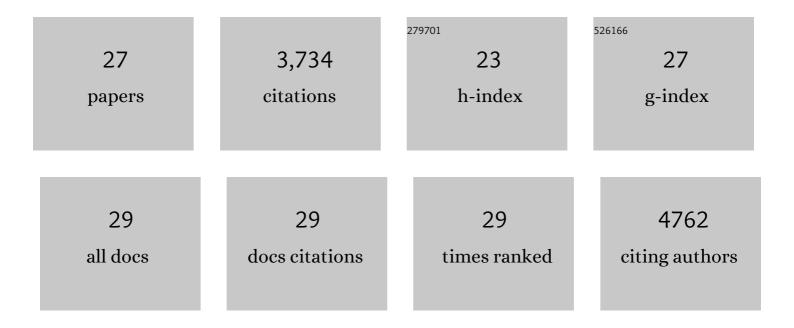
Lex E Flagel

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8189418/publications.pdf Version: 2024-02-01



LEV E FLACEL

#	Article	IF	CITATIONS
1	Gene duplication and evolutionary novelty in plants. New Phytologist, 2009, 183, 557-564.	3.5	725
2	Evolutionary Genetics of Genome Merger and Doubling in Plants. Annual Review of Genetics, 2008, 42, 443-461.	3.2	618
3	Speciation and Introgression between Mimulus nasutus and Mimulus guttatus. PLoS Genetics, 2014, 10, e1004410.	1.5	252
4	Evolutionary rate variation, genomic dominance and duplicate gene expression evolution during allotetraploid cotton speciation. New Phytologist, 2010, 186, 184-193.	3.5	223
5	Efficient soybean transformation using hygromycinÂB selection in the cotyledonary-node method. Planta, 2003, 216, 723-735.	1.6	222
6	Reciprocal Silencing, Transcriptional Bias and Functional Divergence of Homeologs in Polyploid Cotton (Gossypium). Genetics, 2009, 182, 503-517.	1.2	212
7	The Unreasonable Effectiveness of Convolutional Neural Networks in Population Genetic Inference. Molecular Biology and Evolution, 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. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6191-6195.	3.3	143
9	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
10	Homoeologous nonreciprocal recombination in polyploid cotton. New Phytologist, 2010, 186, 123-134.	3.5	136
11	Genetic diversity is indispensable for plant breeding to improve crops. Crop Science, 2021, 61, 839-852.	0.8	107
12	Duplicate gene evolution, homoeologous recombination, and transcriptome characterization in allopolyploid cotton. BMC Genomics, 2012, 13, 302.	1.2	102
13	A majority of cotton genes are expressed in single-celled fiber. Planta, 2007, 227, 319-329.	1.6	97
14	The Evolution of Spinnable Cotton Fiber Entailed Prolonged Development and a Novel Metabolism. PLoS Genetics, 2008, 4, e25.	1.5	93
15	Molecular characterization of Cry1F resistance in fall armyworm, Spodoptera frugiperda from Brazil. Insect Biochemistry and Molecular Biology, 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>). Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 21152-21157.	3.3	61
17	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
18	Parallel Domestication, Convergent Evolution and Duplicated Gene Recruitment in Allopolyploid Cotton. Genetics, 2008, 179, 1725-1733.	1.2	57

Lex E Flagel

#	Article	IF	CITATIONS
19	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
20	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
21	Evidence of Natural Selection Acting on a Polymorphic Hybrid Incompatibility Locus in <i>Mimulus</i> . Genetics, 2015, 199, 543-554.	1.2	40
22	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
23	Coordinated and Fine-Scale Control of Homoeologous Gene Expression in Allotetraploid Cotton. Journal of Heredity, 2009, 100, 487-490.	1.0	34
24	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
25	GOOGA: A platform to synthesize mapping experiments and identify genomic structural diversity. PLoS Computational Biology, 2019, 15, e1006949.	1.5	19
26	Phenetic Comparison of Seven Echinacea Species Based on Immunomodulatory Characteristics. Economic Botany, 2006, 60, 205-211.	0.8	17
27	The utility of genomic prediction models in evolutionary genetics. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20210693.	1.2	13