

Nicolas Bierne

List of Publications by Year in descending order

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89
papers

9,042
citations

65103

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h-index

50605

87
g-index

114
all docs

114
docs citations

114
times ranked

10981
citing authors

#	ARTICLE	IF	CITATIONS
1	Marine transmissible cancer navigates urbanized waters, threatening spillover. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2024, 291, .	2.8	1
2	Urban rendezvous along the seashore: Ports as Darwinian field labs for studying marine evolution in the Anthropocene. <i>Evolutionary Applications</i> , 2023, 16, 560-579.	3.2	13
3	Transcriptomics of mussel transmissible cancer MtrBTN2 suggests accumulation of multiple cancer traits and oncogenic pathways shared among bilaterians. <i>Open Biology</i> , 2023, 13, .	3.7	0
4	Anthropogenic Change and the Process of Speciation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2023, 15, a041455.	5.4	3
5	Prevalence and polymorphism of a mussel transmissible cancer in Europe. <i>Molecular Ecology</i> , 2022, 31, 736-751.	3.6	44
6	Subtle limits to connectivity revealed by outlier loci within two divergent metapopulations of the deep-sea hydrothermal gastropod <i>Lifremeria nautilei</i> . <i>Molecular Ecology</i> , 2022, 31, 2796-2813.	3.6	12
7	Spatial coalescent connectivity through multi-generation dispersal modelling predicts gene flow across marine phyla. <i>Nature Communications</i> , 2022, 13, .	13.2	13
8	DILS: Demographic inferences with linked selection by using ABC. <i>Molecular Ecology Resources</i> , 2021, 21, 2629-2644.	5.0	37
9	Agent-based modeling and genetics reveal the Limfjorden, Denmark, as a well-connected system for mussel larvae. <i>Marine Ecology - Progress Series</i> , 2021, 680, 193-205.	1.9	16
10	An introgression breakthrough left by an anthropogenic contact between two ascidians. <i>Molecular Ecology</i> , 2021, 30, 6718-6732.	3.6	17
11	Traits of a mussel transmissible cancer are reminiscent of a parasitic life style. <i>Scientific Reports</i> , 2021, 11, 24110.	3.4	15
12	Twin introductions by independent invader mussel lineages are both associated with recent admixture with a native congener in Australia. <i>Evolutionary Applications</i> , 2020, 13, 515-532.	3.2	45
13	Replicated anthropogenic hybridisations reveal parallel patterns of admixture in marine mussels. <i>Evolutionary Applications</i> , 2020, 13, 575-599.	3.2	54
14	Anthropogenic hybridization at sea: three evolutionary questions relevant to invasive species management. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190547.	4.2	29
15	The geometry and genetics of hybridization. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 2575-2590.	2.3	22
16	Effective population size and heterozygosity-fitness correlations in a population of the Mediterranean lagoon ecotype of long-snouted seahorse <i>Hippocampus guttulatus</i> . <i>Conservation Genetics</i> , 2019, 20, 1281-1288.	1.5	4
17	Implementation of various approaches to study the prevalence, incidence and progression of disseminated neoplasia in mussel stocks. <i>Journal of Invertebrate Pathology</i> , 2019, 168, 107271.	3.3	26
18	The hidden side of a major marine biogeographic boundary: a wide mosaic hybrid zone at the Atlantic-Mediterranean divide reveals the complex interaction between natural and genetic barriers in mussels. <i>Heredity</i> , 2019, 122, 770-784.	2.7	38

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19	Parallel pattern of differentiation at a genomic island shared between clinal and mosaic hybrid zones in a complex of cryptic seahorse lineages. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 817-835.	2.3	29
20	A single clonal lineage of transmissible cancer identified in two marine mussel species in South America and Europe. <i>ELife</i> , 2019, 8, .	5.9	66
21	Codon Usage Bias in Animals: Disentangling the Effects of Natural Selection, Effective Population Size, and GC-Biased Gene Conversion. <i>Molecular Biology and Evolution</i> , 2018, 35, 1092-1103.	9.2	124
22	Imposex incidence in <i>Stramonita haemastoma</i> (Gastropoda: Muricidae) from the Mediterranean and Atlantic coast after Tributyltin global ban. <i>Journal of Sea Research</i> , 2018, 134, 10-15.	1.7	8
23	Analysis of Genome-Wide Differentiation between Native and Introduced Populations of the Cupped Oysters <i>Crassostrea gigas</i> and <i>Crassostrea angulata</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 2518-2534.	2.6	55
24	The origin and remodeling of genomic islands of differentiation in the European sea bass. <i>Nature Communications</i> , 2018, 9, 2518.	13.2	87
25	Coadapted genomes and selection on hybrids: Fisher's geometric model explains a variety of empirical patterns. <i>Evolution Letters</i> , 2018, 2, 472-498.	3.4	61
26	The divergence history of European blue mussel species reconstructed from Approximate Bayesian Computation: the effects of sequencing techniques and sampling strategies. <i>PeerJ</i> , 2018, 6, e5198.	2.0	26
27	Unexpected mosaic distribution of two hybridizing sibling lineages in the teleplanically dispersing snail <i>Stramonita haemastoma</i> suggests unusual postglacial redistribution or cryptic invasion. <i>Ecology and Evolution</i> , 2017, 7, 9016-9026.	1.9	14
28	Interpreting the genomic landscape of speciation: a road map for finding barriers to gene flow. <i>Journal of Evolutionary Biology</i> , 2017, 30, 1450-1477.	1.6	420
29	Weird genotypes? Don't discard them, transmissible cancer could be an explanation. <i>Evolutionary Applications</i> , 2017, 10, 140-145.	3.2	27
30	Adaptive evolution and segregating load contribute to the genomic landscape of divergence in two tree species connected by episodic gene flow. <i>Molecular Ecology</i> , 2017, 26, 59-76.	3.6	75
31	Editorial Dedicated population genomics for the silent world: the specific questions of marine population genetics. <i>Environmental Epigenetics</i> , 2016, 62, 545-550.	1.9	13
32	Shedding Light on the Grey Zone of Speciation along a Continuum of Genomic Divergence. <i>PLoS Biology</i> , 2016, 14, e2000234.	5.4	403
33	The genetics of speciation: Insights from Fisher's geometric model. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1450-1464.	2.3	53
34	Population genomics of sexual and asexual lineages in fissiparous ribbon worms (Lineus, Nemertea): hybridization, polyploidy and the Meselson effect. <i>Molecular Ecology</i> , 2016, 25, 3356-3369.	3.6	61
35	Population genomic footprints of fine-scale differentiation between habitats in Mediterranean blue tits. <i>Molecular Ecology</i> , 2016, 25, 542-558.	3.6	52
36	Local interspecies introgression is the main cause of extreme levels of intraspecific differentiation in mussels. <i>Molecular Ecology</i> , 2016, 25, 269-286.	3.6	97

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37	Distinguishing contemporary hybridization from past introgression with postgenomic ancestry-informative <sc>SNP</sc>s in strongly differentiated <i>Ciona</i> species. <i>Molecular Ecology</i> , 2016, 25, 5527-5542.	3.6	54
38	Does natural selection explain the fine scale genetic structure at the nuclear exon <i>Gluâ€²</i> in blue mussels from Kerguelen?. <i>Ecology and Evolution</i> , 2015, 5, 1456-1473.	1.9	10
39	Using neutral, selected, and hitchhiker loci to assess connectivity of marine populations in the genomic era. <i>Evolutionary Applications</i> , 2015, 8, 769-786.	3.2	228
40	Additive transcriptomic variation associated with reproductive traits suggest local adaptation in a recently settled population of the Pacific oyster, <i>Crassostrea gigas</i> . <i>BMC Genomics</i> , 2015, 16, 808.	2.9	16
41	European sea bass genome and its variation provide insights into adaptation to euryhalinity and speciation. <i>Nature Communications</i> , 2014, 5, 5770.	13.2	396
42	Evidence for adaptation from standing genetic variation on an antimicrobial peptide gene in the mussel <i>Mytilus edulis</i>. <i>Molecular Ecology</i> , 2014, 23, 3000-3012.	3.6	22
43	Gene-Flow in a Mosaic Hybrid Zone: Is Local Introgression Adaptive?. <i>Genetics</i> , 2014, 197, 939-951.	2.9	62
44	Comparative population genomics in animals uncovers the determinants of genetic diversity. <i>Nature</i> , 2014, 515, 261-263.	36.2	521
45	Can we continue to neglect genomic variation in introgression rates when inferring the history of speciation? A case study in a <sc>M</sc><sc>ytilus</sc> hybrid zone. <i>Journal of Evolutionary Biology</i> , 2014, 27, 1662-1675.	1.6	81
46	Contrasting patterns of genome-wide polymorphism in the native and invasive range of the marine mollusc <sc>C</sc><sc>repidula fornicata</sc>. <i>Molecular Ecology</i> , 2013, 22, 1003-1018.	3.6	44
47	Hybridization and speciation. <i>Journal of Evolutionary Biology</i> , 2013, 26, 229-246.	1.6	1,819
48	Differential introgression from a sister species explains high <i>F</i>_{ST} outlier loci within a mussel species. <i>Journal of Evolutionary Biology</i> , 2013, 26, 14-26.	1.6	51
49	Pervasive selection or is itâ€¦? why are <i>F</i>_{ST} outliers sometimes so frequent?. <i>Molecular Ecology</i> , 2013, 22, 2061-2064.	3.6	119
50	Evolutionary history of x-tox genes in three lepidopteran species: Origin, evolution of primary and secondary structure and alternative splicing, generating a repertoire of immune-related proteins. <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 54-64.	2.7	7
51	A High Load of Non-neutral Amino-Acid Polymorphisms Explains High Protein Diversity Despite Moderate Effective Population Size in a Marine Bivalve With Sweepstakes Reproduction. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 333-341.	1.9	31
52	Reference-Free Population Genomics from Next-Generation Transcriptome Data and the Vertebrateâ€“Invertebrate Gap. <i>PLoS Genetics</i> , 2013, 9, e1003457.	3.4	161
53	Crossing the Species Barrier: Genomic Hotspots of Introgression between Two Highly Divergent <i>Ciona intestinalis</i> Species. <i>Molecular Biology and Evolution</i> , 2013, 30, 1574-1587.	9.2	150
54	Population genomics shed light on the demographic and adaptive histories of European invasion in the Pacific oyster, <i>Crassostrea gigas</i>. <i>Evolutionary Applications</i> , 2013, 6, 1064-1078.	3.2	52

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55	The geography of introgression in a patchy environment and the thorn in the side of ecological speciation. <i>Environmental Epigenetics</i> , 2013, 59, 72-86.	1.9	144
56	A New Barrier to Dispersal Trapped Old Genetic Clines That Escaped the Easter Microplate Tension Zone of the Pacific Vent Mussels. <i>PLoS ONE</i> , 2013, 8, e81555.	2.5	24
57	SNP Detection from De Novo Transcriptome Sequencing in the Bivalve <i>Macoma balthica</i> : Marker Development for Evolutionary Studies. <i>PLoS ONE</i> , 2012, 7, e52302.	2.5	24
58	The coupling hypothesis: why genome scans may fail to map local adaptation genes. <i>Molecular Ecology</i> , 2011, 20, 2044-2072.	3.6	467
59	HETEROZYGOSITY-FITNESS CORRELATIONS: A TIME FOR REAPPRAISAL. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 1202-17.	2.3	297
60	THE DISTINCTIVE FOOTPRINTS OF LOCAL HITCHHIKING IN A VARIED ENVIRONMENT AND GLOBAL HITCHHIKING IN A SUBDIVIDED POPULATION. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 3254-3272.	2.3	81
61	The Flow of Antimicrobial Peptide Genes Through a Genetic Barrier Between <i>Mytilus edulis</i> and <i>M. galloprovincialis</i> . <i>Journal of Molecular Evolution</i> , 2009, 68, 461-474.	1.9	14
62	Speciation in the Deep Sea: Multi-Locus Analysis of Divergence and Gene Flow between Two Hybridizing Species of Hydrothermal Vent Mussels. <i>PLoS ONE</i> , 2009, 4, e6485.	2.5	46
63	Pleistocene separation of mitochondrial lineages of <i>Mytilus</i> spp. mussels from Northern and Southern Hemispheres and strong genetic differentiation among southern populations. <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 84-91.	2.9	108
64	Genetic hitchhiking in a subdivided population of <i>Mytilus edulis</i> . <i>BMC Evolutionary Biology</i> , 2008, 8, 164.	3.1	32
65	Increasing genomic information in bivalves through new EST collections in four species: Development of new genetic markers for environmental studies and genome evolution. <i>Gene</i> , 2008, 408, 27-36.	2.3	132
66	Single Nucleotide polymorphisms and their relationship to codon usage bias in the Pacific oyster <i>Crassostrea gigas</i> . <i>Gene</i> , 2007, 406, 13-22.	2.3	136
67	Evidence for a slightly deleterious effect of intron polymorphisms at the EF1 α gene in the deep-sea hydrothermal vent bivalve <i>Bathymodiolus</i> . <i>Gene</i> , 2007, 406, 99-107.	2.3	14
68	Genomic reticulation indicates mixed ancestry in Southern-Hemisphere <i>Mytilus</i> spp. mussels. <i>Biological Journal of the Linnean Society</i> , 2007, 92, 747-754.	1.6	24
69	Mark-recapture cloning: a straightforward and cost-effective cloning method for population genetics of single-copy nuclear DNA sequences in diploids. <i>Molecular Ecology Notes</i> , 2007, 7, 562-566.	1.6	17
70	Variation in synonymous codon use and DNA polymorphism within the <i>Drosophila</i> genome. <i>Journal of Evolutionary Biology</i> , 2006, 19, 1-11.	1.6	34
71	Fitness landscapes support the dominance theory of post-zygotic isolation in the mussels <i>Mytilus edulis</i> and <i>M. galloprovincialis</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 1253-1260.	2.8	63
72	GC-Biased Segregation of Noncoding Polymorphisms in <i>Drosophila</i> . <i>Genetics</i> , 2006, 172, 221-228.	2.9	55

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73	The Genomic Rate of Adaptive Amino Acid Substitution in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2004, 21, 1350-1360.	9.2	214
74	Introgression patterns in the mosaic hybrid zone between <i>Mytilus edulis</i> and <i>M. galloprovincialis</i> . <i>Molecular Ecology</i> , 2003, 12, 447-461.	3.6	228
75	Direct selection on allozymes is not required to explain heterogeneity among marker loci across a <i>Mytilus</i> hybrid zone. <i>Molecular Ecology</i> , 2003, 12, 2505-2510.	3.6	61
76	Habitat preference and the marine-speciation paradox. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003, 270, 1399-1406.	2.8	143
77	The Problem of Counting Sites in the Estimation of the Synonymous and Nonsynonymous Substitution Rates: Implications for the Correlation Between the Synonymous Substitution Rate and Codon Usage Bias. <i>Genetics</i> , 2003, 165, 1587-1597.	2.9	75
78	ASSORTATIVE FERTILIZATION AND SELECTION AT LARVAL STAGE IN THE MUSSELS <i>MYTILLUS EDULIS</i> AND <i>M. GALLOPROVINCIALIS</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2002, 56, 292.	2.3	12
79	Deleterious mutations in a hybrid zone: can mutational load decrease the barrier to gene flow?. <i>Genetical Research</i> , 2002, 80, 197-204.	0.9	34
80	ASSORTATIVE FERTILIZATION AND SELECTION AT LARVAL STAGE IN THE MUSSELS <i>MYTILLUS EDULIS</i> AND <i>M. GALLOPROVINCIALIS</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2002, 56, 292-298.	2.3	94
81	Can habitat specialisation maintain a mosaic hybrid zone in marine bivalves?. <i>Marine Ecology - Progress Series</i> , 2002, 245, 157-170.	1.9	60
82	Microsatellite Analysis of 6-Hour-Old Embryos Reveals No Preferential Intraspecific Fertilization Between Cupped Oysters <i>Crassostrea gigas</i> and <i>Crassostrea angulata</i> . <i>Marine Biotechnology</i> , 2001, 3, 448-453.	2.3	32
83	Screening for intron-length polymorphisms in penaeid shrimps using exon-primed intron-crossing (EPIC)-PCR. <i>Molecular Ecology</i> , 2000, 9, 233-235.	3.6	57
84	Microsatellite-associated heterosis in hatchery-propagated stocks of the shrimp <i>Penaeus stylirostris</i> . <i>Aquaculture</i> , 2000, 184, 203-219.	3.5	76
85	An Inbreeding Model of Associative Overdominance During a Population Bottleneck. <i>Genetics</i> , 2000, 155, 1981-1990.	2.9	80
86	Three polymorphic microsatellites in the shrimp <i>Penaeus stylirostris</i> . <i>Animal Genetics</i> , 1999, 30, 234-235.	1.7	14
87	Early Effect of Inbreeding as Revealed by Microsatellite Analyses on <i>Ostrea edulis</i> Larvae. <i>Genetics</i> , 1998, 148, 1893-1906.	2.9	165
88	Fine-grained habitat-associated genetic connectivity in an admixed population of mussels in the small isolated Kerguelen Islands. <i>Peer Community Journal</i> , 0, 1, .	0.0	1
89	Introgression between highly divergent sea squirt genomes: an adaptive breakthrough?. <i>Peer Community Journal</i> , 0, 2, .	0.0	8