

# Philipp W Messer

## List of Publications by Year in Descending Order

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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	A homing suppression gene drive with multiplexed gRNAs maintains high drive conversion efficiency and avoids functional resistance alleles.. <i>G3: Genes, Genomes, Genetics</i> , <b>2022</b> ,	3.2	6
78	Experimental demonstration of tethered gene drive systems for confined population modification or suppression. <i>BMC Biology</i> , <b>2022</b> , 20,	7.3	4
77	Modeling CRISPR gene drives for suppression of invasive rodents using a supervised machine learning framework.. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1009660	5	6
76	Design and analysis of CRISPR-based underdominance toxin-antidote gene drives. <i>Evolutionary Applications</i> , <b>2021</b> , 14, 1052-1069	4.8	14
75	Detection of hard and soft selective sweeps from <i>Drosophila melanogaster</i> population genomic data. <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009373	6	7
74	Suppression gene drive in continuous space can result in unstable persistence of both drive and wild-type alleles. <i>Molecular Ecology</i> , <b>2021</b> , 30, 1086-1101	5.7	21
73	Computational and experimental performance of CRISPR homing gene drive strategies with multiplexed gRNAs. <i>Science Advances</i> , <b>2020</b> , 6, eaaz0525	14.3	41
72	Performance analysis of novel toxin-antidote CRISPR gene drive systems. <i>BMC Biology</i> , <b>2020</b> , 18, 27	7.3	31
71	Population Dynamics of Underdominance Gene Drive Systems in Continuous Space. <i>ACS Synthetic Biology</i> , <b>2020</b> , 9, 779-792	5.7	22
70	A toxin-antidote CRISPR gene drive system for regional population modification. <i>Nature Communications</i> , <b>2020</b> , 11, 1082	17.4	56
69	A community-maintained standard library of population genetic models. <i>ELife</i> , <b>2020</b> , 9,	8.9	35
68	The Effects of Quantitative Trait Architecture on Detection Power in Short-Term Artificial Selection Experiments. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 3213-3227	3.2	1
67	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> , <b>2020</b> , 117, 24377-24383	11.5	37
66	Core commitments for field trials of gene drive organisms. <i>Science</i> , <b>2020</b> , 370, 1417-1419	33.3	35
65	Maximum Likelihood Estimation of Fitness Components in Experimental Evolution. <i>Genetics</i> , <b>2019</b> , 211, 1005-1017	4	22
64	CRISPR Gene Drive Efficiency and Resistance Rate Is Highly Heritable with No Common Genetic Loci of Large Effect. <i>Genetics</i> , <b>2019</b> , 212, 333-341	4	31
63	Molecular safeguarding of CRISPR gene drive experiments. <i>ELife</i> , <b>2019</b> , 8,	8.9	65

62	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> , <b>2019</b> , 41, e1900151	4.1	3
61	Evolutionary Modeling in SLiM 3 for Beginners. <i>Molecular Biology and Evolution</i> , <b>2019</b> , 36, 1101-1109	8.3	2
60	SLiM 3: Forward Genetic Simulations Beyond the Wright-Fisher Model. <i>Molecular Biology and Evolution</i> , <b>2019</b> , 36, 632-637	8.3	247
59	Tree-sequence recording in SLiM opens new horizons for forward-time simulation of whole genomes. <i>Molecular Ecology Resources</i> , <b>2019</b> , 19, 552-566	8.4	67
58	The role of the vaginal microbiome in gynaecological cancer. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , <b>2018</b> , 125, 309-315	3.7	73
57	Reducing resistance allele formation in CRISPR gene drive. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 5522-5527	11.5	151
56	Signatures of Insecticide Selection in the Genome of. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 3469-3480	3.2	17
55	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> , <b>2018</b> , 115, 12471-12476	11.5	96
54	asymptoticMK: A Web-Based Tool for the Asymptotic McDonald-Kreitman Test. <i>G3: Genes, Genomes, Genetics</i> , <b>2017</b> , 7, 1569-1575	3.2	19
53	Evolution of Resistance Against CRISPR/Cas9 Gene Drive. <i>Genetics</i> , <b>2017</b> , 205, 827-841	4	189
52	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> , <b>2017</b> , 13, e1006796	6	176
51	SLiM 2: Flexible, Interactive Forward Genetic Simulations. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 2308-2340	8.5	141
50	Plumage Genes and Little Else Distinguish the Genomes of Hybridizing Warblers. <i>Current Biology</i> , <b>2016</b> , 26, 2313-8	6.3	215
49	Adaptively introgressed Neandertal haplotype at the OAS locus functionally impacts innate immune responses in humans. <i>Genome Biology</i> , <b>2016</b> , 17, 246	18.3	70
48	Evaluating the performance of selection scans to detect selective sweeps in domestic dogs. <i>Molecular Ecology</i> , <b>2016</b> , 25, 342-56	5.7	53
47	Can Population Genetics Adapt to Rapid Evolution?. <i>Trends in Genetics</i> , <b>2016</b> , 32, 408-418	8.5	108
46	Recent selective sweeps in North American <i>Drosophila melanogaster</i> show signatures of soft sweeps. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005004	6	251
45	Modeling the Manipulation of Natural Populations by the Mutagenic Chain Reaction. <i>Genetics</i> , <b>2015</b> , 201, 425-31	4	82

44	Quantification of GC-biased gene conversion in the human genome. <i>Genome Research</i> , <b>2015</b> , 25, 1215-28	9.7	75
43	Evolutionary genomics. Conundrum of jumbled mosquito genomes. <i>Science</i> , <b>2015</b> , 347, 27-8	33.3	25
42	Soft selective sweeps in complex demographic scenarios. <i>Genetics</i> , <b>2014</b> , 198, 669-84	4	53
41	Genome-wide signals of positive selection in human evolution. <i>Genome Research</i> , <b>2014</b> , 24, 885-95	9.7	132
40	SLiM: simulating evolution with selection and linkage. <i>Genetics</i> , <b>2013</b> , 194, 1037-9	4	131
39	Population genomics of rapid adaptation by soft selective sweeps. <i>Trends in Ecology and Evolution</i> , <b>2013</b> , 28, 659-69	10.9	324
38	Strong purifying selection at synonymous sites in <i>D. melanogaster</i> . <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003527	6	129
37	Frequent adaptation and the McDonald-Kreitman test. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 8615-20	11.5	147
36	Estimating the strength of selective sweeps from deep population diversity data. <i>Genetics</i> , <b>2012</b> , 191, 593-605	4	37
35	Genome patterns of selection and introgression of haplotypes in natural populations of the house mouse ( <i>Mus musculus</i> ). <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002891	6	105
34	Faster than neutral evolution of constrained sequences: the complex interplay of mutational biases and weak selection. <i>Genome Biology and Evolution</i> , <b>2011</b> , 3, 383-95	3.9	29
33	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> , <b>2011</b> , 108, 20666-71	11.5	135
32	Evidence that adaptation in <i>Drosophila</i> is not limited by mutation at single sites. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1000924	6	201
31	Genome-wide patterns of adaptation to temperate environments associated with transposable elements in <i>Drosophila</i> . <i>PLoS Genetics</i> , <b>2010</b> , 6, e1000905	6	111
30	Measuring the rates of spontaneous mutation from deep and large-scale polymorphism data. <i>Genetics</i> , <b>2009</b> , 182, 1219-32	4	35
29	Inferring the strength of selection in <i>Drosophila</i> under complex demographic models. <i>Molecular Biology and Evolution</i> , <b>2009</b> , 26, 513-26	8.3	18
28	DNA indels in coding regions reveal selective constraints on protein evolution in the human lineage. <i>BMC Evolutionary Biology</i> , <b>2007</b> , 7, 191	3	35
27	The majority of recent short DNA insertions in the human genome are tandem duplications. <i>Molecular Biology and Evolution</i> , <b>2007</b> , 24, 1190-7	8.3	64

26	Effects of long-range correlations in DNA on sequence alignment score statistics. <i>Journal of Computational Biology</i> , <b>2007</b> , 14, 655-68	1.7	8
25	CorGen--measuring and generating long-range correlations for DNA sequence analysis. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, W692-5	20.1	14
24	Alignment Statistics for Long-Range Correlated Genomic Sequences. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 426-440	0.9	2
23	Universality of long-range correlations in expansion-randomization systems. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , <b>2005</b> , 2005, P10004-P10004	1.9	11
22	Solvable sequence evolution models and genomic correlations. <i>Physical Review Letters</i> , <b>2005</b> , 94, 138103-4	37.4	37
21	Molecular safeguarding of CRISPR gene drive experiments		1
20	The Effects of Quantitative Trait Architecture on Detection Power in Artificial Selection Experiments		1
19	Evolution of Resistance Against CRISPR/Cas9 Gene Drive		5
18	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
17	Reducing resistance allele formation in CRISPR gene drives		4
16	A community-maintained standard library of population genetic models		7
15	Detection of hard and soft selective sweeps from <i>Drosophila melanogaster</i> population genomic data		2
14	Tree-sequence recording in SLiM opens new horizons for forward-time simulation of whole genomes		4
13	SLiM 3: Forward genetic simulations beyond the Wright-Fisher model		51
12	Multiple loci of small effect confer wide variability in efficiency and resistance rate of CRISPR gene drive		4
11	Population dynamics of underdominance gene drive systems in continuous space		7
10	A toxin-antidote CRISPR gene drive system for regional population modification		8
9	Performance analysis of novel toxin-antidote CRISPR gene drive systems		11

8	Resistance is futile: A CRISPR homing gene drive targeting a haplolethal gene	13
7	Computational and experimental performance of CRISPR homing gene drive strategies with multiplexed gRNAs	7
6	Suppression gene drive in continuous space can result in unstable persistence of both drive and wild-type alleles	8
5	Design and analysis of CRISPR-based underdominance toxin-antidote gene drives	10
4	Adaptively introgressed Neandertal haplotype at the OAS locus functionally impacts innate immune responses in humans	1
3	Fitness effects of CRISPR endonucleases in <i>Drosophila melanogaster</i> populations	5
2	Experimental demonstration of tethered gene drive systems for confined population modification or suppression	3
1	A homing suppression gene drive with multiplexed gRNAs maintains high drive conversion efficiency and avoids functional resistance alleles	4