

# Alexander E Lipka

## List of Publications by Year in descending order

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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	Multiomics approach reveals a role of translational machinery in shaping maize kernel amino acid composition. <i>Plant Physiology</i> , 2022, 188, 111-133.	4.8	9
2	A multi-trait multi-locus stepwise approach for conducting GWAS on correlated traits. <i>Plant Genome</i> , 2022, 15, e20200.	2.8	4
3	A population-level statistic for assessing Mendelian behavior of genotyping-by-sequencing data from highly duplicated genomes. <i>BMC Bioinformatics</i> , 2022, 23, 101.	2.6	5
4	Assessment of two statistical approaches for variance genome-wide association studies in plants. <i>Heredity</i> , 2022, 129, 93-102.	2.6	1
5	Interpretation of Manhattan Plots and Other Outputs of Genome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2022, , 63-80.	0.9	2
6	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
7	Diversifying maize genomic selection models. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	12
8	Genomic Prediction of Yield Traits in Single-Cross Hybrid Rice ( <i>Oryza sativa</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 692870.	2.3	7
9	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
10	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
11	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
12	Genetic variation associated with PPO-inhibiting herbicide tolerance in sorghum. <i>PLoS ONE</i> , 2020, 15, e0233254.	2.5	4
13	simplePHENOTYPES: SIMulation of pleiotropic, linked and epistatic phenotypes. <i>BMC Bioinformatics</i> , 2020, 21, 491.	2.6	11
14	Exploration of Life-Course Factors Influencing Phenotypic Outcomes in Crops. <i>Plant and Cell Physiology</i> , 2020, 61, 1381-1383.	3.1	1
15	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
16	HAPPI GWAS: Holistic Analysis with Pre- and Post-Integration GWAS. <i>Bioinformatics</i> , 2020, 36, 4655-4657.	4.1	10
17	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
18	The regulatory landscape of early maize inflorescence development. <i>Genome Biology</i> , 2020, 21, 165.	8.8	32

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19	mGWAS Uncovers Gln-Glucosinolate Seed-Specific Interaction and its Role in Metabolic Homeostasis. <i>Plant Physiology</i> , 2020, 183, 483-500.	4.8	24
20	How Well Can Multivariate and Univariate GWAS Distinguish Between True and Spurious Pleiotropy?. <i>Frontiers in Genetics</i> , 2020, 11, 602526.	2.3	12
21	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
22	Genomic Prediction Informed by Biological Processes Expands Our Understanding of the Genetic Architecture Underlying Free Amino Acid Traits in Dry <i>Arabidopsis</i> Seeds. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4227-4239.	1.8	11
23	Training Population Optimization for Genomic Selection in <i>Miscanthus</i>. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2465-2476.	1.8	27
24	Winter hardiness of <i>Miscanthus</i> (III): Genome-wide association and genomic prediction for overwintering ability in <i>Miscanthus sinensis</i>. <i>GCB Bioenergy</i> , 2019, 11, 930-955.	5.6	5
25	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. <i>GCB Bioenergy</i> , 2019, 11, 988-1007.	5.6	7
26	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
27	Winter hardiness of <i>Miscanthus</i> (II): Genetic mapping for overwintering ability and adaptation traits in three interconnected <i>Miscanthus</i> populations. <i>GCB Bioenergy</i> , 2019, 11, 706-726.	5.6	7
28	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
29	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
30	Stability Analysis of Kernel Quality Traits in Exotic-derived Doubled Haploid Maize Lines. <i>Plant Genome</i> , 2019, 12, 170114.	2.8	12
31	Genome-wide Analysis and Prediction of Resistance to Goss's Wilt in Maize. <i>Plant Genome</i> , 2019, 12, 180045.	2.8	17
32	Evaluation of genomic selection and marker-assisted selection in <i>Miscanthus</i> and energycane. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	20
33	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
34	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
35	Population Structure Analyses Provide Insight into the Source Populations Underlying Rural Isolated Communities in Illinois. <i>Human Biology</i> , 2019, 91, 31.	0.2	1
36	Genetic mapping of biomass yield in three interconnected <i>Miscanthus</i> populations. <i>GCB Bioenergy</i> , 2018, 10, 165-185.	5.6	29

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37	Association Mapping of Flowering and Height Traits in Germplasm Enhancement of Maize Doubled Haploid (GEMâ€šDH) Lines. <i>Plant Genome</i> , 2018, 11, 170083.	2.8	33
38	An assessment of the performance of the logistic mixed model for analyzing binary traits in maize and sorghum diversity panels. <i>PLoS ONE</i> , 2018, 13, e0207752.	2.5	9
39	Genetic Architecture of Soybean Yield and Agronomic Traits. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3367-3375.	1.8	98
40	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
41	Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. <i>Plant Cell</i> , 2017, 29, 2374-2392.	6.6	93
42	Selinene Volatiles Are Essential Precursors for Maize Defense Promoting Fungal Pathogen Resistance. <i>Plant Physiology</i> , 2017, 175, 1455-1468.	4.8	61
43	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
44	Engaging rural communities in genetic research: challenges and opportunities. <i>Journal of Community Genetics</i> , 2017, 8, 209-219.	1.2	11
45	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
46	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
47	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
48	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
49	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
50	<i>ZEAXANTHIN EPOXIDASE</i> Activity Potentiates Carotenoid Degradation in Maturing Seed. <i>Plant Physiology</i> , 2016, 171, 1837-1851.	4.8	44
51	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
52	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
53	Host plant preference of <i>Lygus hesperus</i> exposed to three desert-adapted industrial crops. <i>Industrial Crops and Products</i> , 2016, 89, 363-367.	5.2	4
54	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

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55	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
56	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
57	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
58	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
59	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
60	Accelerating the Switchgrass ( <i>Panicum virgatum</i> L.) Breeding Cycle Using Genomic Selection Approaches. <i>PLoS ONE</i> , 2014, 9, e112227.	2.5	65
61	<i>CAROTENOID CLEAVAGE DIOXYGENASE4</i> Is a Negative Regulator of $\beta$ -Carotene Content in <i>Arabidopsis</i> Seeds. <i>Plant Cell</i> , 2014, 25, 4812-4826.	6.6	180
62	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
63	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
64	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
65	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
66	Lessons from Dwarf8 on the Strengths and Weaknesses of Structured Association Mapping. <i>PLoS Genetics</i> , 2013, 9, e1003246.	3.5	115
67	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
68	Natural Variation in Maize Aphid Resistance Is Associated with 2,4-Dihydroxy-7-Methoxy-1,4-Benzoxazin-3-One Glucoside Methyltransferase Activity $\hat{A}$ . <i>Plant Cell</i> , 2013, 25, 2341-2355.	6.6	251
69	Genetic Analysis of Visually Scored Orange Kernel Color in Maize. <i>Crop Science</i> , 2013, 53, 189-200.	1.8	66
70	GAPIT: genome association and prediction integrated tool. <i>Bioinformatics</i> , 2012, 28, 2397-2399.	4.1	2,016
71	Species dependence of [ $^{64}\text{Cu}$ ]Cu-Bis(thiosemicarbazone) radiopharmaceutical binding to serum albumins. <i>Nuclear Medicine and Biology</i> , 2008, 35, 281-286.	0.6	28
72	Genetic mapping of sorghum resistance to an Illinois isolate of <i>Colletotrichum sublineola</i> . <i>Plant Genome</i> , 0, , .	2.8	1