

# Ilan Gronau

## 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.

26

papers

2,184

citations

16

h-index

28

g-index

28

ext. papers

2,780

ext. citations

10.9

avg, IF

4.65

L-index

#	Paper	IF	Citations
26	A community-maintained standard library of population genetic models. <i>ELife</i> , <b>2020</b> , 9,	8.9	35
25	Genomic islands of differentiation in a rapid avian radiation have been driven by recent selective sweeps. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 30554-30563	11.5	9
24	Comparative genomics provides new insights into the remarkable adaptations of the African wild dog ( <i>Lycaon pictus</i> ). <i>Scientific Reports</i> , <b>2019</b> , 9, 8329	4.9	15
23	Comparing evolutionary distances via adaptive distance functions. <i>Journal of Theoretical Biology</i> , <b>2018</b> , 440, 88-99	2.3	
22	Response to Hohenlohe. <i>Science Advances</i> , <b>2017</b> , 3, e1701233	14.3	6
21	Whole-genome sequence analysis shows that two endemic species of North American wolf are admixtures of the coyote and gray wolf. <i>Science Advances</i> , <b>2016</b> , 2, e1501714	14.3	98
20	Worldwide patterns of genomic variation and admixture in gray wolves. <i>Genome Research</i> , <b>2016</b> , 26, 1639-73	9.7	118
19	Ancient gene flow from early modern humans into Eastern Neanderthals. <i>Nature</i> , <b>2016</b> , 530, 429-33	50.4	269
18	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1005851	6	56
17	A method for calculating probabilities of fitness consequences for point mutations across the human genome. <i>Nature Genetics</i> , <b>2015</b> , 47, 276-83	36.3	175
16	Distinguishing noise from signal in patterns of genomic divergence in a highly polymorphic avian radiation. <i>Molecular Ecology</i> , <b>2015</b> , 24, 4238-51	5.7	56
15	Adaptive evolution of testis-specific, recently evolved, clustered miRNAs in <i>Drosophila</i> . <i>Rna</i> , <b>2014</b> , 20, 1195-209	5.8	27
14	Genome-wide inference of ancestral recombination graphs. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004342	6	200
13	Genome sequencing highlights the dynamic early history of dogs. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004016	6	372
12	Genome-wide inference of natural selection on human transcription factor binding sites. <i>Nature Genetics</i> , <b>2013</b> , 45, 723-9	36.3	95
11	Inference of natural selection from interspersed genomic elements based on polymorphism and divergence. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 1159-71	8.3	58
10	Replacing and additive horizontal gene transfer in <i>Streptococcus</i> . <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 3309-20	8.3	23

9	Fast and reliable reconstruction of phylogenetic trees with indistinguishable edges. <i>Random Structures and Algorithms</i> , <b>2012</b> , 40, 350-384	0.8	9
8	Bayesian inference of ancient human demography from individual genome sequences. <i>Nature Genetics</i> , <b>2011</b> , 43, 1031-4	36.3	387
7	Recursive construction and error correction of DNA molecules and libraries from synthetic and natural DNA. <i>Methods in Enzymology</i> , <b>2011</b> , 498, 207-45	1.7	1
6	Adaptive distance measures for resolving K2P quartets: metric separation versus stochastic noise. <i>Journal of Computational Biology</i> , <b>2010</b> , 17, 1509-18	1.7	3
5	Towards optimal distance functions for stochastic substitution models. <i>Journal of Theoretical Biology</i> , <b>2009</b> , 260, 294-307	2.3	8
4	Recursive construction of perfect DNA molecules from imperfect oligonucleotides. <i>Molecular Systems Biology</i> , <b>2008</b> , 4, 191	12.2	47
3	Optimal implementations of UPGMA and other common clustering algorithms. <i>Information Processing Letters</i> , <b>2007</b> , 104, 205-210	0.8	102
2	Neighbor joining algorithms for inferring phylogenies via LCA distances. <i>Journal of Computational Biology</i> , <b>2007</b> , 14, 1-15	1.7	8
1	A community-maintained standard library of population genetic models		7