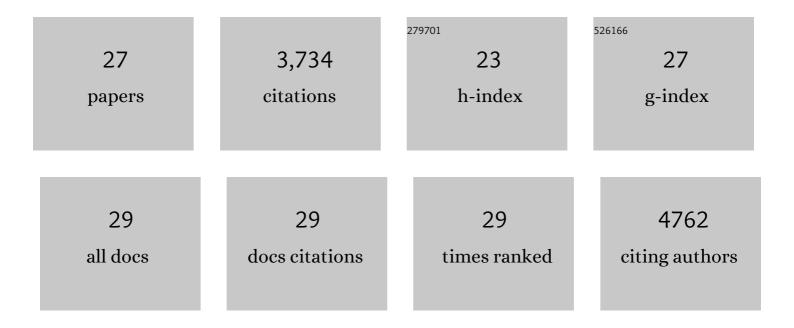
Lex E Flagel

List of Publications by Year in descending order

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LEV E FLACEL

#	Article	IF	CITATIONS
1	Genetic diversity is indispensable for plant breeding to improve crops. Crop Science, 2021, 61, 839-852.	0.8	107
2	The utility of genomic prediction models in evolutionary genetics. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20210693.	1.2	13
3	Molecular characterization of Cry1F resistance in fall armyworm, Spodoptera frugiperda from Brazil. Insect Biochemistry and Molecular Biology, 2020, 116, 103280.	1.2	63
4	Evaluating maize phenotypic variance, heritability, and yield relationships at multiple biological scales across agronomically relevant environments. Plant, Cell and Environment, 2020, 43, 880-902.	2.8	24
5	GOOGA: A platform to synthesize mapping experiments and identify genomic structural diversity. PLoS Computational Biology, 2019, 15, e1006949.	1.5	19
6	The Unreasonable Effectiveness of Convolutional Neural Networks in Population Genetic Inference. Molecular Biology and Evolution, 2019, 36, 220-238.	3.5	151
7	Development and characterization of the first dsRNA-resistant insect population from western corn rootworm, Diabrotica virgifera virgifera LeConte. PLoS ONE, 2018, 13, e0197059.	1.1	139
8	Rapid molecular evolution across amniotes of the IIS/TOR network. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7055-7060.	3.3	59
9	Evidence of Natural Selection Acting on a Polymorphic Hybrid Incompatibility Locus in <i>Mimulus</i> . Genetics, 2015, 199, 543-554.	1.2	40
10	Speciation and Introgression between Mimulus nasutus and Mimulus guttatus. PLoS Genetics, 2014, 10, e1004410.	1.5	252
11	The Standing Pool of Genomic Structural Variation in a Natural Population of Mimulus guttatus. Genome Biology and Evolution, 2014, 6, 53-64.	1.1	42
12	Duplicate gene evolution, homoeologous recombination, and transcriptome characterization in allopolyploid cotton. BMC Genomics, 2012, 13, 302.	1.2	102
13	Parallel up-regulation of the profilin gene family following independent domestication of diploid and allopolyploid cotton (<i>Gossypium</i>). Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 21152-21157.	3.3	61
14	Homoeologous nonreciprocal recombination in polyploid cotton. New Phytologist, 2010, 186, 123-134.	3.5	136
15	Evolutionary rate variation, genomic dominance and duplicate gene expression evolution during allotetraploid cotton speciation. New Phytologist, 2010, 186, 184-193.	3.5	223
16	Reciprocal Silencing, Transcriptional Bias and Functional Divergence of Homeologs in Polyploid Cotton (Gossypium). Genetics, 2009, 182, 503-517.	1.2	212
17	Coordinated and Fine-Scale Control of Homoeologous Gene Expression in Allotetraploid Cotton. Journal of Heredity, 2009, 100, 487-490.	1.0	34
18	Gene duplication and evolutionary novelty in plants. New Phytologist, 2009, 183, 557-564.	3.5	725

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#	Article	IF	CITATIONS
19	Evolutionary Genetics of Genome Merger and Doubling in Plants. Annual Review of Genetics, 2008, 42, 443-461.	3.2	618
20	Phylogenetic, morphological, and chemotaxonomic incongruence in the North American endemic genus <i>Echinacea</i> . American Journal of Botany, 2008, 95, 756-765.	0.8	34
21	The Evolution of Spinnable Cotton Fiber Entailed Prolonged Development and a Novel Metabolism. PLoS Genetics, 2008, 4, e25.	1.5	93
22	Parallel Domestication, Convergent Evolution and Duplicated Gene Recruitment in Allopolyploid Cotton. Genetics, 2008, 179, 1725-1733.	1.2	57
23	Partitioned expression of duplicated genes during development and evolution of a single cell in a polyploid plant. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6191-6195.	3.3	143
24	A majority of cotton genes are expressed in single-celled fiber. Planta, 2007, 227, 319-329.	1.6	97
25	Phenetic Comparison of Seven Echinacea Species Based on Immunomodulatory Characteristics. Economic Botany, 2006, 60, 205-211.	0.8	17
26	T-DNA locus structure in a large population of soybean plants transformed using the Agrobacterium-mediated cotyledonary-node method. Plant Biotechnology Journal, 2004, 2, 289-300.	4.1	47
27	Efficient soybean transformation using hygromycinÂB selection in the cotyledonary-node method. Planta, 2003, 216, 723-735.	1.6	222