

Nicolas Bierne

List of Publications by Year in descending order

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89
papers

9,042
citations

65103

42
h-index

50605

87
g-index

114
all docs

114
docs citations

114
times ranked

10981
citing authors

#	ARTICLE	IF	CITATIONS
1	Hybridization and speciation. <i>Journal of Evolutionary Biology</i> , 2013, 26, 229-246.	1.6	1,819
2	Comparative population genomics in animals uncovers the determinants of genetic diversity. <i>Nature</i> , 2014, 515, 261-263.	36.2	521
3	The coupling hypothesis: why genome scans may fail to map local adaptation genes. <i>Molecular Ecology</i> , 2011, 20, 2044-2072.	3.6	467
4	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
5	Shedding Light on the Grey Zone of Speciation along a Continuum of Genomic Divergence. <i>PLoS Biology</i> , 2016, 14, e2000234.	5.4	403
6	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
7	HETEROZYGOSITY-FITNESS CORRELATIONS: A TIME FOR REAPPRAISAL. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 1202-17.	2.3	297
8	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
9	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
10	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
11	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
12	Reference-Free Population Genomics from Next-Generation Transcriptome Data and the Vertebrateâ€“Invertebrate Gap. <i>PLoS Genetics</i> , 2013, 9, e1003457.	3.4	161
13	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
14	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
15	Habitat preference and the marine-speciation paradox. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003, 270, 1399-1406.	2.8	143
16	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
17	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
18	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

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19	Pervasive selection or is it? why are <i>ST</i> outliers sometimes so frequent?. <i>Molecular Ecology</i> , 2013, 22, 2061-2064.	3.6	119
20	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
21	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
22	ASSORTATIVE FERTILIZATION AND SELECTION AT LARVAL STAGE IN THE MUSSELS <i>MYTILUS EDULIS</i> AND <i>M. GALLOPROVINCIALIS</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2002, 56, 292-298.	2.3	94
23	The origin and remolding of genomic islands of differentiation in the European sea bass. <i>Nature Communications</i> , 2018, 9, 2518.	13.2	87
24	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
25	Can we continue to neglect genomic variation in introgression rates when inferring the history of speciation? A case study in a <i>M</i> <i>ytillus</i> hybrid zone. <i>Journal of Evolutionary Biology</i> , 2014, 27, 1662-1675.	1.6	81
26	An Inbreeding Model of Associative Overdominance During a Population Bottleneck. <i>Genetics</i> , 2000, 155, 1981-1990.	2.9	80
27	Microsatellite-associated heterosis in hatchery-propagated stocks of the shrimp <i>Penaeus stylirostris</i> . <i>Aquaculture</i> , 2000, 184, 203-219.	3.5	76
28	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
29	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
30	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
31	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
32	Gene-Flow in a Mosaic Hybrid Zone: Is Local Introgression Adaptive?. <i>Genetics</i> , 2014, 197, 939-951.	2.9	62
33	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
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	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
36	Can habitat specialisation maintain a mosaic hybrid zone in marine bivalves?. <i>Marine Ecology - Progress Series</i> , 2002, 245, 157-170.	1.9	60

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37	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
38	GC-Biased Segregation of Noncoding Polymorphisms in <i>Drosophila</i> . <i>Genetics</i> , 2006, 172, 221-228.	2.9	55
39	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
40	Distinguishing contemporary hybridization from past introgression with postgenomic ancestry-informative <i>SNPs</i> in strongly differentiated <i>Ciona</i> species. <i>Molecular Ecology</i> , 2016, 25, 5527-5542.	3.6	54
41	Replicated anthropogenic hybridisations reveal parallel patterns of admixture in marine mussels. <i>Evolutionary Applications</i> , 2020, 13, 575-599.	3.2	54
42	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
43	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
44	Population genomic footprints of fine-scale differentiation between habitats in Mediterranean blue tits. <i>Molecular Ecology</i> , 2016, 25, 542-558.	3.6	52
45	Differential introgression from a sister species explains high <i>F_{ST}</i> outlier loci within a mussel species. <i>Journal of Evolutionary Biology</i> , 2013, 26, 14-26.	1.6	51
46	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
47	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
48	Contrasting patterns of genome-wide polymorphism in the native and invasive range of the marine mollusc <i>Crrepidula fornicata</i> . <i>Molecular Ecology</i> , 2013, 22, 1003-1018.	3.6	44
49	Prevalence and polymorphism of a mussel transmissible cancer in Europe. <i>Molecular Ecology</i> , 2022, 31, 736-751.	3.6	44
50	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
51	DILS: Demographic inferences with linked selection by using ABC. <i>Molecular Ecology Resources</i> , 2021, 21, 2629-2644.	5.0	37
52	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
53	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
54	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

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55	Genetic hitchhiking in a subdivided population of <i>Mytilus edulis</i> . BMC Evolutionary Biology, 2008, 8, 164.	3.1	32
56	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. G3: Genes, Genomes, Genetics, 2013, 3, 333-341.	1.9	31
57	Parallel pattern of differentiation at a genomic island shared between clinal and mosaic hybrid zones in a complex of cryptic seahorse lineages. Evolution; International Journal of Organic Evolution, 2019, 73, 817-835.	2.3	29
58	Anthropogenic hybridization at sea: three evolutionary questions relevant to invasive species management. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190547.	4.2	29
59	Weird genotypes? Don't discard them, transmissible cancer could be an explanation. Evolutionary Applications, 2017, 10, 140-145.	3.2	27
60	Implementation of various approaches to study the prevalence, incidence and progression of disseminated neoplasia in mussel stocks. Journal of Invertebrate Pathology, 2019, 168, 107271.	3.3	26
61	The divergence history of European blue mussel species reconstructed from Approximate Bayesian Computation: the effects of sequencing techniques and sampling strategies. PeerJ, 2018, 6, e5198.	2.0	26
62	Genomic reticulation indicates mixed ancestry in Southern-Hemisphere <i>Mytilus</i> spp. mussels. Biological Journal of the Linnean Society, 2007, 92, 747-754.	1.6	24
63	SNP Detection from De Novo Transcriptome Sequencing in the Bivalve <i>Macoma balthica</i> : Marker Development for Evolutionary Studies. PLoS ONE, 2012, 7, e52302.	2.5	24
64	A New Barrier to Dispersal Trapped Old Genetic Clines That Escaped the Easter Microplate Tension Zone of the Pacific Vent Mussels. PLoS ONE, 2013, 8, e81555.	2.5	24
65	Evidence for adaptation from standing genetic variation on an antimicrobial peptide gene in the mussel <i>Mytilus edulis</i> . Molecular Ecology, 2014, 23, 3000-3012.	3.6	22
66	The geometry and genetics of hybridization. Evolution; International Journal of Organic Evolution, 2020, 74, 2575-2590.	2.3	22
67	Mark-recapture cloning: a straightforward and cost-effective cloning method for population genetics of single-copy nuclear DNA sequences in diploids. Molecular Ecology Notes, 2007, 7, 562-566.	1.6	17
68	An introgression breakthrough left by an anthropogenic contact between two ascidians. Molecular Ecology, 2021, 30, 6718-6732.	3.6	17
69	Additive transcriptomic variation associated with reproductive traits suggest local adaptation in a recently settled population of the Pacific oyster, <i>Crassostrea gigas</i> . BMC Genomics, 2015, 16, 808.	2.9	16
70	Agent-based modeling and genetics reveal the Limfjorden, Denmark, as a well-connected system for mussel larvae. Marine Ecology - Progress Series, 2021, 680, 193-205.	1.9	16
71	Traits of a mussel transmissible cancer are reminiscent of a parasitic life style. Scientific Reports, 2021, 11, 24110.	3.4	15
72	Three polymorphic microsatellites in the shrimp <i>Penaeus stylirostris</i> . Animal Genetics, 1999, 30, 234-235.	1.7	14

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73	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
74	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
75	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
76	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
77	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
78	Spatial coalescent connectivity through multi-generation dispersal modelling predicts gene flow across marine phyla. <i>Nature Communications</i> , 2022, 13, .	13.2	13
79	ASSORTATIVE FERTILIZATION AND SELECTION AT LARVAL STAGE IN THE MUSSELS <i>MYTILUS EDULIS</i> AND <i>M. GALLOPROVINCIALIS</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2002, 56, 292.	2.3	12
80	Subtle limits to connectivity revealed by outlier loci within two divergent metapopulations of the deep-sea hydrothermal gastropod <i>Ifrimeria nautilei</i> . <i>Molecular Ecology</i> , 2022, 31, 2796-2813.	3.6	12
81	Does natural selection explain the fine scale genetic structure at the nuclear exon <i>Glu5a2</i> in blue mussels from Kerguelen?. <i>Ecology and Evolution</i> , 2015, 5, 1456-1473.	1.9	10
82	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
83	Introgression between highly divergent sea squirt genomes: an adaptive breakthrough?. <i>Peer Community Journal</i> , 0, 2, .	0.0	8
84	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
85	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
86	Anthropogenic Change and the Process of Speciation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2023, 15, a041455.	5.4	3
87	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
88	Marine transmissible cancer navigates urbanized waters, threatening spillover. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2024, 291, .	2.8	1
89	Transcriptomics of mussel transmissible cancer <i>MtrBTN2</i> suggests accumulation of multiple cancer traits and oncogenic pathways shared among bilaterians. <i>Open Biology</i> , 2023, 13, .	3.7	0