Aaron J Lorenz

List of Publications by Year
in descending order

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63	4,551	186265	123424
papers	citations	28 h-index	61 g-index

70	70	70	4316
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomic selection in plant breeding: from theory to practice. Briefings in Functional Genomics, 2010, 9, 166-177.	2.7	996
2	Plant Breeding with Genomic Selection: Gain per Unit Time and Cost. Crop Science, 2010, 50, 1681-1690.	1.8	547
3	Genomic Selection in Plant Breeding. Advances in Agronomy, 2011, 110, 77-123.	5.2	395
4	Genotyping by sequencing for genomic prediction in a soybean breeding population. BMC Genomics, 2014, 15, 740.	2.8	191
5	A Population Structure and Genomeâ€Wide Association Analysis on the USDA Soybean Germplasm Collection. Plant Genome, 2015, 8, eplantgenome2015.04.0024.	2.8	174
6	Association mapping and geneâ€“gene interaction for stem rust resistance in CIMMYT spring wheat germplasm. Theoretical and Applied Genetics, 2011, 123, 1257-1268.	3.6	158
7	Adding Genetically Distant Individuals to Training Populations Reduces Genomic Prediction Accuracy in Barley. Crop Science, 2015, 55, 2657-2667.	1.8	150
8	Genome-Enabled Prediction Models for Yield Related Traits in Chickpea. Frontiers in Plant Science, 2016, 7, 1666.	3.6	127
9	Allelic variants of OsHKT1;1 underlie the divergence between indica and japonica subspecies of rice (Oryza sativa) for root sodium content. PLoS Genetics, 2017, 13, e1006823.	3.5	118
10	Performance of Single Nucleotide Polymorphisms versus Haplotypes for Genome-Wide Association Analysis in Barley. PLoS ONE, 2010, 5, e14079.	2.5	118
11	Resource Allocation for Maximizing Prediction Accuracy and Genetic Gain of Genomic Selection in Plant Breeding: A Simulation Experiment. G3: Genes, Genomes, Genetics, 2013, 3, 481-491.	1.8	114
12	Genomic Prediction of Single Crosses in the Early Stages of a Maize Hybrid Breeding Pipeline. G3: Genes, Genomes, Genetics, 2016, 6, 3443-3453.	1.8	107
13	The effect of artificial selection on phenotypic plasticity in maize. Nature Communications, 2017, 8, 1348.	12.8	105
14	Prospects of Genomic Prediction in the USDA Soybean Germplasm Collection: Historical Data Creates Robust Models for Enhancing Selection of Accessions. G3: Genes, Genomes, Genetics, 2016, 6, 2329-2341.	1.8	90
15	On crop height estimation with UAVs. , 2014, , .		89
16	Genome-Wide Analysis of Grain Yield Stability and Environmental Interactions in a Multiparental Soybean Population. G3: Genes, Genomes, Genetics, 2018, 8, 519-529.	1.8	75
17	Genomic Selection in Preliminary Yield Trials in a Winter Wheat Breeding Program. G3: Genes, Genomes, Genetics, 2018, 8, 2735-2747.	1.8	74
18	The importance of dominance and genotype-by-environment interactions on grain yield variation in a large-scale public cooperative maize experiment. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	52

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19	Genetic variation in seminal and nodal root angle and their association with grain yield of maize under water-stressed field conditions. Plant and Soil, 2015, 397, 213-225.	3.7	50
20	Correlating detergent fiber analysis and dietary fiber analysis data for corn stover collected by NIRS. Cellulose, 2009, 16, 577-585.	4.9	44
21	Evaluating Methods of Updating Training Data in Long-Term Genomewide Selection. G3: Genes, Genomes, Genetics, 2017, 7, 1499-1510.	1.8	44
22	Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. Frontiers in Genetics, 2020, 11, 592769.	2.3	44
23	Quantitative Determination of Phytate and Inorganic Phosphorus for Maize Breeding. Crop Science, 2007, 47, 600-604.	1.8	39
24	Maize genomes to fields (G2F): 2014â€“2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. BMC Research Notes, 2020, 13, 71.	1.4	38
25	Dissecting the Genetic Basis of Local Adaptation in Soybean. Scientific Reports, 2017, 7, 17195.	3.3	37
26	Genomeâ€wide Association Mapping of Qualitatively Inherited Traits in a Germplasm Collection. Plant Genome, 2017, 10, plantgenome2016.06.0054.	2.8	37
27	Leveraging genomic prediction to scan germplasm collection for crop improvement. PLoS ONE, 2017, 12, e0179191.	2.5	35
28	Dominance Effects and Functional Enrichments Improve Prediction of Agronomic Traits in Hybrid Maize. Genetics, 2020, 215, 215-230.	2.9	35
29	Multi-trait Improvement by Predicting Genetic Correlations in Breeding Crosses. G3: Genes, Genomes, Genetics, 2019, 9, 3153-3165.	1.8	34
30	Greenhouse screening of maize genotypes for deep root mass and related root traits and their association with grain yield under water-deficit conditions in the field. Euphytica, 2016, 207, 79-94.	1.2	30
31	Genomeâ€Wide Association Mapping of Hostâ€Plant Resistance to Soybean Aphid. Plant Genome, 2018, 11, 180011.	2.8	29
32	Genome-wide association study and genomic selection for tolerance of soybean biomass to soybean cyst nematode infestation. PLoS ONE, 2020, 15, e0235089.	2.5	28
33	Cell Wall Composition and Ruminant Digestibility of Various Maize Tissues Across Development. Bioenergy Research, 2010, 3, 28-37.	3.9	24
34	Genetic Variation and Breeding Potential of Phytate and Inorganic Phosphorus in a Maize Population. Crop Science, 2008, 48, 79-84.	1.8	22
35	Soybean iron deficiency chlorosis high-throughput phenotyping using an unmanned aircraft system. Plant Methods, 2019, 15, 97.	4.3	21
36	Relative utility of agronomic, phenological, and morphological traits for assessing genotypeâ€byâ€environment interaction in maize inbreds. Crop Science, 2020, 60, 62-81.	1.8	21

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37	The phylogenetic relationships of US maize germplasm. Nature Genetics, 2013, 45, 844-845.	21.4	19
38	Training Population Design and Resource Allocation for Genomic Selection in Plant Breeding. , 2017, , 7-22.		17
39	Plant Breeding for Intercropping in Temperate Field Crop Systems: A Review. Frontiers in Plant Science, 2022, 13, 843065.	3.6	17
40	Iron deficiency in soybean. Crop Science, 2022, 62, 36-52.	1.8	16
41	Environmental Reviews and Case Studies: Bringing Unmanned Aerial Systems Closer to the Environment. Environmental Practice, 2015, 17, 188-200.	0.3	15
42	Belowground microbial communities respond to water deficit and are shaped by decades of maize hybrid breeding. Environmental Microbiology, 2020, 22, 889-904.	3.8	15
43	Identification and Fineâ€Mapping of a Soybean Quantitative Trait Locus on Chromosome 5 Conferring Tolerance to Iron Deficiency Chlorosis. Plant Genome, 2019, 12, 190007.	2.8	14
44	The utility of genomic prediction models in evolutionary genetics. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20210693.	2.6	13
45	Optimization of training sets for genomic prediction of early-stage single crosses in maize. Theoretical and Applied Genetics, 2021, 134, 687-699.	3.6	13
46	Implementation of genomic selection in public-sector plant breeding programs: Current status and opportunities. Crop Breeding and Applied Biotechnology, 2021, 21, .	0.4	13
47	Mapping Quantitative Trait Loci for Resistance to Goss's Bacterial Wilt and Leaf Blight in North American Maize by Joint Linkage Analysis. Crop Science, 2016, 56, 2306-2313.	1.8	12
48	Response Surface Analysis of Genomic Prediction Accuracy Values Using Quality Control Covariates in Soybean. Evolutionary Bioinformatics, 2019, 15, 117693431983130.	1.2	12
49	Optimization of temporal UASâ€based imagery analysis to estimate plant maturity date for soybean breeding. The Plant Phenome Journal, 2021, 4, e20018.	2.0	11
50	Evaluation of Nonparametric Models for Genomic Prediction of Earlyâ€Stage Single Crosses in Maize. Crop Science, 2019, 59, 1411-1423.	1.8	9
51	Tx741, Tx777, Tx779, Tx780, and Tx782 Inbred Maize Lines for Yield and Southern United States Stress Adaptation. Journal of Plant Registrations, 2019, 13, 258-269.	0.5	9
52	Selection for Silage Yield and Composition Did Not Affect Genomic Diversity Within the Wisconsin Quality Synthetic Maize Population. G3: Genes, Genomes, Genetics, 2015, 5, 541-549.	1.8	8
53	Environmental Stability Study of Soybeans with Modified Carbohydrate Profiles in Maturity Groups 0 to V. Crop Science, 2019, 59, 1531-1543.	1.8	8
54	Genome-Wide Association and Gene Co-expression Network Analyses Reveal Complex Genetics of Resistance to Gossâ€™s Wilt of Maize. G3: Genes, Genomes, Genetics, 2019, 9, 3139-3152.	1.8	6

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55	Genomic Dissection of Nonhost Resistance to Wheat Stem Rust in Brachypodium distachyon. Molecular Plant-Microbe Interactions, 2019, 32, 392-400.	2.6	4
56	Registration of â€˜NE10589â€™ (Husker Genetics Brand Ruth) hard red winter wheat. Journal of Plant Registrations, 2020, 14, 388-397.	0.5	4
57	Variation in Soybean Aphid (Hemiptera: Aphididae) Biotypes Within Fields. Journal of Economic Entomology, 2021, 114, 1336-1344.	1.8	4
58	Development of a controlled-environment assay to induce iron deficiency chlorosis in soybean by adjusting calcium carbonates, pH, and nodulation. Plant Methods, 2022, 18, 36.	4.3	4
59	Candidate Genes Modulating Reproductive Timing in Elite US Soybean Lines Identified in Soybean Alleles of Arabidopsis Flowering Orthologs With Divergent Latitude Distribution. Frontiers in Plant Science, 2022, 13, 889066.	3.6	4
60	Changes in Dynamic Leaf Traits in Maize Associated with Year of Hybrid Release. Crop Science, 2018, 58, 551-563.	1.8	3
61	Mining Fiskeby III and Mandarin (Ottawa) Expression Profiles to Understand Iron Stress Tolerant Responses in Soybean. International Journal of Molecular Sciences, 2021, 22, 11032.	4.1	3
62	Characterizing introgression-by-environment interactions using maize near isogenic lines. Theoretical and Applied Genetics, 2020, 133, 2761-2773.	3.6	2
63	Registration of M10â€207102 soybean germplasm: A highâ€yielding, earlyâ€maturity line with elevated protein. Journal of Plant Registrations, 2022, 16, 132-136.	0.5	2