

Katrina M Dlugosch

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5890385/publications.pdf>

Version: 2024-02-01

32
papers

3,048
citations

586496

16
h-index

511568

30
g-index

68
all docs

68
docs citations

68
times ranked

4807
citing authors

#	ARTICLE	IF	CITATIONS
1	Where we've been and where we're going: the importance of source communities in predicting establishment success from phylogenetic relationships. <i>Ecography</i> , 2022, 2022, .	2.1	7
2	Both source and recipient range phylogenetic community structure can predict the outcome of avian introductions. <i>Ecography</i> , 2022, 2022, .	2.1	0
3	Pilot RNA-seq data from 24 species of vascular plants at Harvard Forest. <i>Applications in Plant Sciences</i> , 2021, 9, e11409.	0.8	3
4	The evolution of invasiveness: a mechanistic view of trade-offs involving defenses. <i>American Journal of Botany</i> , 2020, 107, 953-956.	0.8	4
5	TagSeq for gene expression in non-model plants: A pilot study at the Santa Rita Experimental Range NEON core site. <i>Applications in Plant Sciences</i> , 2020, 8, e11398.	0.8	4
6	Expansion history and environmental suitability shape effective population size in a plant invasion. <i>Molecular Ecology</i> , 2019, 28, 2546-2558.	2.0	21
7	Native and Invading Yellow Starthistle (<i>Centaurea solstitialis</i>) Microbiomes Differ in Composition and Diversity of Bacteria. <i>MSphere</i> , 2019, 4, .	1.3	20
8	Potential limits to the benefits of admixture during biological invasion. <i>Molecular Ecology</i> , 2019, 28, 100-113.	2.0	20
9	Population Genomics of Colonization and Invasion. <i>Population Genomics</i> , 2018, , 655-683.	0.2	14
10	Leveraging contemporary species introductions to test phylogenetic hypotheses of trait evolution. <i>Current Opinion in Plant Biology</i> , 2018, 42, 95-102.	3.5	3
11	Chloroplast sequence variation and the efficacy of peptide nucleic acids for blocking host amplification in plant microbiome studies. <i>Microbiome</i> , 2018, 6, 144.	4.9	74
12	Invasions and extinctions through the looking glass of evolutionary ecology. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160031.	1.8	96
13	Population genomic analyses reveal a history of range expansion and trait evolution across the native and invaded range of yellow starthistle (<i>Centaurea solstitialis</i>). <i>Molecular Ecology</i> , 2017, 26, 1131-1147.	2.0	63
14	Evolution of invasiveness through increased resource use in a vacant niche. <i>Nature Plants</i> , 2015, 1, .	4.7	78
15	Novel spatial analysis methods reveal scale-dependent spread and infer limiting factors of invasion by Sahara mustard. <i>Ecography</i> , 2015, 38, 311-320.	2.1	10
16	The devil is in the details: genetic variation in introduced populations and its contributions to invasion. <i>Molecular Ecology</i> , 2015, 24, 2095-2111.	2.0	263
17	Allele Identification for Transcriptome-Based Population Genomics in the Invasive Plant <i>Centaurea solstitialis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 359-367.	0.8	65
18	Genomics of Compositae weeds: EST libraries, microarrays, and evidence of introgression. <i>American Journal of Botany</i> , 2012, 99, 209-218.	0.8	80

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19	Allele Identification in Assembled Genomic Sequence Datasets. <i>Methods in Molecular Biology</i> , 2012, 888, 197-211.	0.4	2
20	Increased growth in sunflower correlates with reduced defences and altered gene expression in response to biotic and abiotic stress. <i>Molecular Ecology</i> , 2011, 20, 4683-4694.	2.0	68
21	NU-IN: Nucleotide evolution and input module for the EvoSimulator genome simulation platform. <i>BMC Research Notes</i> , 2010, 3, 217.	0.6	1
22	EvoPipes.net: Bioinformatic Tools for Ecological and Evolutionary Genomics. <i>Evolutionary Bioinformatics</i> , 2010, 6, EBO.S5861.	0.6	83
23	Evolution of Weediness and Invasiveness: Charting the Course for Weed Genomics. <i>Weed Science</i> , 2009, 57, 451-462.	0.8	82
24	SCARF: maximizing next-generation EST assemblies for evolutionary and population genomic analyses. <i>Bioinformatics</i> , 2009, 25, 535-536.	1.8	13
25	Invading populations of an ornamental shrub show rapid life history evolution despite genetic bottlenecks. <i>Ecology Letters</i> , 2008, 11, 701-709.	3.0	241
26	Founding events in species invasions: genetic variation, adaptive evolution, and the role of multiple introductions. <i>Molecular Ecology</i> , 2008, 17, 431-449.	2.0	1,468
27	Can we stop transgenes from taking a walk on the wild side?. <i>Molecular Ecology</i> , 2008, 17, 1167-1169.	2.0	14
28	Genotypes on the move: some things old and some things new shape the genetics of colonization during species invasions. <i>Molecular Ecology</i> , 2008, 17, 4583-4585.	2.0	21
29	Molecular and morphological evidence for and against gene flow in sympatric apomicts of the North American <i>Crepis</i> agamic complex (Asteraceae) This paper is one of a selection of papers published in the Special Issue on Systematics Research.. <i>Botany</i> , 2008, 86, 877-885.	0.5	9
30	Molecular and quantitative trait variation across the native range of the invasive species <i>Hypericum canariense</i> : evidence for ancient patterns of colonization via preadaptation?. <i>Molecular Ecology</i> , 2007, 16, 4269-4283.	2.0	58
31	Invasions as a Tool for Basic Research. <i>Conservation Biology</i> , 2007, 21, 1376-1377.	2.4	0
32	Nectar and hostplant scarcity limit populations of an endangered Oregon butterfly. <i>Oecologia</i> , 1999, 119, 231-238.	0.9	97