Nicholas H Barton

List of Publications by Year
in descending order

#	Article	IF	Citations
1	A COMPARISON OF THREE INDIRECT METHODS FOR ESTIMATING AVERAGE LEVELS OF GENE FLOW. Evolution; International Journal of Organic Evolution, 1989, 43, 1349-1368.	2.3	1,204
2	Understanding quantitative genetic variation. Nature Reviews Genetics, 2002, 3, 11-21.	16.3	727
3	PERSPECTIVE: A CRITIQUE OF SEWALL WRIGHT'S SHIFTING BALANCE THEORY OF EVOLUTION. Evolution; International Journal of Organic Evolution, 1997, 51, 643-671.	2.3	486
4	GENETIC ANALYSIS OF A HYBRID ZONE BETWEEN THE FIRE-BELLIED TOADS,<i>BOMBINA BOMBINA</i>AND<i>B. VARIEGATA</i>, NEAR CRACOW IN SOUTHERN POLAND. Evolution; International Journal of Organic Evolution, 1986, 40, 1141-1159.	2.3	287
5	STRONG NATURAL SELECTION IN A WARNING-COLOR HYBRID ZONE. Evolution; International Journal of Organic Evolution, 1989, 43, 421-431.	2.3	234
6	The Effects of Genetic and Geographic Structure on Neutral Variation. Annual Review of Ecology, Evolution, and Systematics, 2003, 34, 99-125.	8.3	215
7	Local introduction and heterogeneous spatial spread of dengue-suppressing Wolbachia through an urban population of Aedes aegypti. PLoS Biology, 2017, 15, e2001894.	5.6	202
8	Perspective: A Critique of Sewall Wright's Shifting Balance Theory of Evolution. Evolution; International Journal of Organic Evolution, 1997, 51, 643.	2.3	198
9	Genetic Analysis of a Hybrid Zone Between the Fire-Bellied Toads, Bombina bombina and B. variegata, Near Cracow in Southern Poland. Evolution; International Journal of Organic Evolution, 1986, 40, 1141.	2.3	190
10	Strong Natural Selection in a Warning-Color Hybrid Zone. Evolution; International Journal of Organic Evolution, 1989, 43, 421.	2.3	190
11	Thinking About the Evolution of Complex Traits in the Era of Genome-Wide Association Studies. Annual Review of Genomics and Human Genetics, 2019, 20, 461-493.	6.2	186
12	THE GENETIC STRUCTURE OF THE HYBRID ZONE BETWEEN THE FIRE-BELLIED TOADS<i>BOMBINA BOMBINA</i>AND<i>B. VARIEGATA</i>: COMPARISONS BETWEEN TRANSECTS AND BETWEEN LOCI. Evolution; International Journal of Organic Evolution, 1991, 45, 237-261.	2.3	181
13	Limits to adaptation along environmental gradients. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6401-6406.	7.1	176
14	The sources of adaptive variation. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20162864.	2.6	174
15	THE EVOLUTION OF STRONG REPRODUCTIVE ISOLATION. Evolution; International Journal of Organic Evolution, 2009, 63, 1171-1190.	2.3	127
16	Why structure matters. ELife, 2019, 8, .	6.0	107
17	Limits to the Rate of Adaptive Substitution in Sexual Populations. PLoS Genetics, 2012, 8, e1002740.	3.5	98
18	Tread Lightly Interpreting Polygenic Tests of Selection. Genetics, 2018, 208, 1351-1355.	2.9	98

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19	RAPID LABORATORY EVOLUTION OF ADULT LIFE-HISTORY TRAITS IN<i>DROSOPHILA MELANOGASTER</i>IN RESPONSE TO TEMPERATURE. Evolution; International Journal of Organic Evolution, 1995, 49, 538-544.	2.3	83
20	THE GENETIC STRUCTURE OF A HYBRID ZONE BETWEEN TWO CHROMOSOME RACES OF THE <i>SCELOPORUS GRAMMICUS</i> COMPLEX (SAURIA, PHRYNOSOMATIDAE) IN CENTRAL MEXICO. Evolution; International Journal of Organic Evolution, 1995, 49, 9-36.	2.3	80
21	HYBRIDIZATION OFBOMBINA BOMBINAANDB. VARIEGATA(ANURA, DISCOGLOSSIDAE) AT A SHARP ECOTONE IN WESTERN UKRAINE: COMPARISONS ACROSS TRANSECTS AND OVER TIME. Evolution; International Journal of Organic Evolution, 2006, 60, 583-600.	2.3	71
22	Deploying dengue-suppressing Wolbachia : Robust models predict slow but effective spatial spread in Aedes aegypti. Theoretical Population Biology, 2017, 115, 45-60.	1.1	71
23	The Spread of an Inversion with Migration and Selection. Genetics, 2018, 208, 377-382.	2.9	70
24	The contribution of statistical physics to evolutionary biology. Trends in Ecology and Evolution, 2011, 26, 424-432.	8.7	67
25	Evolving evolvability. Nature, 2000, 407, 457-458.	27.8	62
26	Inferring Recent Demography from Isolation by Distance of Long Shared Sequence Blocks. Genetics, 2017, 205, 1335-1351.	2.9	61
27	An integrative genomic analysis of the Longshanks selection experiment for longer limbs in mice. ELife, 2019, 8, .	6.0	58
28	A NEW MODEL FOR EXTINCTION AND RECOLONIZATION IN TWO DIMENSIONS: QUANTIFYING PHYLOGEOGRAPHY. Evolution; International Journal of Organic Evolution, 2010, 64, 2701-2715.	2.3	57
29	Mating system variation in hybrid zones: facilitation, barriers and asymmetries to gene flow. New Phytologist, 2019, 224, 1035-1047.	7.3	46
30	Haplotype tagging reveals parallel formation of hybrid races in two butterfly species. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	46
31	Estimating Barriers to Gene Flow from Distorted Isolation-by-Distance Patterns. Genetics, 2018, 208, 1231-1245.	2.9	37
32	Introgression of a Block of Genome Under Infinitesimal Selection. Genetics, 2018, 209, 1279-1303.	2.9	33
33	Likelihoodâ€based inference of population history from lowâ€coverage <i>de novo</i> genome assemblies. Molecular Ecology, 2014, 23, 198-211.	3.9	28
34	The â€œNew Synthesisâ€ Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	27
35	On the completion of speciation. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190530.	4.0	26
36	Coalescent simulation in continuous space. Bioinformatics, 2013, 29, 955-956.	4.1	24

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37	VARIATION IN MATING CALL ACROSS THE HYBRID ZONE BETWEEN THE FIRE-BELLIED TOADS <i>BOMBINA BOMBINA</i> AND <i>B. VARIEGATA</i>. Evolution; International Journal of Organic Evolution, 1992, 46, 595-607.	2.3	20
38	Polygenic local adaptation in metapopulations: A stochastic ecoâ€evolutionary model. Evolution; International Journal of Organic Evolution, 2021, 75, 1030-1045.	2.3	20
39	A likelihoodâ€based comparison of population histories in a parasitoid guild. Molecular Ecology, 2012, 21, 4605-4617.	3.9	19
40	Evolutionary Pathways for the Generation of New Self-Incompatibility Haplotypes in a Nonself-Recognition System. Genetics, 2018, 209, 861-883.	2.9	19
41	Replicability of Introgression Under Linked, Polygenic Selection. Genetics, 2018, 210, 1411-1427.	2.9	17
42	When Does Frequency-Independent Selection Maintain Genetic Variation?. Genetics, 2017, 207, 653-668.	2.9	16
43	Homage to Felsenstein 1981, or why are there so few/many species?. Evolution; International Journal of Organic Evolution, 2021, 75, 978-988.	2.3	13
44	A General Approximation for the Dynamics of Quantitative Traits. Genetics, 2016, 202, 1523-1548.	2.9	10
45	Efficient inference of paternity and sibship inference given known maternity via hierarchical clustering. Molecular Ecology Resources, 2018, 18, 988-999.	4.8	9
46	Why did theÂ<i>Wolbachia</i>Âtransinfection cross the road? drift, deterministic dynamics, and disease control. Evolution Letters, 2022, 6, 92-105.	3.3	6
47	Diverse forms of selection in evolution and computer science. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10398-10399.	7.1	5
48	Sewall Wright on Evolution in Mendelian Populations and the â€œShifting Balanceâ€. Genetics, 2016, 202, 3-4.	2.9	4
49	The consequences of an introgression event. Molecular Ecology, 2018, 27, 4973-4975.	3.9	4
50	The response of a metapopulation to a changing environment. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20210009.	4.0	4
51	Richard Hudson and Norman Kaplan on the Coalescent Process. Genetics, 2016, 202, 865-866.	2.9	3
52	Dynamic maximum entropy provides accurate approximation of structured population dynamics. PLoS Computational Biology, 2021, 17, e1009661.	3.2	1