

Lex E Flagel

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

3,734
citations

279701

23
h-index

526166

27
g-index

29
all docs

29
docs citations

29
times ranked

4762
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene duplication and evolutionary novelty in plants. <i>New Phytologist</i> , 2009, 183, 557-564.	3.5	725
2	Evolutionary Genetics of Genome Merger and Doubling in Plants. <i>Annual Review of Genetics</i> , 2008, 42, 443-461.	3.2	618
3	Speciation and Introgression between <i>Mimulus nasutus</i> and <i>Mimulus guttatus</i> . <i>PLoS Genetics</i> , 2014, 10, e1004410.	1.5	252
4	Evolutionary rate variation, genomic dominance and duplicate gene expression evolution during allotetraploid cotton speciation. <i>New Phytologist</i> , 2010, 186, 184-193.	3.5	223
5	Efficient soybean transformation using hygromycin selection in the cotyledonary-node method. <i>Planta</i> , 2003, 216, 723-735.	1.6	222
6	Reciprocal Silencing, Transcriptional Bias and Functional Divergence of Homeologs in Polyploid Cotton (<i>Gossypium</i>). <i>Genetics</i> , 2009, 182, 503-517.	1.2	212
7	The Unreasonable Effectiveness of Convolutional Neural Networks in Population Genetic Inference. <i>Molecular Biology and Evolution</i> , 2019, 36, 220-238.	3.5	151
8	Partitioned expression of duplicated genes during development and evolution of a single cell in a polyploid plant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6191-6195.	3.3	143
9	Development and characterization of the first dsRNA-resistant insect population from western corn rootworm, <i>Diabrotica virgifera virgifera</i> LeConte. <i>PLoS ONE</i> , 2018, 13, e0197059.	1.1	139
10	Homoeologous nonreciprocal recombination in polyploid cotton. <i>New Phytologist</i> , 2010, 186, 123-134.	3.5	136
11	Genetic diversity is indispensable for plant breeding to improve crops. <i>Crop Science</i> , 2021, 61, 839-852.	0.8	107
12	Duplicate gene evolution, homoeologous recombination, and transcriptome characterization in allopolyploid cotton. <i>BMC Genomics</i> , 2012, 13, 302.	1.2	102
13	A majority of cotton genes are expressed in single-celled fiber. <i>Planta</i> , 2007, 227, 319-329.	1.6	97
14	The Evolution of Spinnable Cotton Fiber Entailed Prolonged Development and a Novel Metabolism. <i>PLoS Genetics</i> , 2008, 4, e25.	1.5	93
15	Molecular characterization of Cry1F resistance in fall armyworm, <i>Spodoptera frugiperda</i> from Brazil. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 116, 103280.	1.2	63
16	Parallel up-regulation of the profilin gene family following independent domestication of diploid and allopolyploid cotton (<i>Gossypium</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 21152-21157.	3.3	61
17	Rapid molecular evolution across amniotes of the IIS/TOR network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7055-7060.	3.3	59
18	Parallel Domestication, Convergent Evolution and Duplicated Gene Recruitment in Allopolyploid Cotton. <i>Genetics</i> , 2008, 179, 1725-1733.	1.2	57

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19	T-DNA locus structure in a large population of soybean plants transformed using the Agrobacterium-mediated cotyledonary-node method. <i>Plant Biotechnology Journal</i> , 2004, 2, 289-300.	4.1	47
20	The Standing Pool of Genomic Structural Variation in a Natural Population of <i>Mimulus guttatus</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 53-64.	1.1	42
21	Evidence of Natural Selection Acting on a Polymorphic Hybrid Incompatibility Locus in <i>Mimulus</i> . <i>Genetics</i> , 2015, 199, 543-554.	1.2	40
22	Phylogenetic, morphological, and chemotaxonomic incongruence in the North American endemic genus <i>Echinacea</i> . <i>American Journal of Botany</i> , 2008, 95, 756-765.	0.8	34
23	Coordinated and Fine-Scale Control of Homoeologous Gene Expression in Allotetraploid Cotton. <i>Journal of Heredity</i> , 2009, 100, 487-490.	1.0	34
24	Evaluating maize phenotypic variance, heritability, and yield relationships at multiple biological scales across agronomically relevant environments. <i>Plant, Cell and Environment</i> , 2020, 43, 880-902.	2.8	24
25	GOOGA: A platform to synthesize mapping experiments and identify genomic structural diversity. <i>PLoS Computational Biology</i> , 2019, 15, e1006949.	1.5	19
26	Phenetic Comparison of Seven <i>Echinacea</i> Species Based on Immunomodulatory Characteristics. <i>Economic Botany</i> , 2006, 60, 205-211.	0.8	17
27	The utility of genomic prediction models in evolutionary genetics. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20210693.	1.2	13