Ilan Gronau

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1694428/publications.pdf

Version: 2024-02-01

430754 610775 3,136 26 18 24 citations h-index g-index papers 28 28 28 5327 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Bayesian inference of ancient human demography from individual genome sequences. Nature Genetics, 2011, 43, 1031-1034.	9.4	526
2	Genome Sequencing Highlights the Dynamic Early History of Dogs. PLoS Genetics, 2014, 10, e1004016.	1.5	481
3	Ancient gene flow from early modern humans into Eastern Neanderthals. Nature, 2016, 530, 429-433.	13.7	392
4	Genome-Wide Inference of Ancestral Recombination Graphs. PLoS Genetics, 2014, 10, e1004342.	1.5	323
5	A method for calculating probabilities of fitness consequences for point mutations across the human genome. Nature Genetics, 2015, 47, 276-283.	9.4	247
6	Worldwide patterns of genomic variation and admixture in gray wolves. Genome Research, 2016, 26, 163-173.	2.4	160
7	Whole-genome sequence analysis shows that two endemic species of North American wolf are admixtures of the coyote and gray wolf. Science Advances, 2016, 2, e1501714.	4.7	150
8	Optimal implementations of UPGMA and other common clustering algorithms. Information Processing Letters, 2007, 104, 205-210.	0.4	147
9	Genome-wide inference of natural selection on human transcription factor binding sites. Nature Genetics, 2013, 45, 723-729.	9.4	121
10	A community-maintained standard library of population genetic models. ELife, 2020, 9, .	2.8	112
11	Inference of Natural Selection from Interspersed Genomic Elements Based on Polymorphism and Divergence. Molecular Biology and Evolution, 2013, 30, 1159-1171.	3 . 5	77
12	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. PLoS Genetics, 2016, 12, e1005851.	1.5	77
13	Distinguishing noise from signal in patterns of genomic divergence in a highly polymorphic avian radiation. Molecular Ecology, 2015, 24, 4238-4251.	2.0	72
14	Recursive construction of perfect DNA molecules from imperfect oligonucleotides. Molecular Systems Biology, 2008, 4, 191.	3.2	50
15	Adaptive evolution of testis-specific, recently evolved, clustered miRNAs in <i>Drosophila</i> . Rna, 2014, 20, 1195-1209.	1.6	47
16	Genomic islands of differentiation in a rapid avian radiation have been driven by recent selective sweeps. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 30554-30565.	3.3	40
17	Replacing and Additive Horizontal Gene Transfer in Streptococcus. Molecular Biology and Evolution, 2012, 29, 3309-3320.	3.5	33
18	Comparative genomics provides new insights into the remarkable adaptations of the African wild dog (Lycaon pictus). Scientific Reports, 2019, 9, 8329.	1.6	23

#	ARTICLE	IF	CITATION
19	Neighbor Joining Algorithms for Inferring Phylogenies via LCA Distances. Journal of Computational Biology, 2007, 14, 1-15.	0.8	15
20	Fast and reliable reconstruction of phylogenetic trees with indistinguishable edges. Random Structures and Algorithms, 2012, 40, 350-384.	0.6	12
21	Towards optimal distance functions for stochastic substitution models. Journal of Theoretical Biology, 2009, 260, 294-307.	0.8	9
22	Response to Hohenlohe <i>et al</i> Science Advances, 2017, 3, e1701233.	4.7	6
23	Adaptive Distance Measures for Resolving K2P Quartets: Metric Separation versus Stochastic Noise. Journal of Computational Biology, 2010, 17, 1509-1518.	0.8	3
24	Recursive Construction and Error Correction of DNA Molecules and Libraries from Synthetic and Natural DNA. Methods in Enzymology, 2011, 498, 207-245.	0.4	1
25	Comparing evolutionary distances via adaptive distance functions. Journal of Theoretical Biology, 2018, 440, 88-99.	0.8	0
26	Optimal Design of Synthetic DNA Sequences Without Unwanted Binding Sites. Journal of Computational Biology, 0, , .	0.8	0