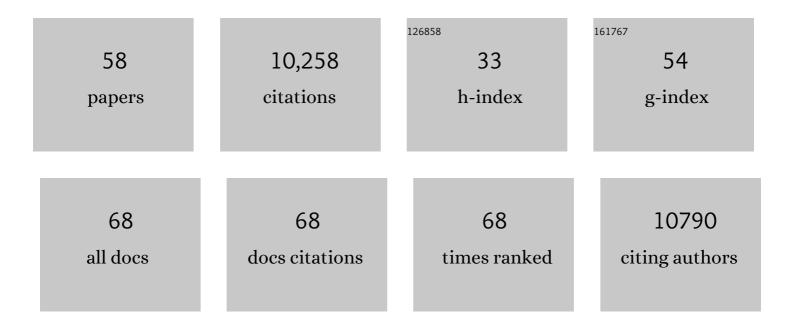
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Maximum likelihood estimation of a migration matrix and effective population sizes in n subpopulations by using a coalescent approach. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 4563-4568.	3.3	1,610
2	Maximum-Likelihood Estimation of Migration Rates and Effective Population Numbers in Two Populations Using a Coalescent Approach. Genetics, 1999, 152, 763-773.	1.2	902
3	Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. Bioinformatics, 2006, 22, 341-345.	1.8	785
4	PERSPECTIVE: GENE DIVERGENCE, POPULATION DIVERGENCE, AND THE VARIANCE IN COALESCENCE TIME IN PHYLOGEOGRAPHIC STUDIES. Evolution; International Journal of Organic Evolution, 2000, 54, 1839-1854.	1.1	757
5	PERSPECTIVE: GENE DIVERGENCE, POPULATION DIVERGENCE, AND THE VARIANCE INCOALESCENCE TIME IN PHYLOGEOGRAPHIC STUDIES. Evolution; International Journal of Organic Evolution, 2000, 54, 1839.	1.1	604
6	Unified Framework to Evaluate Panmixia and Migration Direction Among Multiple Sampling Locations. Genetics, 2010, 185, 313-326.	1.2	583
7	BEAGLE: An Application Programming Interface and High-Performance Computing Library for Statistical Phylogenetics. Systematic Biology, 2012, 61, 170-173.	2.7	555
8	The utility of single nucleotide polymorphisms in inferences of population history. Trends in Ecology and Evolution, 2003, 18, 249-256.	4.2	544
9	Estimating Divergence Times from Molecular Data on Phylogenetic and Population Genetic Timescales. Annual Review of Ecology, Evolution, and Systematics, 2002, 33, 707-740.	6.7	521
10	Strength and tempo of directional selection in the wild. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 9157-9160.	3.3	401
11	Early Origin and Recent Expansion of Plasmodium falciparum. Science, 2003, 300, 318-321.	6.0	365
12	Effect of unsampled populations on the estimation of population sizes and migration rates between sampled populations. Molecular Ecology, 2004, 13, 827-836.	2.0	263
13	Host Switch Leads to Emergence of Plasmodium vivax Malaria in Humans. Molecular Biology and Evolution, 2005, 22, 1686-1693.	3.5	199
14	Gene flow and population structure in the Mexican blind cavefish complex (Astyanax mexicanus). BMC Evolutionary Biology, 2012, 12, 9.	3.2	174
15	How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use?. , 2001, , 42-79.		163
16	Global Migration Dynamics Underlie Evolution and Persistence of Human Influenza A (H3N2). PLoS Pathogens, 2010, 6, e1000918.	2.1	151
17	In defence of model-based inference in phylogeography. Molecular Ecology, 2010, 19, 436-446.	2.0	141
18	Usefulness of Single Nucleotide Polymorphism Data for Estimating Population Parameters. Genetics, 2000, 156, 439-447.	1.2	126

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19	The Strength of Phenotypic Selection in Natural Populations. American Naturalist, 2001, 157, 245.	1.0	114
20	A synthesis of genetic connectivity in deepâ€sea fauna and implications for marine reserve design. Molecular Ecology, 2016, 25, 3276-3298.	2.0	109
21	Phylogeographic patterns of genetic diversity in eastern Mediterranean water frogs were determined by geological processes and climate change in the Late Cenozoic. Journal of Biogeography, 2010, 37, 2111-2124.	1.4	101
22	GEOLOGICALLY DATED SEA BARRIERS CALIBRATE A PROTEIN CLOCK FOR AEGEAN WATER FROGS. Evolution; International Journal of Organic Evolution, 1996, 50, 1676-1687.	1.1	98
23	Widespread unidirectional transfer of mitochondrial DNA: a case in western Palaearctic water frogs. Journal of Evolutionary Biology, 2008, 21, 668-681.	0.8	96
24	Spontaneous heterosis in larval life-history traits of hemiclonal frog hybrids. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 2171-2176.	3.3	79
25	Geologically Dated Sea Barriers Calibrate a Protein Clock for Aegean Water Frogs. Evolution; International Journal of Organic Evolution, 1996, 50, 1676.	1.1	73
26	Global diversity and oceanic divergence of humpback whales (<i>Megaptera novaeangliae</i>). Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20133222.	1.2	66
27	Genetic structuring and migration patterns of Atlantic bigeye tuna, Thunnus obesus (Lowe, 1839). BMC Evolutionary Biology, 2008, 8, 252.	3.2	53
28	Population Genetic Inference With MIGRATE. Current Protocols in Bioinformatics, 2019, 68, e87.	25.8	53
29	Strong and stable geographic differentiation of swamp buffalo maternal and paternal lineages indicates domestication in the China/Indochina border region. Molecular Ecology, 2016, 25, 1530-1550.	2.0	49
30	Genetic compatibility between sexual and clonal genomes in local populations of the hybridogeneticRana esculenta complex. Evolutionary Ecology, 1996, 10, 531-543.	0.5	46
31	Exceptional maternal lineage diversity in brown bears (<i>Ursus arctos</i>) from Turkey. Zoological Journal of the Linnean Society, 2016, 176, 463-477.	1.0	44
32	Likelihoods on coalescents: a Monte Carlo sampling approach to inferring parameters from population samples of molecular data. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 1999, , 163-185.	1.0	44
33	Multigene analysis suggests ecological speciation in the fungal pathogen <i>Claviceps purpurea</i> . Molecular Ecology, 2008, 17, 2276-2286.	2.0	43
34	Evaluating marginal likelihood with thermodynamic integration method and comparison with several other numerical methods. Water Resources Research, 2016, 52, 734-758.	1.7	41
35	Genetic data reveal that water frogs of Cyprus (genus <i>Pelophylax</i>) are an endemic species of Messinian origin. Zoosystematics and Evolution, 2012, 88, 261-283.	0.4	37
36	Genetic Divergence and Evolution of Reproductive Isolation in Eastern Mediterranean Water Frogs. , 2010, , 373-403.		35

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37	Evolution of serum albumin intron-1 is shaped by a 5′ truncated non-long terminal repeat retrotransposon in western Palearctic water frogs (Neobatrachia). Molecular Phylogenetics and Evolution, 2009, 53, 784-791.	1.2	29
38	Estimation of the Population Scaled Mutation Rate From Microsatellite Data. Genetics, 2007, 177, 1967-1968.	1.2	24
39	Fractional coalescent. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6244-6249.	3.3	24
40	Assortative Mating Drives Linkage Disequilibrium between Sperm and Egg Recognition Protein Loci in the Sea Urchin Strongylocentrotus purpuratus. Molecular Biology and Evolution, 2015, 32, 859-870.	3.5	20
41	Microsatellites: A tool for evolutionary genetic studies of western Palearctic water frogs. Zoosystematics and Evolution, 2001, 77, 43-50.	0.4	15
42	Biogeographic models of gene flow in two waterfowl of the Australoâ€Papuan tropics. Ecology and Evolution, 2012, 2, 2803-2814.	0.8	14
43	A possible explanation for the population size discrepancy in tuna (genus Thunnus) estimated from mitochondrial DNA and microsatellite data. Molecular Phylogenetics and Evolution, 2013, 66, 463-468.	1.2	14
44	Genetic Variation of Anastrepha suspensa (Diptera: Tephritidae) in Florida and the Caribbean Using Microsatellite DNA Markers. Journal of Economic Entomology, 2010, 103, 2214-2222.	0.8	13
45	Balancing a Cline by Influx of Migrants: A Genetic Transition in Water Frogs of Eastern Greece. Journal of Heredity, 2013, 104, 57-71.	1.0	13
46	When did Neanderthals and modern humans diverge?. Evolutionary Anthropology, 2003, 11, 60-63.	1.7	12
47	Hemiclone diversity in the hybridogenetic frog Rana esculenta outside the area of clone formation: the view from protein electrophoresis. Journal of Zoological Systematics and Evolutionary Research, 2007, 46, 070907105857002-???.	0.6	11
48	Pathways of cryptic invasion in a fish parasite traced using coalescent analysis and epidemiological survey. Biological Invasions, 2013, 15, 1907-1923.	1.2	9
49	Population Genetics of HIV: Parameter Estimation Using Genealogy-based Methods. , 2002, , 217-252.		5
50	A Continuous Method for Gene Flow. Genetics, 2013, 194, 687-696.	1.2	4
51	Population divergence time estimation using individual lineage label switching. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	4
52	Developmental disturbances in Rana esculenta tadpoles and metamorphs. Zoosystematics and Evolution, 2008, 77, 79-86.	0.4	3
53	Are hybrid clonals species? A case for enlightened anarchy. Amphibia - Reptilia, 1996, 17, 315-320.	0.1	2
54	Genetic diversity and population structure of Leishmania (Viannia) braziliensis in the Peruvian jungle. PLoS Neglected Tropical Diseases, 2022, 16, e0010374.	1.3	2

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55	Statistical analyses of population genetic data. Trends in Ecology and Evolution, 1997, 12, 488.	4.2	1
56	Quasi-Monte Carlo method in population genetics parameter estimation. Mathematics and Computers in Simulation, 2014, 103, 33-38.	2.4	1
57	STATISTICAL METHODS IN (MOLECULAR) EVOLUTION. Evolution; International Journal of Organic Evolution, 2006, 60, 421-423.	1.1	Ο
58	STATISTICAL METHODS IN (MOLECULAR) EVOLUTION1. Evolution; International Journal of Organic Evolution, 2006, 60, 421.	1.1	0