

Peter Beerli

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

10,258
citations

126858

33
h-index

161767

54
g-index

68
all docs

68
docs citations

68
times ranked

10790
citing authors

#	ARTICLE	IF	CITATIONS
1	Population divergence time estimation using individual lineage label switching. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	4
2	Genetic diversity and population structure of <i>Leishmania (Viannia) braziliensis</i> in the Peruvian jungle. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010374.	1.3	2
3	Population Genetic Inference With MIGRATE. <i>Current Protocols in Bioinformatics</i> , 2019, 68, e87.	25.8	53
4	Fractional coalescent. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6244-6249.	3.3	24
5	Exceptional maternal lineage diversity in brown bears (<i>Ursus arctos</i>) from Turkey. <i>Zoological Journal of the Linnean Society</i> , 2016, 176, 463-477.	1.0	44
6	Evaluating marginal likelihood with thermodynamic integration method and comparison with several other numerical methods. <i>Water Resources Research</i> , 2016, 52, 734-758.	1.7	41
7	Strong and stable geographic differentiation of swamp buffalo maternal and paternal lineages indicates domestication in the China/Indochina border region. <i>Molecular Ecology</i> , 2016, 25, 1530-1550.	2.0	49
8	A synthesis of genetic connectivity in deep-sea fauna and implications for marine reserve design. <i>Molecular Ecology</i> , 2016, 25, 3276-3298.	2.0	109
9	Assortative Mating Drives Linkage Disequilibrium between Sperm and Egg Recognition Protein Loci in the Sea Urchin <i>Strongylocentrotus purpuratus</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 859-870.	3.5	20
10	Quasi-Monte Carlo method in population genetics parameter estimation. <i>Mathematics and Computers in Simulation</i> , 2014, 103, 33-38.	2.4	1
11	Global diversity and oceanic divergence of humpback whales (<i>Megaptera novaeangliae</i>). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20133222.	1.2	66
12	A Continuous Method for Gene Flow. <i>Genetics</i> , 2013, 194, 687-696.	1.2	4
13	Pathways of cryptic invasion in a fish parasite traced using coalescent analysis and epidemiological survey. <i>Biological Invasions</i> , 2013, 15, 1907-1923.	1.2	9
14	Balancing a Cline by Influx of Migrants: A Genetic Transition in Water Frogs of Eastern Greece. <i>Journal of Heredity</i> , 2013, 104, 57-71.	1.0	13
15	A possible explanation for the population size discrepancy in tuna (genus <i>Thunnus</i>) estimated from mitochondrial DNA and microsatellite data. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 463-468.	1.2	14
16	BEAGLE: An Application Programming Interface and High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , 2012, 61, 170-173.	2.7	555
17	Biogeographic models of gene flow in two waterfowl of the Australo-Papuan tropics. <i>Ecology and Evolution</i> , 2012, 2, 2803-2814.	0.8	14
18	Genetic data reveal that water frogs of Cyprus (genus <i>Pelophylax</i>) are an endemic species of Messinian origin. <i>Zoosystematics and Evolution</i> , 2012, 88, 261-283.	0.4	37

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19	Gene flow and population structure in the Mexican blind cavefish complex (<i>Astyanax mexicanus</i>). <i>BMC Evolutionary Biology</i> , 2012, 12, 9.	3.2	174
20	In defence of model-based inference in phylogeography. <i>Molecular Ecology</i> , 2010, 19, 436-446.	2.0	141
21	Phylogeographic patterns of genetic diversity in eastern Mediterranean water frogs were determined by geological processes and climate change in the Late Cenozoic. <i>Journal of Biogeography</i> , 2010, 37, 2111-2124.	1.4	101
22	Global Migration Dynamics Underlie Evolution and Persistence of Human Influenza A (H3N2). <i>PLoS Pathogens</i> , 2010, 6, e1000918.	2.1	151
23	Genetic Divergence and Evolution of Reproductive Isolation in Eastern Mediterranean Water Frogs. , 2010, , 373-403.		35
24	Unified Framework to Evaluate Panmixia and Migration Direction Among Multiple Sampling Locations. <i>Genetics</i> , 2010, 185, 313-326.	1.2	583
25	Genetic Variation of <i>Anastrepha suspensa</i> (Diptera: Tephritidae) in Florida and the Caribbean Using Microsatellite DNA Markers. <i>Journal of Economic Entomology</i> , 2010, 103, 2214-2222.	0.8	13
26	Evolution of serum albumin intron-1 is shaped by a 5â€² truncated non-long terminal repeat retrotransposon in western Palearctic water frogs (<i>Neobatrachia</i>). <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 784-791.	1.2	29
27	Developmental disturbances in <i>Rana esculenta</i> tadpoles and metamorphs. <i>Zoosystematics and Evolution</i> , 2008, 77, 79-86.	0.4	3
28	Widespread unidirectional transfer of mitochondrial DNA: a case in western Palearctic water frogs. <i>Journal of Evolutionary Biology</i> , 2008, 21, 668-681.	0.8	96
29	Multigene analysis suggests ecological speciation in the fungal pathogen <i>Claviceps purpurea</i> . <i>Molecular Ecology</i> , 2008, 17, 2276-2286.	2.0	43
30	Genetic structuring and migration patterns of Atlantic bigeye tuna, <i>Thunnus obesus</i> (Lowe, 1839). <i>BMC Evolutionary Biology</i> , 2008, 8, 252.	3.2	53
31	Estimation of the Population Scaled Mutation Rate From Microsatellite Data. <i>Genetics</i> , 2007, 177, 1967-1968.	1.2	24
32	Hemiclone diversity in the hybridogenetic frog <i>Rana esculenta</i> outside the area of clone formation: the view from protein electrophoresis. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2007, 46, 070907105857002-???	0.6	11
33	STATISTICAL METHODS IN (MOLECULAR) EVOLUTION. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 421-423.	1.1	0
34	Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. <i>Bioinformatics</i> , 2006, 22, 341-345.	1.8	785
35	STATISTICAL METHODS IN (MOLECULAR) EVOLUTION1. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 421.	1.1	0
36	Host Switch Leads to Emergence of <i>Plasmodium vivax</i> Malaria in Humans. <i>Molecular Biology and Evolution</i> , 2005, 22, 1686-1693.	3.5	199

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37	Effect of unsampled populations on the estimation of population sizes and migration rates between sampled populations. <i>Molecular Ecology</i> , 2004, 13, 827-836.	2.0	263
38	When did Neanderthals and modern humans diverge?. <i>Evolutionary Anthropology</i> , 2003, 11, 60-63.	1.7	12
39	The utility of single nucleotide polymorphisms in inferences of population history. <i>Trends in Ecology and Evolution</i> , 2003, 18, 249-256.	4.2	544
40	Early Origin and Recent Expansion of <i>Plasmodium falciparum</i> . <i>Science</i> , 2003, 300, 318-321.	6.0	365
41	Estimating Divergence Times from Molecular Data on Phylogenetic and Population Genetic Timescales. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2002, 33, 707-740.	6.7	521
42	Population Genetics of HIV: Parameter Estimation Using Genealogy-based Methods. , 2002, , 217-252.		5
43	Maximum likelihood estimation of a migration matrix and effective population sizes in n subpopulations by using a coalescent approach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 4563-4568.	3.3	1,610
44	How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use?. , 2001, , 42-79.		163
45	Strength and tempo of directional selection in the wild. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 9157-9160.	3.3	401
46	Microsatellites: A tool for evolutionary genetic studies of western Palearctic water frogs. <i>Zoosystematics and Evolution</i> , 2001, 77, 43-50.	0.4	15
47	The Strength of Phenotypic Selection in Natural Populations. <i>American Naturalist</i> , 2001, 157, 245.	1.0	114
48	PERSPECTIVE: GENE DIVERGENCE, POPULATION DIVERGENCE, AND THE VARIANCE IN COALESCENCE TIME IN PHYLOGEOGRAPHIC STUDIES. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 1839-1854.	1.1	757
49	PERSPECTIVE: GENE DIVERGENCE, POPULATION DIVERGENCE, AND THE VARIANCE IN COALESCENCE TIME IN PHYLOGEOGRAPHIC STUDIES. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 1839.	1.1	604
50	Usefulness of Single Nucleotide Polymorphism Data for Estimating Population Parameters. <i>Genetics</i> , 2000, 156, 439-447.	1.2	126
51	Spontaneous heterosis in larval life-history traits of hemiclinal frog hybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 2171-2176.	3.3	79
52	Maximum-Likelihood Estimation of Migration Rates and Effective Population Numbers in Two Populations Using a Coalescent Approach. <i>Genetics</i> , 1999, 152, 763-773.	1.2	902
53	Likelihoods on coalescents: a Monte Carlo sampling approach to inferring parameters from population samples of molecular data. <i>Lecture Notes-monograph Series / Institute of Mathematical Statistics</i> , 1999, , 163-185.	1.0	44
54	Statistical analyses of population genetic data. <i>Trends in Ecology and Evolution</i> , 1997, 12, 488.	4.2	1

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55	Geologically Dated Sea Barriers Calibrate a Protein Clock for Aegean Water Frogs. <i>Evolution; International Journal of Organic Evolution</i> , 1996, 50, 1676.	1.1	73
56	GEOLOGICALLY DATED SEA BARRIERS CALIBRATE A PROTEIN CLOCK FOR AEGEAN WATER FROGS. <i>Evolution; International Journal of Organic Evolution</i> , 1996, 50, 1676-1687.	1.1	98
57	Genetic compatibility between sexual and clonal genomes in local populations of the hybridogenetic <i>Rana esculenta</i> complex. <i>Evolutionary Ecology</i> , 1996, 10, 531-543.	0.5	46
58	Are hybrid clonals species? A case for enlightened anarchy. <i>Amphibia - Reptilia</i> , 1996, 17, 315-320.	0.1	2