

Philipp W Messer

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

79
papers

4,421
citations

35
h-index

66
g-index

93
ext. papers

6,102
ext. citations

7.6
avg, IF

6.38
L-index

#	Paper	IF	Citations
79	Population genomics of rapid adaptation by soft selective sweeps. <i>Trends in Ecology and Evolution</i> , 2013 , 28, 659-69	10.9	324
78	Recent selective sweeps in North American <i>Drosophila melanogaster</i> show signatures of soft sweeps. <i>PLoS Genetics</i> , 2015 , 11, e1005004	6	251
77	SLiM 3: Forward Genetic Simulations Beyond the Wright-Fisher Model. <i>Molecular Biology and Evolution</i> , 2019 , 36, 632-637	8.3	247
76	Plumage Genes and Little Else Distinguish the Genomes of Hybridizing Warblers. <i>Current Biology</i> , 2016 , 26, 2313-8	6.3	215
75	Evidence that adaptation in <i>Drosophila</i> is not limited by mutation at single sites. <i>PLoS Genetics</i> , 2010 , 6, e1000924	6	201
74	Evolution of Resistance Against CRISPR/Cas9 Gene Drive. <i>Genetics</i> , 2017 , 205, 827-841	4	189
73	Novel CRISPR/Cas9 gene drive constructs reveal insights into mechanisms of resistance allele formation and drive efficiency in genetically diverse populations. <i>PLoS Genetics</i> , 2017 , 13, e1006796	6	176
72	Reducing resistance allele formation in CRISPR gene drive. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 5522-5527	11.5	151
71	Frequent adaptation and the McDonald-Kreitman test. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 8615-20	11.5	147
70	SLiM 2: Flexible, Interactive Forward Genetic Simulations. <i>Molecular Biology and Evolution</i> , 2017 , 34, 2308-240	8.40	141
69	Heterozygote advantage as a natural consequence of adaptation in diploids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 20666-71	11.5	135
68	Genome-wide signals of positive selection in human evolution. <i>Genome Research</i> , 2014 , 24, 885-95	9.7	132
67	SLiM: simulating evolution with selection and linkage. <i>Genetics</i> , 2013 , 194, 1037-9	4	131
66	Strong purifying selection at synonymous sites in <i>D. melanogaster</i> . <i>PLoS Genetics</i> , 2013 , 9, e1003527	6	129
65	Genome-wide patterns of adaptation to temperate environments associated with transposable elements in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2010 , 6, e1000905	6	111
64	Can Population Genetics Adapt to Rapid Evolution?. <i>Trends in Genetics</i> , 2016 , 32, 408-418	8.5	108
63	Genome patterns of selection and introgression of haplotypes in natural populations of the house mouse (<i>Mus musculus</i>). <i>PLoS Genetics</i> , 2012 , 8, e1002891	6	105

62	Narrow thermal tolerance and low dispersal drive higher speciation in tropical mountains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 12471-12476	11.5	96
61	Modeling the Manipulation of Natural Populations by the Mutagenic Chain Reaction. <i>Genetics</i> , 2015 , 201, 425-31	4	82
60	Quantification of GC-biased gene conversion in the human genome. <i>Genome Research</i> , 2015 , 25, 1215-28	9.7	75
59	The role of the vaginal microbiome in gynaecological cancer. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2018 , 125, 309-315	3.7	73
58	Adaptively introgressed Neandertal haplotype at the OAS locus functionally impacts innate immune responses in humans. <i>Genome Biology</i> , 2016 , 17, 246	18.3	70
57	Tree-sequence recording in SLiM opens new horizons for forward-time simulation of whole genomes. <i>Molecular Ecology Resources</i> , 2019 , 19, 552-566	8.4	67
56	Molecular safeguarding of CRISPR gene drive experiments. <i>ELife</i> , 2019 , 8,	8.9	65
55	The majority of recent short DNA insertions in the human genome are tandem duplications. <i>Molecular Biology and Evolution</i> , 2007 , 24, 1190-7	8.3	64
54	A toxin-antidote CRISPR gene drive system for regional population modification. <i>Nature Communications</i> , 2020 , 11, 1082	17.4	56
53	Soft selective sweeps in complex demographic scenarios. <i>Genetics</i> , 2014 , 198, 669-84	4	53
52	Evaluating the performance of selection scans to detect selective sweeps in domestic dogs. <i>Molecular Ecology</i> , 2016 , 25, 342-56	5.7	53
51	SLiM 3: Forward genetic simulations beyond the Wright-Fisher model		51
50	Computational and experimental performance of CRISPR homing gene drive strategies with multiplexed gRNAs. <i>Science Advances</i> , 2020 , 6, eaaz0525	14.3	41
49	Estimating the strength of selective sweeps from deep population diversity data. <i>Genetics</i> , 2012 , 191, 593-605	4	37
48	Solvable sequence evolution models and genomic correlations. <i>Physical Review Letters</i> , 2005 , 94, 138103	7.4	37
47	A CRISPR homing gene drive targeting a haplolethal gene removes resistance alleles and successfully spreads through a cage population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 24377-24383	11.5	37
46	Measuring the rates of spontaneous mutation from deep and large-scale polymorphism data. <i>Genetics</i> , 2009 , 182, 1219-32	4	35
45	DNA indels in coding regions reveal selective constraints on protein evolution in the human lineage. <i>BMC Evolutionary Biology</i> , 2007 , 7, 191	3	35

44	A community-maintained standard library of population genetic models. <i>ELife</i> , 2020 , 9,	8.9	35
43	Core commitments for field trials of gene drive organisms. <i>Science</i> , 2020 , 370, 1417-1419	33.3	35
42	CRISPR Gene Drive Efficiency and Resistance Rate Is Highly Heritable with No Common Genetic Loci of Large Effect. <i>Genetics</i> , 2019 , 212, 333-341	4	31
41	Performance analysis of novel toxin-antidote CRISPR gene drive systems. <i>BMC Biology</i> , 2020 , 18, 27	7.3	31
40	Faster than neutral evolution of constrained sequences: the complex interplay of mutational biases and weak selection. <i>Genome Biology and Evolution</i> , 2011 , 3, 383-95	3.9	29
39	Evolutionary genomics. Conundrum of jumbled mosquito genomes. <i>Science</i> , 2015 , 347, 27-8	33.3	25
38	Maximum Likelihood Estimation of Fitness Components in Experimental Evolution. <i>Genetics</i> , 2019 , 211, 1005-1017	4	22
37	Population Dynamics of Underdominance Gene Drive Systems in Continuous Space. <i>ACS Synthetic Biology</i> , 2020 , 9, 779-792	5.7	22
36	Suppression gene drive in continuous space can result in unstable persistence of both drive and wild-type alleles. <i>Molecular Ecology</i> , 2021 , 30, 1086-1101	5.7	21
35	asymptoticMK: A Web-Based Tool for the Asymptotic McDonald-Kreitman Test. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 1569-1575	3.2	19
34	Inferring the strength of selection in <i>Drosophila</i> under complex demographic models. <i>Molecular Biology and Evolution</i> , 2009 , 26, 513-26	8.3	18
33	Signatures of Insecticide Selection in the Genome of <i>Drosophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 3469-3480	3.2	17
32	CorGen--measuring and generating long-range correlations for DNA sequence analysis. <i>Nucleic Acids Research</i> , 2006 , 34, W692-5	20.1	14
31	Design and analysis of CRISPR-based underdominance toxin-antidote gene drives. <i>Evolutionary Applications</i> , 2021 , 14, 1052-1069	4.8	14
30	Resistance is futile: A CRISPR homing gene drive targeting a haplolethal gene		13
29	Universality of long-range correlations in expansion and randomization systems. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2005 , 2005, P10004-P10004	1.9	11
28	Novel CRISPR/Cas9 gene drive constructs in <i>Drosophila</i> reveal insights into mechanisms of resistance allele formation and drive efficiency in genetically diverse populations		11
27	Performance analysis of novel toxin-antidote CRISPR gene drive systems		11

26	Design and analysis of CRISPR-based underdominance toxin-antidote gene drives		10
25	Effects of long-range correlations in DNA on sequence alignment score statistics. <i>Journal of Computational Biology</i> , 2007 , 14, 655-68	1.7	8
24	A toxin-antidote CRISPR gene drive system for regional population modification		8
23	Suppression gene drive in continuous space can result in unstable persistence of both drive and wild-type alleles		8
22	A community-maintained standard library of population genetic models		7
21	Population dynamics of underdominance gene drive systems in continuous space		7
20	Computational and experimental performance of CRISPR homing gene drive strategies with multiplexed gRNAs		7
19	Detection of hard and soft selective sweeps from <i>Drosophila melanogaster</i> population genomic data. <i>PLoS Genetics</i> , 2021 , 17, e1009373	6	7
18	Modeling CRISPR gene drives for suppression of invasive rodents using a supervised machine learning framework.. <i>PLoS Computational Biology</i> , 2021 , 17, e1009660	5	6
17	A homing suppression gene drive with multiplexed gRNAs maintains high drive conversion efficiency and avoids functional resistance alleles.. <i>G3: Genes, Genomes, Genetics</i> , 2022 ,	3.2	6
16	Evolution of Resistance Against CRISPR/Cas9 Gene Drive		5
15	Fitness effects of CRISPR endonucleases in <i>Drosophila melanogaster</i> populations		5
14	Reducing resistance allele formation in CRISPR gene drives		4
13	Tree-sequence recording in SLiM opens new horizons for forward-time simulation of whole genomes		4
12	Multiple loci of small effect confer wide variability in efficiency and resistance rate of CRISPR gene drive		4
11	A homing suppression gene drive with multiplexed gRNAs maintains high drive conversion efficiency and avoids functional resistance alleles		4
10	Experimental demonstration of tethered gene drive systems for confined population modification or suppression. <i>BMC Biology</i> , 2022 , 20,	7.3	4
9	Experimental demonstration of tethered gene drive systems for confined population modification or suppression		3

8	Gene Drives: Dynamics and Regulatory Matters-A Report from the Workshop "Evaluation of Spatial and Temporal Control of Gene Drives," April 4-5, 2019, Vienna. <i>BioEssays</i> , 2019 , 41, e1900151	4.1	3
7	Detection of hard and soft selective sweeps from <i>Drosophila melanogaster</i> population genomic data		2
6	Evolutionary Modeling in SLiM 3 for Beginners. <i>Molecular Biology and Evolution</i> , 2019 , 36, 1101-1109	8.3	2
5	Alignment Statistics for Long-Range Correlated Genomic Sequences. <i>Lecture Notes in Computer Science</i> , 2006 , 426-440	0.9	2
4	Molecular safeguarding of CRISPR gene drive experiments		1
3	The Effects of Quantitative Trait Architecture on Detection Power in Artificial Selection Experiments		1
2	Adaptively introgressed Neandertal haplotype at the OAS locus functionally impacts innate immune responses in humans		1
1	The Effects of Quantitative Trait Architecture on Detection Power in Short-Term Artificial Selection Experiments. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 3213-3227	3.2	1