabolite composition: Genome-wide association studies applied to a nontargeted metabolome. Crop Science, 2021, 61, 591-603.	1.8	9
2	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.	3.6	20
3	Heritable temporal gene expression patterns correlate with metabolomic seed content in developing hexaploid oat seed. Plant Biotechnology Journal, 2020, 18, 1211-1222.	8.3	19
4	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.	3.6	18
5	Mass spectrometry-based analytical developments to link iron speciation to iron bioavailability in maize. Food Chemistry, 2019, 294, 414-422.	8.2	3
6	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.	1.8	44
7	Integrating Coexpression Networks with GWAS to Prioritize Causal Genes in Maize. Plant Cell, 2018, 30, 2922-2942.	6.6	137
8	NLR locus-mediated trade-off between abiotic and biotic stress adaptation in Arabidopsis. Nature Plants, 2017, 3, 17072.	9.3	53
9	Chromatographic Methods to Evaluate Nutritional Quality in Oat. Methods in Molecular Biology, 2017, 1536, 115-125.	0.9	3
10	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.	5.7	53
11	The Interaction of Genotype and Environment Determines Variation in the Maize Kernel Ionome. G3: Genes, Genomes, Genetics, 2016, 6, 4175-4183.	1.8	41
12	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.	2.8	5
13	Genomics of Mineral Nutrient Biofortification: Calcium, Iron and Zinc. , 2014, , 431-454.		9
14	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.	2.5	64
15	Compositional Analysis of Genetically Modified (GM) Crops: Key Issues and Future Needs. Journal of Agricultural and Food Chemistry, 2013, 61, 8248-8253.	5.2	11
16	Ionomic Characterization of Maize Kernels in the Intermated B73 Ã— Mo17 Population. Crop Science, 2013, 53, 208-220.	1.8	65
17	Leveraging Non-Targeted Metabolite Profiling via Statistical Genomics. PLoS ONE, 2013, 8, e57667.	2.5	17
18	Biofortified maize (Zea mays L.) provides more bioavailable iron than standard maize: Studies in poultry (Gallus gallus) and an in vitro digestion/Caco-2 model. FASEB Journal, 2012, 26, 1019.1.	0.5	0

#	Article	IF	Citations
19	Genetic and Physiological Analysis of Iron Biofortification in Maize Kernels. PLoS ONE, 2011, 6, e20429.	2.5	77
20	Mechanisms of Aluminum Tolerance. , 2011, , 133-153.		8
21	Iron biofortification of maize grain. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 327-329.	0.8	20
22	Weighted Correlation Network Analysis (WGCNA) Applied to the Tomato Fruit Metabolome. PLoS ONE, 2011, 6, e26683.	2.5	168
23	Association and Linkage Analysis of Aluminum Tolerance Genes in Maize. PLoS ONE, 2010, 5, e9958.	2.5	91
24	Physiological and Genetic Characterization of End-of-Day Far-Red Light Response in Maize Seedlings Â Â. Plant Physiology, 2010, 154, 173-186.	4.8	47
25	Natural Genetic Variation in Selected Populations of Arabidopsis thaliana Is Associated with Ionomic Differences. PLoS ONE, 2010, 5, e11081.	2.5	78
26	Iron bioavailability from maizeâ€based diets fed to iron deficient broiler chickens. FASEB Journal, 2010, 24, 208.8.	0.5	1
27	Maize Al Tolerance. , 2009, , 367-380.		2
28	Using metabolomics to estimate unintended effects in transgenic crop plants: problems, promises, and opportunities. Journal of Biomolecular Techniques, 2008, 19, 159-66.	1.5	29
29	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.	4.8	184
30	A gene in the multidrug and toxic compound extrusion (MATE) family confers aluminum tolerance in sorghum. Nature Genetics, 2007, 39, 1156-1161.	21.4	665
31	A method for cellular localization of gene expression via quantitative in situ hybridization in plants. Plant Journal, 2007, 50, 159-187.	5.7	40
32	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.	7.1	509
33	The Physiology, Genetics and Molecular Biology of Plant Aluminum Resistance and Toxicity. Plant and Soil, 2005, 274, 175-195.	3.7	597
34	The physiology, genetics and molecular biology of plant aluminum resistance and toxicity. Plant Ecophysiology, 2005, , 175-195.	1.5	65
35	HOW DO CROP PLANTS TOLERATE ACID SOILS? MECHANISMS OF ALUMINUM TOLERANCE AND PHOSPHOROUS EFFICIENCY. Annual Review of Plant Biology, 2004, 55, 459-493.	18.7	1,460
36	Identification and Characterization of Aluminum Tolerance Loci in Arabidopsis (Landsberg erecta Ã—) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Plant Physiology, 2003, 132, 936-948.	4.8	147

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37	Mechanisms of metal resistance in plants: aluminum and heavy metals. Plant and Soil, 2002, 247, 109-119.	3.7	66
38	Developmental Patterns of Chromatin Structure and DNA Methylation Responsible for Epigenetic Expression of a Maize Regulatory Gene. Genetics, 2000, 155, 1889-1902.	2.9	45