

Philipp W Messer

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

7,159
citations

94433

37
h-index

133252

59
g-index

93
all docs

93
docs citations

93
times ranked

7388
citing authors

#	ARTICLE	IF	CITATIONS
1	SLiM 3: Forward Genetic Simulations Beyond the Wrightâ€Fisher Model. <i>Molecular Biology and Evolution</i> , 2019, 36, 632-637.	8.9	628
2	Population genomics of rapid adaptation by soft selective sweeps. <i>Trends in Ecology and Evolution</i> , 2013, 28, 659-669.	8.7	471
3	Recent Selective Sweeps in North American <i>Drosophila melanogaster</i> Show Signatures of Soft Sweeps. <i>PLoS Genetics</i> , 2015, 11, e1005004.	3.5	392
4	Plumage Genes and Little Else Distinguish the Genomes of Hybridizing Warblers. <i>Current Biology</i> , 2016, 26, 2313-2318.	3.9	302
5	Evidence that Adaptation in <i>Drosophila</i> Is Not Limited by Mutation at Single Sites. <i>PLoS Genetics</i> , 2010, 6, e1000924.	3.5	255
6	Evolution of Resistance Against CRISPR/Cas9 Gene Drive. <i>Genetics</i> , 2017, 205, 827-841.	2.9	250
7	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.	3.5	246
8	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.	7.1	233
9	Frequent adaptation and the McDonaldâ€Kreitman test. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8615-8620.	7.1	231
10	SLiM 2: Flexible, Interactive Forward Genetic Simulations. <i>Molecular Biology and Evolution</i> , 2017, 34, 230-240.	8.9	207
11	Genome-wide signals of positive selection in human evolution. <i>Genome Research</i> , 2014, 24, 885-895.	5.5	200
12	SLiM: Simulating Evolution with Selection and Linkage. <i>Genetics</i> , 2013, 194, 1037-1039.	2.9	192
13	Strong Purifying Selection at Synonymous Sites in <i>D. melanogaster</i> . <i>PLoS Genetics</i> , 2013, 9, e1003527.	3.5	187
14	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, 20666-20671.	7.1	174
15	Can Population Genetics Adapt to Rapid Evolution?. <i>Trends in Genetics</i> , 2016, 32, 408-418.	6.7	171
16	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.	7.1	161
17	Treeâ€sequence recording in SLiM opens new horizons for forwardâ€time simulation of whole genomes. <i>Molecular Ecology Resources</i> , 2019, 19, 552-566.	4.8	154
18	Genome-Wide Patterns of Adaptation to Temperate Environments Associated with Transposable Elements in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2010, 6, e1000905.	3.5	137

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19	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.	3.5	128
20	Quantification of GC-biased gene conversion in the human genome. <i>Genome Research</i> , 2015, 25, 1215-1228.	5.5	127
21	Adaptively introgressed Neandertal haplotype at the OAS locus functionally impacts innate immune responses in humans. <i>Genome Biology</i> , 2016, 17, 246.	8.8	117
22	The role of the vaginal microbiome in gynaecological cancer. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2018, 125, 309-315.	2.3	114
23	A community-maintained standard library of population genetic models. <i>ELife</i> , 2020, 9, .	6.0	112
24	Modeling the Manipulation of Natural Populations by the Mutagenic Chain Reaction. <i>Genetics</i> , 2015, 201, 425-431.	2.9	111
25	A toxin-antidote CRISPR gene drive system for regional population modification. <i>Nature Communications</i> , 2020, 11, 1082.	12.8	100
26	Molecular safeguarding of CRISPR gene drive experiments. <i>ELife</i> , 2019, 8, .	6.0	100
27	The Majority of Recent Short DNA Insertions in the Human Genome Are Tandem Duplications. <i>Molecular Biology and Evolution</i> , 2007, 24, 1190-1197.	8.9	91
28	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.	7.1	91
29	Computational and experimental performance of CRISPR homing gene drive strategies with multiplexed gRNAs. <i>Science Advances</i> , 2020, 6, eaaz0525.	10.3	79
30	Soft Selective Sweeps in Complex Demographic Scenarios. <i>Genetics</i> , 2014, 198, 669-684.	2.9	69
31	Evaluating the performance of selection scans to detect selective sweeps in domestic dogs. <i>Molecular Ecology</i> , 2016, 25, 342-356.	3.9	69
32	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.	3.9	68
33	Core commitments for field trials of gene drive organisms. <i>Science</i> , 2020, 370, 1417-1419.	12.6	67
34	Performance analysis of novel toxin-antidote CRISPR gene drive systems. <i>BMC Biology</i> , 2020, 18, 27.	3.8	63
35	Measuring the Rates of Spontaneous Mutation From Deep and Large-Scale Polymorphism Data. <i>Genetics</i> , 2009, 182, 1219-1232.	2.9	51
36	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.	2.9	49

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37	Population Dynamics of Underdominance Gene Drive Systems in Continuous Space. <i>ACS Synthetic Biology</i> , 2020, 9, 779-792.	3.8	47
38	Estimating the Strength of Selective Sweeps from Deep Population Diversity Data. <i>Genetics</i> , 2012, 191, 593-605.	2.9	46
39	Solvable Sequence Evolution Models and Genomic Correlations. <i>Physical Review Letters</i> , 2005, 94, 138103.	7.8	43
40	DNA indels in coding regions reveal selective constraints on protein evolution in the human lineage. <i>BMC Evolutionary Biology</i> , 2007, 7, 191.	3.2	42
41	Detection of hard and soft selective sweeps from <i>Drosophila melanogaster</i> population genomic data. <i>PLoS Genetics</i> , 2021, 17, e1009373.	3.5	35
42	asymptoticMK: A Web-Based Tool for the Asymptotic McDonald-Kreitman Test. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1569-1575.	1.8	34
43	Signatures of Insecticide Selection in the Genome of <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3469-3480.	1.8	33
44	Design and analysis of CRISPR-based underdominance toxin-antidote gene drives. <i>Evolutionary Applications</i> , 2021, 14, 1052-1069.	3.1	33
45	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, 12, .	1.8	32
46	Faster than Neutral Evolution of Constrained Sequences: The Complex Interplay of Mutational Biases and Weak Selection. <i>Genome Biology and Evolution</i> , 2011, 3, 383-395.	2.5	30
47	Conundrum of jumbled mosquito genomes. <i>Science</i> , 2015, 347, 27-28.	12.6	29
48	Maximum Likelihood Estimation of Fitness Components in Experimental Evolution. <i>Genetics</i> , 2019, 211, 1005-1017.	2.9	29
49	Inferring the Strength of Selection in <i>Drosophila</i> under Complex Demographic Models. <i>Molecular Biology and Evolution</i> , 2008, 26, 513-526.	8.9	28
50	Modeling CRISPR gene drives for suppression of invasive rodents using a supervised machine learning framework. <i>PLoS Computational Biology</i> , 2021, 17, e1009660.	3.2	22
51	CorGen—measuring and generating long-range correlations for DNA sequence analysis. <i>Nucleic Acids Research</i> , 2006, 34, W692-W695.	14.5	18
52	Evolutionary Modeling in SLiM 3 for Beginners. <i>Molecular Biology and Evolution</i> , 2019, 36, 1101-1109.	8.9	18
53	Universality of long-range correlations in expansion-randomization systems. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2005, 2005, P10004-P10004.	2.3	12
54	Experimental demonstration of tethered gene drive systems for confined population modification or suppression. <i>BMC Biology</i> , 2022, 20, .	3.8	12

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55	Effects of Long-Range Correlations in DNA on Sequence Alignment Score Statistics. Journal of Computational Biology, 2007, 14, 655-668.	1.6	11
56	The Effects of Quantitative Trait Architecture on Detection Power in Short-Term Artificial Selection Experiments. G3: Genes, Genomes, Genetics, 2020, 10, 3213-3227.	1.8	5
57	Gene Drives: Dynamics and Regulatory Mattersâ€”A Report from the Workshop â€œEvaluation of Spatial and Temporal Control of Gene Drives,â€”April 4â€”5, 2019, Vienna. BioEssays, 2019, 41, 1900151.	2.5	3
58	Alignment Statistics for Long-Range Correlated Genomic Sequences. Lecture Notes in Computer Science, 2006, , 426-440.	1.3	2
59	Predicting the genomic resolution of bulk segregant analysis. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	1