Michael DeGiorgio

List of Publications by Year
in descending order

63 papers	5,730 citations	186265 28 h-index	144013 57 g-index
67 all docs	67 docs citations	67 times ranked	8303 citing authors

#	Article	IF	Citations
1	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. Nature, 2014, 505, 87-91.	27.8	821
2	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. Nature, 2014, 506, 225-229.	27.8	500
3	Genomic evidence for the Pleistocene and recent population history of Native Americans. Science, 2015, 349, aab3884.	12.6	449
4	Genomic analyses inform on migration events during the peopling of Eurasia. Nature, 2016, 538, 238-242.	27.8	360
5	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. Genome Research, 2015, 25, 459-466.	5.5	348
6	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. Nature, 2014, 507, 225-228.	27.8	328
7	The genetic prehistory of the New World Arctic. Science, 2014, 345, 1255832.	12.6	264
8	SweepFinder2: increased sensitivity, robustness and flexibility. Bioinformatics, 2016, 32, 1895-1897.	4.1	238
9	Genetic Signatures Reveal High-Altitude Adaptation in a Set of Ethiopian Populations. Molecular Biology and Evolution, 2013, 30, 1877-1888.	8.9	173
10	Explaining worldwide patterns of human genetic variation using a coalescent-based serial founder model of migration outward from Africa. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16057-16062.	7.1	161
11	A Model-Based Approach for Identifying Signatures of Ancient Balancing Selection in Genetic Data. PLoS Genetics, 2014, 10, e1004561.	3.5	159
12	Detecting recent selective sweeps while controlling for mutation rate and background selection. Molecular Ecology, 2016, 25, 142-156.	3.9	157
13	Properties of Consensus Methods for Inferring Species Trees from Gene Trees. Systematic Biology, 2009, 58, 35-54.	5.6	135
14	A time transect of exomes from a Native American population before and after European contact. Nature Communications, 2016, 7, 13175.	12.8	134
15	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. Cell, 2019, 179, 736-749.e15.	28.9	126
16	Whole-Exome Sequencing of 2,000 Danish Individuals and the Role of Rare Coding Variants in Type 2 Diabetes. American Journal of Human Genetics, 2013, 93, 1072-1086.	6.2	124
17	A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. American Journal of Human Genetics, 2014, 95, 584-589.	6.2	119
18	Ancient individuals from the North American Northwest Coast reveal 10,000 years of regional genetic continuity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4093-4098.	7.1	100

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19	Empty Niches after Extinctions Increase Population Sizes of Modern Corals. Current Biology, 2016, 26, 3190-3194.	3.9	79
20	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. Current Biology, 2014, 24, R1035-R1037.	3.9	73
21	Detection and Classification of Hard and Soft Sweeps from Unphased Genotypes by Multilocus Genotype Identity. Genetics, 2018, 210, 1429-1452.	2.9	69
22	VolcanoFinder: Genomic scans for adaptive introgression. PLoS Genetics, 2020, 16, e1008867.	3.5	62
23	Fast and Consistent Estimation of Species Trees Using Supermatrix Rooted Triples. Molecular Biology and Evolution, 2010, 27, 552-569.	8.9	61
24	Archaic Hominin Introgression in Africa Contributes to Functional Salivary MUC7 Genetic Variation. Molecular Biology and Evolution, 2017, 34, 2704-2715.	8.9	57
25	Robustness to Divergence Time Underestimation When Inferring Species Trees from Estimated Gene Trees. Systematic Biology, 2014, 63, 66-82.	5.6	54
26	Coalescence-Time Distributions in a Serial Founder Model of Human Evolutionary History. Genetics, 2011, 189, 579-593.	2.9	41
27	<i>bammds:</i> a tool for assessing the ancestry of low-depth whole-genome data using multidimensional scaling (MDS). Bioinformatics, 2014, 30, 2962-2964.	4.1	40
28	Patterns of Genetic Coding Variation in a Native American Population before and after European Contact. American Journal of Human Genetics, 2018, 102, 806-815.	6.2	33
29	Fast and robust detection of ancestral selective sweeps. Molecular Ecology, 2017, 26, 6871-6891.	3.9	31
30	Localizing and Classifying Adaptive Targets with Trend Filtered Regression. Molecular Biology and Evolution, 2019, 36, 252-270.	8.9	31
31	Admixture and Ancestry Inference from Ancient and Modern Samples through Measures of Population Genetic Drift. Human Biology, 2017, 89, 21.	0.2	30
32	A Likelihood Approach for Uncovering Selective Sweep Signatures from Haplotype Data. Molecular Biology and Evolution, 2020, 37, 3023-3046.	8.9	28
33	An Unbiased Estimator of Gene Diversity in Samples Containing Related Individuals. Molecular Biology and Evolution, 2008, 26, 501-512.	8.9	26
34	An Unbiased Estimator of Gene Diversity with Improved Variance for Samples Containing Related and Inbred Individuals of any Ploidy. G3: Genes, Genomes, Genetics, 2017, 7, 671-691.	1.8	26
35	Detection of Shared Balancing Selection in the Absence of Trans-Species Polymorphism. Molecular Biology and Evolution, 2019, 36, 177-199.	8.9	26
36	Flexible Mixture Model Approaches That Accommodate Footprint Size Variability for Robust Detection of Balancing Selection. Molecular Biology and Evolution, 2020, 37, 3267-3291.	8.9	23

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37	An empirical evaluation of two-stage species tree inference strategies using a multilocus dataset from North American pines. BMC Evolutionary Biology, 2014, 14, 67.	3.2	21
38	Geographic Sampling Scheme as a Determinant of the Major Axis of Genetic Variation in Principal Components Analysis. Molecular Biology and Evolution, 2013, 30, 480-488.	8.9	20
39	Selection and thermostability suggest G-quadruplexes are novel functional elements of the human genome. Genome Research, 2021, 31, 1136-1149.	5.5	20
40	Learning the properties of adaptive regions with functional data analysis. PLoS Genetics, 2020, 16, e1008896.	3.5	16
41	Reverse Transcription Errors and RNAâ€"DNA Differences at Short Tandem Repeats. Molecular Biology and Evolution, 2016, 33, 2744-2758.	8.9	15
42	High Levels of Copy Number Variation of Ampliconic Genes across Major Human Y Haplogroups. Genome Biology and Evolution, 2018, 10, 1333-1350.	2.5	15
43	Identifying and Classifying Shared Selective Sweeps from Multilocus Data. Genetics, 2020, 215, 143-171.	2.9	14
44	Consistency and inconsistency of consensus methods for inferring species trees from gene trees in the presence of ancestral population structure. Theoretical Population Biology, 2016, 110, 12-24.	1.1	13
45	Ampliconic Genes on the Great Ape Y Chromosomes: Rapid Evolution of Copy Number but Conservation of Expression Levels. Genome Biology and Evolution, 2020, 12, 842-859.	2.5	13
46	A spatially aware likelihood test to detect sweeps from haplotype distributions. PLoS Genetics, 2022, 18, e1010134.	3.5	13
47	The roles of balancing selection and recombination in the evolution of rattlesnake venom. Nature Ecology and Evolution, 2022, 6, 1367-1380.	7.8	13
48	A High-Resolution View of Adaptive Event Dynamics in a Plasmid. Genome Biology and Evolution, 2019, 11, 3022-3034.	2.5	11
49	Ancient and modern genomics of the Ohlone Indigenous population of California. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2111533119.	7.1	10
50	Unbiased Estimation of Gene Diversity in Samples Containing Related Individuals: Exact Variance and Arbitrary Ploidy. Genetics, 2010, 186, 1367-1387.	2.9	8
51	Learning Retention Mechanisms and Evolutionary Parameters of Duplicate Genes from Their Expression Data. Molecular Biology and Evolution, 2021, 38, 1209-1224.	8.9	8
52	The genomic prehistory of the Indigenous peoples of Uruguay. , 2022, 1, .		7
53	Computational and Statistical Analyses of Insertional Polymorphic Endogenous Retroviruses in a Non-Model Organism. Computation, 2014, 2, 221-245.	2.0	5
54	Maximum Likelihood Estimation of Species Trees from Gene Trees in the Presence of Ancestral Population Structure. Genome Biology and Evolution, 2020, 12, 3977-3995.	2.5	5

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55	Understanding the Adaptive Evolutionary Histories of South American Ancient and Present-Day Populations via Genomics. Genes, 2021, 12, 360.	2.4	3
56	`BalLeRMix`+: mixture model approaches for robust joint identification of both positive selection and long-term balancing selection. Bioinformatics, 2022, 38, 861-863.	4.1	3
57	Properties and unbiased estimation of F- and D-statistics in samples containing related and inbred individuals. Genetics, 2022, 220, .	2.9	2
58	*PhyloWGA*: chromosome-aware phylogenetic interrogation of whole genome alignments. Bioinformatics, 2021, 37, 1923-1925.	4.1	1
59	Of Traits and Trees: Probabilistic Distances under Continuous Trait Models for Dissecting the Interplay among Phylogeny, Model, and Data. Systematic Biology, 2021, 70, 660-680.	5.6	1
60	VolcanoFinder: Genomic scans for adaptive introgression. , 2020, 16, e1008867.		0
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