StÃ©phanie Manel

List of Publications by Year
in descending order

70 papers	6,923 citations	172207 29 h-index	91712 69 g-index
76 all docs	76 docs citations	76 times ranked	8553 citing authors

#	Article	IF	Citations
1	Landscape genetics: combining landscape ecology and population genetics. Trends in Ecology and Evolution, 2003, 18, 189-197.	4.2	1,907
2	Assignment methods: matching biological questions with appropriate techniques. Trends in Ecology and Evolution, 2005, 20, 136-142.	4.2	645
3	Ten years of landscape genetics. Trends in Ecology and Evolution, 2013, 28, 614-621.	4.2	527
4	Detecting selection along environmental gradients: analysis of eight methods and their effectiveness for outbreeding and selfing populations. Molecular Ecology, 2013, 22, 1383-1399.	2.0	334
5	Considering adaptive genetic variation in climate change vulnerability assessment reduces species range loss projections. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10418-10423.	3.3	308
6	Alternative methods for predicting species distribution: an illustration with Himalayan river birds. Journal of Applied Ecology, 1999, 36, 734-747.	1.9	254
7	Adaptive Genetic Variation on the Landscape: Methods and Cases. Annual Review of Ecology, Evolution, and Systematics, 2012, 43, 23-43.	3.8	250
8	Perspectives on the use of landscape genetics to detect genetic adaptive variation in the field. Molecular Ecology, 2010, 19, 3760-3772.	2.0	237
9	Environmental DNA illuminates the dark diversity of sharks. Science Advances, 2018, 4, eaap9661.	4.7	222
10	Broadâ€scale adaptive genetic variation in alpine plants is driven by temperature and precipitation. Molecular Ecology, 2012, 21, 3729-3738.	2.0	161
11	Genetic diversity in widespread species is not congruent with species richness in alpine plant communities. Ecology Letters, 2012, 15, 1439-1448.	3.0	135
12	Landscape genetics of plants. Trends in Plant Science, 2010, 15, 675-683.	4.3	129
13	Forecasting changes in population genetic structure of alpine plants in response to global warming. Molecular Ecology, 2012, 21, 2354-2368.	2.0	127
14	Low Connectivity between Mediterranean Marine Protected Areas: A Biophysical Modeling Approach for the Dusky Grouper Epinephelus marginatus. PLoS ONE, 2013, 8, e68564.	1.1	117
15	Global determinants of freshwater and marine fish genetic diversity. Nature Communications, 2020, 11, 692.	5.8	97
16	Land ahead: using genome scans to identify molecular markers of adaptive relevance. Plant Ecology and Diversity, 2008, 1, 273-283.	1.0	94
17	Biologically representative and wellâ€connected marine reserves enhance biodiversity persistence in conservation planning. Conservation Letters, 2018, 11, e12439.	2.8	91
18	Integrative approach for landscape-based graph connectivity analysis: a case study with the common frog (Rana temporaria) in human-dominated landscapes. Landscape Ecology, 2012, 27, 267-279.	1.9	77

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19	Genomic resources and their influence on the detection of the signal of positive selection in genome scans. Molecular Ecology, 2016, 25, 170-184.	2.0	74
20	Comparing environmental DNA metabarcoding and underwater visual census to monitor tropical reef fishes. Environmental DNA, 2021, 3, 142-156.	3.1	61
21	Opportunities and challenges of macrogenetic studies. Nature Reviews Genetics, 2021, 22, 791-807.	7.7	55
22	Long-Distance Benefits of Marine Reserves: Myth or Reality?. Trends in Ecology and Evolution, 2019, 34, 342-354.	4.2	50
23	GAPeDNA: Assessing and mapping global species gaps in genetic databases for eDNA metabarcoding. Diversity and Distributions, 2021, 27, 1880-1892.	1.9	50
24	Combining six genome scan methods to detect candidate genes to salinity in the Mediterranean striped red mullet (Mullus surmuletus). BMC Genomics, 2018, 19, 217.	1.2	44
25	Extending networks of protected areas to optimize connectivity and population growth rate. Ecography, 2015, 38, 273-282.	2.1	43
26	Global mismatch between fishing dependency and larval supply from marine reserves. Nature Communications, 2017, 8, 16039.	5.8	40
27	Comparing the performance of 12S mitochondrial primers for fish environmental DNA across ecosystems. Environmental DNA, 2021, 3, 1113-1127.	3.1	38
28	Blind assessment of vertebrate taxonomic diversity across spatial scales by clustering environmental DNA metabarcoding sequences. Ecography, 2020, 43, 1779-1790.	2.1	37
29	Benchmarking bioinformatic tools for fast and accurate eDNA metabarcoding species identification. Molecular Ecology Resources, 2021, 21, 2565-2579.	2.2	35
30	Insights into the genetic relationships among plants of Beta section Beta using SNP markers. Theoretical and Applied Genetics, 2017, 130, 1857-1866.	1.8	32
31	Geographic isolation and larval dispersal shape seascape genetic patterns differently according to spatial scale. Evolutionary Applications, 2018, 11, 1437-1447.	1.5	30
32	Soil environment is a key driver of adaptation in <i>Medicago truncatula</i>: new insights from landscape genomics. New Phytologist, 2018, 219, 378-390.	3.5	29
33	Environmental DNA metabarcoding reveals and unpacks a biodiversity conservation paradox in Mediterranean marine reserves. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20210112.	1.2	28
34	How many replicates to accurately estimate fish biodiversity using environmental DNA on coral reefs?. Ecology and Evolution, 2021, 11, 14630-14643.	0.8	28
35	Taxonomic, spatial and adaptive genetic variation of Beta section Beta. Theoretical and Applied Genetics, 2016, 129, 257-271.	1.8	27
36	Reviewing the Ecosystem Services, Societal Goods, and Benefits of Marine Protected Areas. Frontiers in Marine Science, 2021, 8, .	1.2	27

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37	Pleistocene climate changes, and not agricultural spread, accounts for range expansion and admixture in the dominant grassland speciesLolium perenneL.. Journal of Biogeography, 2019, 46, 1451.	1.4	26
38	Ecological traits shape genetic diversity patterns across the Mediterranean Sea: a quantitative review on fishes. Journal of Biogeography, 2016, 43, 845-857.	1.4	22
39	Developing educational resources for population genetics in R: an open and collaborative approach. Molecular Ecology Resources, 2017, 17, 120-128.	2.2	21
40	Spatial graphs highlight how multiâ€generational dispersal shapes landscape genetic patterns. Ecography, 2020, 43, 1167-1179.	2.1	21
41	Restricted dispersal in a sea of gene flow. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20210458.	1.2	21
42	Evolving spatial conservation prioritization with intraspecific genetic data. Trends in Ecology and Evolution, 2022, 37, 553-564.	4.2	21
43	Combining Genotype, Phenotype, and Environment to Infer Potential Candidate Genes. Journal of Heredity, 2017, 108, esw077.	1.0	20
44	Canonical correlations reveal adaptive loci and phenotypic responses to climate in perennial ryegrass. Molecular Ecology Resources, 2021, 21, 849-870.	2.2	20
45	Predicting genotype environmental range from genomeâ€“environment associations. Molecular Ecology, 2018, 27, 2823-2833.	2.0	18
46	Detecting aquatic and terrestrial biodiversity in a tropical estuary using environmental DNA. Biotropica, 2021, 53, 1606-1619.	0.8	18
47	Genetic variation of loci potentially under selection confounds speciesâ€“genetic diversity correlations in a fragmented habitat. Molecular Ecology, 2017, 26, 431-443.	2.0	17
48	Preserving genetic connectivity in the European Alps protected area network. Biological Conservation, 2018, 218, 99-109.	1.9	16
49	Marine Conservation and Marine Protected Areas. Population Genomics, 2019, , 423-446.	0.2	15
50	Ecological and genomic vulnerability to climate change across native populations of Robusta coffee (<i>Coffea canephora</i>). Global Change Biology, 2022, 28, 4124-4142.	4.2	15
51	Detection of the elusive Dwarf sperm whale (<i>Kogia sima</i>) using environmental DNA at Malpelo island (Eastern Pacific, Colombia). Ecology and Evolution, 2021, 11, 2956-2962.	0.8	14
52	Cross-ocean patterns and processes in fish biodiversity on coral reefs through the lens of eDNA metabarcoding. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20220162.	1.2	14
53	Towards an integrated ecosystem of <scp>R</scp> packages for the analysis of population genetic data. Molecular Ecology Resources, 2017, 17, 1-4.	2.2	13
54	McSwan: A joint site frequency spectrum method to detect and date selective sweeps across multiple population genomes. Molecular Ecology Resources, 2019, 19, 283-295.	2.2	13

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55	MetaPopGen: an <scp>r</scp> package to simulate population genetics in large size metapopulations. Molecular Ecology Resources, 2015, 15, 1153-1162.	2.2	12
56	Maximizing regional biodiversity requires a mosaic of protection levels. PLoS Biology, 2021, 19, e3001195.	2.6	11
57	Evaluating bioinformatics pipelines for populationâ€level inference using environmental DNA. Environmental DNA, 2022, 4, 674-686.	3.1	10
58	New genomic resources for three exploited Mediterranean fishes. Genomics, 2020, 112, 4297-4303.	1.3	8
59	Climate differently influences the genomic patterns of two sympatric marine fish species. Journal of Animal Ecology, 2022, 91, 1180-1195.	1.3	8
60	Genomic insights into the historical and contemporary demographics of the grey reef shark. Heredity, 2022, 128, 225-235.	1.2	8
61	Ecological indicators based on quantitative eDNA metabarcoding: the case of marine reserves. Ecological Indicators, 2022, 140, 108966.	2.6	8
62	The interplay of riverscape features and exotic introgression on the genetic structure of the Mexican golden trout (<i>Oncorhynchus chrysogaster</i>), a simulation approach. Journal of Biogeography, 2018, 45, 1500-1514.	1.4	7
63	Adaptive potential of <i>Coffea canephora</i> from Uganda in response to climate change. Molecular Ecology, 2022, 31, 1800-1819.	2.0	7
64	Identifying barriers to gene flow and hierarchical conservation units from seascape genomics: a modelling framework applied to a marine predator. Ecography, 2022, 2022, .	2.1	7
65	Long-Distance Marine Connectivity: Poorly Understood but Potentially Important. Trends in Ecology and Evolution, 2019, 34, 688-689.	4.2	5
66	Species ecology explains the spatial components of genetic diversity in tropical reef fishes. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20211574.	1.2	3
67	Applying convolutional neural networks to speed up environmental DNA annotation in a highly diverse ecosystem. Scientific Reports, 2022, 12, .	1.6	2
68	MetaPopGen 2.0: A multilocus genetic simulator to model populations of large size. Molecular Ecology Resources, 2021, 21, 596-608.	2.2	1
69	Reply to Kershaw and Rosenbaum. Trends in Ecology and Evolution, 2014, 29, 70-71.	4.2	0
70	Smoothing technical and computational obstacles in geneâ€environment associations. Molecular Ecology Resources, 2019, 19, 1385-1387.	2.2	0