

Alexander E Lipka

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

5,913
citations

186265

28
h-index

85541

71
g-index

82
all docs

82
docs citations

82
times ranked

6966
citing authors

#	ARTICLE	IF	CITATIONS
1	GAPIT: genome association and prediction integrated tool. <i>Bioinformatics</i> , 2012, 28, 2397-2399.	4.1	2,016
2	Switchgrass Genomic Diversity, Ploidy, and Evolution: Novel Insights from a Network-Based SNP Discovery Protocol. <i>PLoS Genetics</i> , 2013, 9, e1003215.	3.5	608
3	Natural Variation in Maize Aphid Resistance Is Associated with 2,4-Dihydroxy-7-Methoxy-1,4-Benzoxazin-3-One Glucoside Methyltransferase Activity. <i>Plant Cell</i> , 2013, 25, 2341-2355.	6.6	251
4	CAROTENOID CLEAVAGE DIOXYGENASE4 Is a Negative Regulator of Î²-Carotene Content in <i>Arabidopsis</i> Seeds. <i>Plant Cell</i> , 2014, 25, 4812-4826.	6.6	180
5	A Foundation for Provitamin A Biofortification of Maize: Genome-Wide Association and Genomic Prediction Models of Carotenoid Levels. <i>Genetics</i> , 2014, 198, 1699-1716.	2.9	180
6	From association to prediction: statistical methods for the dissection and selection of complex traits in plants. <i>Current Opinion in Plant Biology</i> , 2015, 24, 110-118.	7.1	166
7	Genome-Wide Association Study and Pathway-Level Analysis of Tocochromanol Levels in Maize Grain. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1287-1299.	1.8	152
8	Genomic Selection for Predicting <i>Fusarium</i> Head Blight Resistance in a Wheat Breeding Program. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.01.0003.	2.8	145
9	Single-cell RNA sequencing of developing maize ears facilitates functional analysis and trait candidate gene discovery. <i>Developmental Cell</i> , 2021, 56, 557-568.e6.	7.0	129
10	Genome-Wide Analysis of Branched-Chain Amino Acid Levels in <i>Arabidopsis</i> Seeds. <i>Plant Cell</i> , 2014, 25, 4827-4843.	6.6	121
11	Lessons from Dwarf8 on the Strengths and Weaknesses of Structured Association Mapping. <i>PLoS Genetics</i> , 2013, 9, e1003246.	3.5	115
12	Genomic Prediction of Single Crosses in the Early Stages of a Maize Hybrid Breeding Pipeline. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3443-3453.	1.8	107
13	Characterization of Biosynthetic Pathways for the Production of the Volatile Homoterpenes DMNT and TMTT in <i>Zea mays</i> . <i>Plant Cell</i> , 2016, 28, 2651-2665.	6.6	105
14	Genetic Architecture of Soybean Yield and Agronomic Traits. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3367-3375.	1.8	98
15	Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. <i>Plant Cell</i> , 2017, 29, 2374-2392.	6.6	93
16	Characterization of Disease Resistance Loci in the USDA Soybean Germplasm Collection Using Genome-Wide Association Studies. <i>Phytopathology</i> , 2016, 106, 1139-1151.	2.2	91
17	Evaluation of RR-BLUP Genomic Selection Models that Incorporate Peak Genome-Wide Association Study Signals in Maize and Sorghum. <i>Plant Genome</i> , 2019, 12, 180052.	2.8	89
18	polyRAD: Genotype Calling with Uncertainty from Sequencing Data in Polyploids and Diploids. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 663-673.	1.8	76

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19	Genetic Analysis of Visually Scored Orange Kernel Color in Maize. <i>Crop Science</i> , 2013, 53, 189-200.	1.8	66
20	Accelerating the Switchgrass (<i>Panicum virgatum</i> L.) Breeding Cycle Using Genomic Selection Approaches. <i>PLoS ONE</i> , 2014, 9, e112227.	2.5	65
21	Selinene Volatiles Are Essential Precursors for Maize Defense Promoting Fungal Pathogen Resistance. <i>Plant Physiology</i> , 2017, 175, 1455-1468.	4.8	61
22	NLR locus-mediated trade-off between abiotic and biotic stress adaptation in <i>Arabidopsis</i> . <i>Nature Plants</i> , 2017, 3, 17072.	9.3	53
23	Time dependent genetic analysis links field and controlled environment phenotypes in the model C4 grass <i>Setaria</i> . <i>PLoS Genetics</i> , 2017, 13, e1006841.	3.5	53
24	Quantitative trait locus analysis of <i>Verticillium</i> wilt resistance in an introgressed recombinant inbred population of Upland cotton. <i>Molecular Breeding</i> , 2014, 33, 709-720.	2.1	48
25	<i>ZEAXANTHIN EPOXIDASE</i> Activity Potentiates Carotenoid Degradation in Maturing Seed. <i>Plant Physiology</i> , 2016, 171, 1837-1851.	4.8	44
26	Multi-Trait Genome-Wide Association Studies Reveal Loci Associated with Maize Inflorescence and Leaf Architecture. <i>Plant and Cell Physiology</i> , 2020, 61, 1427-1437.	3.1	38
27	Identification of haplotypes at the <i>Rsv4</i> genomic region in soybean associated with durable resistance to soybean mosaic virus. <i>Theoretical and Applied Genetics</i> , 2016, 129, 453-468.	3.6	37
28	Accumulation of 5-hydroxynorvaline in maize (<i>Zea mays</i>) leaves is induced by insect feeding and abiotic stress. <i>Journal of Experimental Botany</i> , 2015, 66, 593-602.	4.8	36
29	Association Mapping of Flowering and Height Traits in Germplasm Enhancement of Maize Doubled Haploid (GEMâ€œDH) Lines. <i>Plant Genome</i> , 2018, 11, 170083.	2.8	33
30	Optical topometry and machine learning to rapidly phenotype stomatal patterning traits for maize QTL mapping. <i>Plant Physiology</i> , 2021, 187, 1462-1480.	4.8	33
31	Gibberellins Promote Brassinosteroids Action and Both Increase Heterosis for Plant Height in Maize (<i>Zea mays</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1039.	3.6	32
32	The regulatory landscape of early maize inflorescence development. <i>Genome Biology</i> , 2020, 21, 165.	8.8	32
33	Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. <i>Plant Cell</i> , 2021, 33, 882-900.	6.6	31
34	Genetic mapping of biomass yield in three interconnected <i>Miscanthus</i> populations. <i>GCB Bioenergy</i> , 2018, 10, 165-185.	5.6	29
35	Species dependence of [⁶⁴ Cu]Cu-Bis(thiosemicarbazone) radiopharmaceutical binding to serum albumins. <i>Nuclear Medicine and Biology</i> , 2008, 35, 281-286.	0.6	28
36	Training Population Optimization for Genomic Selection in <i>Miscanthus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2465-2476.	1.8	27

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37	Chemical variation for leaf cuticular waxes and their levels revealed in a diverse panel of <i>Brassica napus</i> L .. <i>Industrial Crops and Products</i> , 2016, 79, 77-83.	5.2	26
38	Genome-Wide Association Study of Brown Stem Rot Resistance in Soybean across Multiple Populations. <i>Plant Genome</i> , 2016, 9, plantgenome2015.08.0064.	2.8	25
39	Brassinosteroid and gibberellin control of seedling traits in maize (<i>Zea mays</i> L.). <i>Plant Science</i> , 2017, 263, 132-141.	3.6	25
40	Genomic regions influencing aggressive behavior in honey bees are defined by colony allele frequencies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17135-17141.	7.1	24
41	mGWAS Uncovers Gln-Glucosinolate Seed-Specific Interaction and its Role in Metabolic Homeostasis. <i>Plant Physiology</i> , 2020, 183, 483-500.	4.8	24
42	Genome-wide association and genomic prediction identifies associated loci and predicts the sensitivity of Tobacco ringspot virus in soybean plant introductions. <i>BMC Genomics</i> , 2016, 17, 153.	2.8	23
43	Evaluation of genomic selection and marker-assisted selection in <i>Miscanthus</i> and energycane. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	20
44	Genomic Selection Using Maize Ex-Plant Variety Protection Germplasm for the Prediction of Nitrogen-Use Traits. <i>Crop Science</i> , 2019, 59, 212-220.	1.8	19
45	Biomass yield in a genetically diverse <i>Miscanthus sinensis</i> germplasm panel evaluated at five locations revealed individuals with exceptional potential. <i>GCB Bioenergy</i> , 2019, 11, 1125-1145.	5.6	18
46	An assessment of true and false positive detection rates of stepwise epistatic model selection as a function of sample size and number of markers. <i>Heredity</i> , 2019, 122, 660-671.	2.6	18
47	Genome-Wide Analysis and Prediction of Resistance to Goss's Wilt in Maize. <i>Plant Genome</i> , 2019, 12, 180045.	2.8	17
48	Genetic Analysis of the Transition from Wild to Domesticated Cotton (<i>Gossypium hirsutum</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 731-754.	1.8	14
49	The Use of Targeted Marker Subsets to Account for Population Structure and Relatedness in Genome-Wide Association Studies of Maize (<i>Zea mays</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2365-2374.	1.8	12
50	Stability Analysis of Kernel Quality Traits in Exotic-Derived Doubled Haploid Maize Lines. <i>Plant Genome</i> , 2019, 12, 170114.	2.8	12
51	How Well Can Multivariate and Univariate GWAS Distinguish Between True and Spurious Pleiotropy?. <i>Frontiers in Genetics</i> , 2020, 11, 602526.	2.3	12
52	Diversifying maize genomic selection models. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	12
53	An Assessment of the Factors Influencing the Prediction Accuracy of Genomic Prediction Models Across Multiple Environments. <i>Frontiers in Genetics</i> , 2021, 12, 689319.	2.3	12
54	Engaging rural communities in genetic research: challenges and opportunities. <i>Journal of Community Genetics</i> , 2017, 8, 209-219.	1.2	11

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55	simplePHENOTYPES: SIMulation of pleiotropic, linked and epistatic phenotypes. BMC Bioinformatics, 2020, 21, 491.	2.6	11
56	Genomic Prediction Informed by Biological Processes Expands Our Understanding of the Genetic Architecture Underlying Free Amino Acid Traits in Dry <i>Arabidopsis</i> Seeds. G3: Genes, Genomes, Genetics, 2020, 10, 4227-4239.	1.8	11
57	HAPPI GWAS: Holistic Analysis with Pre- and Post-Integration GWAS. Bioinformatics, 2020, 36, 4655-4657.	4.1	10
58	An assessment of the performance of the logistic mixed model for analyzing binary traits in maize and sorghum diversity panels. PLoS ONE, 2018, 13, e0207752.	2.5	9
59	Multiomics approach reveals a role of translational machinery in shaping maize kernel amino acid composition. Plant Physiology, 2022, 188, 111-133.	4.8	9
60	Genome-wide association and genomic prediction for biomass yield in a genetically diverse <i>Miscanthus sinensis</i> germplasm panel phenotyped at five locations in Asia and North America. GCB Bioenergy, 2019, 11, 988-1007.	5.6	7
61	Winter hardiness of <i>Miscanthus</i> (II): Genetic mapping for overwintering ability and adaptation traits in three interconnected <i>Miscanthus</i> populations. GCB Bioenergy, 2019, 11, 706-726.	5.6	7
62	Genomic Prediction of Yield Traits in Single-Cross Hybrid Rice (<i>Oryza sativa</i> L.). Frontiers in Genetics, 2021, 12, 692870.	2.3	7
63	Winter hardiness of <i>Miscanthus</i> (III): Genome-wide association and genomic prediction for overwintering ability in <i>Miscanthus sinensis</i> . GCB Bioenergy, 2019, 11, 930-955.	5.6	5
64	A population-level statistic for assessing Mendelian behavior of genotyping-by-sequencing data from highly duplicated genomes. BMC Bioinformatics, 2022, 23, 101.	2.6	5
65	Host plant preference of <i>Lygus hesperus</i> exposed to three desert-adapted industrial crops. Industrial Crops and Products, 2016, 89, 363-367.	5.2	4
66	Genetic variation associated with PPO-inhibiting herbicide tolerance in sorghum. PLoS ONE, 2020, 15, e0233254.	2.5	4
67	A multi-trait multi-locus stepwise approach for conducting GWAS on correlated traits. Plant Genome, 2022, 15, e20200.	2.8	4
68	Interpretation of Manhattan Plots and Other Outputs of Genome-Wide Association Studies. Methods in Molecular Biology, 2022, , 63-80.	0.9	2
69	Exploration of Life-Course Factors Influencing Phenotypic Outcomes in Crops. Plant and Cell Physiology, 2020, 61, 1381-1383.	3.1	1
70	Population Structure Analyses Provide Insight into the Source Populations Underlying Rural Isolated Communities in Illinois. Human Biology, 2019, 91, 31.	0.2	1
71	Assessment of two statistical approaches for variance genome-wide association studies in plants. Heredity, 2022, 129, 93-102.	2.6	1
72	Genetic mapping of sorghum resistance to an Illinois isolate of <i>Colletotrichum sublineola</i> . Plant Genome, 0, , .	2.8	1