

Giorgio Bertorelle

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

2,374
citations

331670

21
h-index

361022

35
g-index

38
all docs

38
docs citations

38
times ranked

4358
citing authors

#	ARTICLE	IF	CITATIONS
1	ABC as a flexible framework to estimate demography over space and time: some cons, many pros. <i>Molecular Ecology</i> , 2010, 19, 2609-2625.	3.9	379
2	The origin of European cattle: Evidence from modern and ancient DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8113-8118.	7.1	271
3	Computer simulations: tools for population and evolutionary genetics. <i>Nature Reviews Genetics</i> , 2012, 13, 110-122.	16.3	221
4	Survival and divergence in a small group: The extraordinary genomic history of the endangered Apennine brown bear stragglers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9589-E9597.	7.1	140
5	Partial genomic survival of cave bears in living brown bears. <i>Nature Ecology and Evolution</i> , 2018, 2, 1563-1570.	7.8	132
6	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	124
7	The genetic impact of demographic decline and reintroduction in the wild boar (<i>Sus scrofa</i>): A microsatellite analysis. <i>Molecular Ecology</i> , 2003, 12, 585-595.	3.9	118
8	Decreased Nucleotide and Expression Diversity and Modified Coexpression Patterns Characterize Domestication in the Common Bean. <i>Plant Cell</i> , 2014, 26, 1901-1912.	6.6	103
9	Comparative evaluation of potential indicators and temporal sampling protocols for monitoring genetic erosion. <i>Evolutionary Applications</i> , 2014, 7, 984-998.	3.1	102
10	Genetic load: genomic estimates and applications in non-model animals. <i>Nature Reviews Genetics</i> , 2022, 23, 492-503.	16.3	82
11	The genetic structure of natural and reintroduced roe deer (<i>Capreolus capreolus</i>) populations in the Alps and central Italy, with reference to the mitochondrial DNA phylogeography of Europe. <i>Molecular Ecology</i> , 2002, 11, 1285-1297.	3.9	73
12	Sample Planning Optimization Tool for conservation and population Genetics (<scp>SPOTG</scp>): a software for choosing the appropriate number of markers and samples. <i>Methods in Ecology and Evolution</i> , 2013, 4, 299-303.	5.2	66
13	The number of markers and samples needed for detecting bottlenecks under realistic scenarios, with and without recovery: a simulation-based study. <i>Molecular Ecology</i> , 2013, 22, 3444-3450.	3.9	64
14	From Nucleotides to Satellite Imagery: Approaches to Identify and Manage the Invasive Pathogen <i>Xylella fastidiosa</i> and Its Insect Vectors in Europe. <i>Sustainability</i> , 2020, 12, 4508.	3.2	64
15	Population dynamic of the extinct European aurochs: genetic evidence of a north-south differentiation pattern and no evidence of post-glacial expansion. <i>BMC Evolutionary Biology</i> , 2010, 10, 83.	3.2	51
16	Full circumpolar migration ensures evolutionary unity in the Emperor penguin. <i>Nature Communications</i> , 2016, 7, 11842.	12.8	43
17	The Complete Mitochondrial Genome of an 11,450-year-old Aurochsen (<i>Bos primigenius</i>) from Central Italy. <i>BMC Evolutionary Biology</i> , 2011, 11, 32.	3.2	39
18	The rise and fall of an alien: why the successful colonizer <i>Littorina saxatilis</i> failed to invade the Mediterranean Sea. <i>Biological Invasions</i> , 2022, 24, 3169-3187.	2.4	39

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19	4P: fast computing of population genetics statistics from large <scp>DNA</scp> polymorphism panels. <i>Ecology and Evolution</i> , 2015, 5, 172-175.	1.9	36
20	High variance in reproductive success generates a false signature of a genetic bottleneck in populations of constant size: a simulation study. <i>BMC Bioinformatics</i> , 2013, 14, 309.	2.6	29
21	Ancient genomes reveal early Andean farmers selected common beans while preserving diversity. <i>Nature Plants</i> , 2021, 7, 123-128.	9.3	29
22	Divergence and hybridization in sea turtles: Inferences from genome data show evidence of ancient gene flow between species. <i>Molecular Ecology</i> , 2021, 30, 6178-6192.	3.9	24
23	Population Dynamics and Structural Effects at Short and Long Range Support the Hypothesis of the Selective Advantage of the G614 SARS-CoV-2 Spike Variant. <i>Molecular Biology and Evolution</i> , 2021, 38, 1966-1979.	8.9	23
24	Conservation of the endangered Mediterranean tortoise <i>Testudo hermanni hermanni</i> : The contribution of population genetics and historical demography. <i>Biological Conservation</i> , 2016, 195, 279-291.	4.1	19
25	Genetic Variation and Population Structure in the Endangered Hermann's Tortoise: The Roles of Geography and Human-Mediated Processes. <i>Journal of Heredity</i> , 2014, 105, 70-81.	2.4	18
26	Mapping the geographic origin of captive and confiscated Hermann's tortoises: A genetic toolkit for conservation and forensic analyses. <i>Forensic Science International: Genetics</i> , 2021, 51, 102447.	3.1	13
27	The Biarno case in northern Italy: is the temporal dynamic of swine mitochondrial DNA lineages in Europe related to domestication?. <i>Scientific Reports</i> , 2015, 5, 16514.	3.3	12
28	New, Flexible Bayesian Approaches to Revolutionize Conservation Genetics. <i>Conservation Biology</i> , 2004, 18, 584-584.	4.7	11
29	Candidate genes involved in the evolution of viviparity: a RAD sequencing experiment in the lizard <i>Zootoca vivipara</i> (Squamata: Lacertidae). <i>Zoological Journal of the Linnean Society</i> , 2018, 183, 196-207.	2.3	11
30	Population structure, genomic diversity and demographic history of Komodo dragons inferred from whole-genome sequencing. <i>Molecular Ecology</i> , 2021, 30, 6309-6324.	3.9	11
31	Ancient, but not recent, population declines have had a genetic impact on alpine yellow-bellied toad populations, suggesting potential for complete recovery. <i>Conservation Genetics</i> , 2016, 17, 727-743.	1.5	6
32	Mitochondrial dna variation and divergence in three Hermann's tortoise (<i>Testudo hermanni</i>) populations. <i>Journal of Heredity</i> , 2015, 106, 100-108.	0.6	5
33	Phylogenomic proof of Recurrent Demipolyploidization and Evolutionary Stalling of the Triploid Bridge in <i>Arundo</i> (Poaceae). <i>International Journal of Molecular Sciences</i> , 2020, 21, 5247.	4.1	5
34	Bears in Human-Modified Landscapes: The Case Studies of the Cantabrian, Apennine, and Pindos Mountains. <i>Journal of Heredity</i> , 2020, 111, 260-272.		5
35	Identification of natural selection in genomic data with deep convolutional neural network. <i>BioData Mining</i> , 2021, 14, 51.	4.0	4
36	Population Genetic Structure of a Centipede Species with High Levels of Developmental Instability. <i>PLoS ONE</i> , 2015, 10, e0126245.	2.5	2