

# 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	Predicting the genomic resolution of bulk segregant analysis. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	1
2	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
3	Experimental demonstration of tethered gene drive systems for confined population modification or suppression. <i>BMC Biology</i> , 2022, 20, .	3.8	12
4	Design and analysis of CRISPR-based underdominance toxin-antidote gene drives. <i>Evolutionary Applications</i> , 2021, 14, 1052-1069.	3.1	33
5	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
6	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
7	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
8	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.	1.8	5
9	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
10	Core commitments for field trials of gene drive organisms. <i>Science</i> , 2020, 370, 1417-1419.	12.6	67
11	Computational and experimental performance of CRISPR homing gene drive strategies with multiplexed gRNAs. <i>Science Advances</i> , 2020, 6, eaaz0525.	10.3	79
12	Performance analysis of novel toxin-antidote CRISPR gene drive systems. <i>BMC Biology</i> , 2020, 18, 27.	3.8	63
13	Population Dynamics of Underdominance Gene Drive Systems in Continuous Space. <i>ACS Synthetic Biology</i> , 2020, 9, 779-792.	3.8	47
14	A toxin-antidote CRISPR gene drive system for regional population modification. <i>Nature Communications</i> , 2020, 11, 1082.	12.8	100
15	A community-maintained standard library of population genetic models. <i>ELife</i> , 2020, 9, .	6.0	112
16	Maximum Likelihood Estimation of Fitness Components in Experimental Evolution. <i>Genetics</i> , 2019, 211, 1005-1017.	2.9	29
17	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
18	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, 1900151.	2.5	3

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19	Evolutionary Modeling in SLiM 3 for Beginners. <i>Molecular Biology and Evolution</i> , 2019, 36, 1101-1109.	8.9	18
20	SLiM 3: Forward Genetic Simulations Beyond the Wrightâ€Fisher Model. <i>Molecular Biology and Evolution</i> , 2019, 36, 632-637.	8.9	628
21	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
22	Molecular safeguarding of CRISPR gene drive experiments. <i>ELife</i> , 2019, 8, .	6.0	100
23	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
24	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
25	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
26	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
27	asymptoticMK: A Web-Based Tool for the Asymptotic McDonaldâ€Kreitman Test. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1569-1575.	1.8	34
28	Evolution of Resistance Against CRISPR/Cas9 Gene Drive. <i>Genetics</i> , 2017, 205, 827-841.	2.9	250
29	SLiM 2: Flexible, Interactive Forward Genetic Simulations. <i>Molecular Biology and Evolution</i> , 2017, 34, 230-240.	8.9	207
30	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
31	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
32	Evaluating the performance of selection scans to detect selective sweeps in domestic dogs. <i>Molecular Ecology</i> , 2016, 25, 342-356.	3.9	69
33	Can Population Genetics Adapt to Rapid Evolution?. <i>Trends in Genetics</i> , 2016, 32, 408-418.	6.7	171
34	Plumage Genes and Little Else Distinguish the Genomes of Hybridizing Warblers. <i>Current Biology</i> , 2016, 26, 2313-2318.	3.9	302
35	Quantification of GC-biased gene conversion in the human genome. <i>Genome Research</i> , 2015, 25, 1215-1228.	5.5	127
36	Conundrum of jumbled mosquito genomes. <i>Science</i> , 2015, 347, 27-28.	12.6	29

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37	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
38	Modeling the Manipulation of Natural Populations by the Mutagenic Chain Reaction. <i>Genetics</i> , 2015, 201, 425-431.	2.9	111
39	Soft Selective Sweeps in Complex Demographic Scenarios. <i>Genetics</i> , 2014, 198, 669-684.	2.9	69
40	Genome-wide signals of positive selection in human evolution. <i>Genome Research</i> , 2014, 24, 885-895.	5.5	200
41	SLiM: Simulating Evolution with Selection and Linkage. <i>Genetics</i> , 2013, 194, 1037-1039.	2.9	192
42	Population genomics of rapid adaptation by soft selective sweeps. <i>Trends in Ecology and Evolution</i> , 2013, 28, 659-669.	8.7	471
43	Strong Purifying Selection at Synonymous Sites in <i>D. melanogaster</i> . <i>PLoS Genetics</i> , 2013, 9, e1003527.	3.5	187
44	Frequent adaptation and the McDonald-Kreitman test. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8615-8620.	7.1	231
45	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
46	Estimating the Strength of Selective Sweeps from Deep Population Diversity Data. <i>Genetics</i> , 2012, 191, 593-605.	2.9	46
47	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
48	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
49	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
50	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
51	Measuring the Rates of Spontaneous Mutation From Deep and Large-Scale Polymorphism Data. <i>Genetics</i> , 2009, 182, 1219-1232.	2.9	51
52	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
53	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
54	Effects of Long-Range Correlations in DNA on Sequence Alignment Score Statistics. <i>Journal of Computational Biology</i> , 2007, 14, 655-668.	1.6	11

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55	DNA indels in coding regions reveal selective constraints on protein evolution in the human lineage. BMC Evolutionary Biology, 2007, 7, 191.	3.2	42
56	CorGen—measuring and generating long-range correlations for DNA sequence analysis. Nucleic Acids Research, 2006, 34, W692-W695.	14.5	18
57	Alignment Statistics for Long-Range Correlated Genomic Sequences. Lecture Notes in Computer Science, 2006, , 426-440.	1.3	2
58	Universality of long-range correlations in expansion—randomization systems. Journal of Statistical Mechanics: Theory and Experiment, 2005, 2005, P10004-P10004.	2.3	12
59	Solvable Sequence Evolution Models and Genomic Correlations. Physical Review Letters, 2005, 94, 138103.	7.8	43