

Richard Nichols

List of Publications by Year in descending order

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117
papers

11,394
citations

47006

47
h-index

30922

102
g-index

123
all docs

123
docs citations

123
times ranked

13174
citing authors

#	ARTICLE	IF	CITATIONS
1	Hybridization and speciation. <i>Journal of Evolutionary Biology</i> , 2013, 26, 229-246.	1.7	1,735
2	Evaluating loci for use in the genetic analysis of population structure. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1996, 263, 1619-1626.	2.6	1,577
3	Spatial patterns of genetic variation generated by different forms of dispersal during range expansion. <i>Heredity</i> , 1996, 77, 282-291.	2.6	683
4	Gene trees and species trees are not the same. <i>Trends in Ecology and Evolution</i> , 2001, 16, 358-364.	8.7	535
5	A method for quantifying differentiation between populations at multi-allelic loci and its implications for investigating identity and paternity. <i>Genetica</i> , 1995, 96, 3-12.	1.1	492
6	DNA profile match probability calculation: how to allow for population stratification, relatedness, database selection and single bands. <i>Forensic Science International</i> , 1994, 64, 125-140.	2.2	445
7	Y genetic data support the Neolithic demic diffusion model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11008-11013.	7.1	259
8	The genetic consequences of long distance dispersal during colonization. <i>Heredity</i> , 1994, 72, 312-317.	2.6	249
9	Dates from the molecular clock: how wrong can we be?. <i>Trends in Ecology and Evolution</i> , 2007, 22, 180-184.	8.7	240
10	“Ghost” alleles of the Mauritius kestrel. <i>Nature</i> , 2000, 403, 616-616.	27.8	197
11	<i>Culex pipiens</i> in London Underground tunnels: differentiation between surface and subterranean populations. <i>Heredity</i> , 1999, 82, 7-15.	2.6	196
12	Collapse of Amphibian Communities Due to an Introduced Ranavirus. <i>Current Biology</i> , 2014, 24, 2586-2591.	3.9	182
13	Application of DNA Microarrays to Study the Evolutionary Genomics of <i>Yersinia pestis</i> and <i>Yersinia pseudotuberculosis</i> . <i>Genome Research</i> , 2003, 13, 2018-2029.	5.5	154
14	Next Generation Sequencing Reveals Genome Downsizing in Allotetraploid <i>Nicotiana tabacum</i> , Predominantly through the Elimination of Paternally Derived Repetitive DNAs. <i>Molecular Biology and Evolution</i> , 2011, 28, 2843-2854.	8.9	150
15	Bringing genetic diversity to the forefront of conservation policy and management. <i>Conservation Genetics Resources</i> , 2013, 5, 593-598.	0.8	145
16	Phylogenetic Analysis of Varicella-Zoster Virus: Evidence of Intercontinental Spread of Genotypes and Recombination. <i>Journal of Virology</i> , 2002, 76, 1971-1979.	3.4	139
17	Transition-Transversion Bias Is Not Universal: A Counter Example from Grasshopper Pseudogenes. <i>PLoS Genetics</i> , 2007, 3, e22.	3.5	128
18	Analysis of the giant genomes of <i>Fritillaria</i> (<i>Liliaceae</i>) indicates that a lack of DNA removal characterizes extreme expansions in genome size. <i>New Phytologist</i> , 2015, 208, 596-607.	7.3	122

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19	Genome size and ploidy influence angiosperm species' biomass under nitrogen and phosphorus limitation. <i>New Phytologist</i> , 2016, 210, 1195-1206.	7.3	117
20	Diploidization and genome size change in allopolyploids is associated with differential dynamics of low- and high-copy sequences. <i>Plant Journal</i> , 2013, 74, 829-839.	5.7	112
21	SEVERE INBREEDING DEPRESSION AND RAPID FITNESS REBOUND IN THE BUTTERFLY <i>BICYCLUS ANYNANA</i> (SATYRIDAE). <i>Evolution; International Journal of Organic Evolution</i> , 1996, 50, 2000-2013.	2.3	97
22	The persistence of Pliocene populations through the Pleistocene climatic cycles: evidence from the phylogeography of an Iberian lizard. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2001, 268, 1625-1630.	2.6	95
23	Mating patterns, relatedness and the basis of natal philopatry in the brown long-eared bat, <i>Plecotus auritus</i> . <i>Molecular Ecology</i> , 2001, 10, 1309-1321.	3.9	95
24	Deep Sequencing of Viral Genomes Provides Insight into the Evolution and Pathogenesis of Varicella Zoster Virus and Its Vaccine in Humans. <i>Molecular Biology and Evolution</i> , 2014, 31, 397-409.	8.9	91
25	Spatial patterns of genetic variation generated by different forms of dispersal during range expansion. <i>Heredity</i> , 1996, 77, 282-291.	2.6	90
26	Estimating the Number of Subpopulations (<i>K</i>) in Structured Populations. <i>Genetics</i> , 2016, 203, 1827-1839.	2.9	87
27	Evidence for Directional Selection at a Novel Major Histocompatibility Class I Marker in Wild Common Frogs (<i>Rana temporaria</i>) Exposed to a Viral Pathogen (<i>Ranavirus</i>). <i>PLoS ONE</i> , 2009, 4, e4616.	2.5	86
28	Sperm precedence and homogamy across a hybrid zone in the alpine grasshopper <i>Podisma pedestris</i> . <i>Heredity</i> , 1989, 62, 343-353.	2.6	83
29	Patterns of colonization in a metapopulation of grey seals. <i>Nature</i> , 2002, 416, 424-427.	27.8	81
30	Unidirectional diploid-tetraploid introgression among British birch trees with shifting ranges shown by restriction site-associated markers. <i>Molecular Ecology</i> , 2016, 25, 2413-2426.	3.9	78
31	Independent, Rapid and Targeted Loss of Highly Repetitive DNA in Natural and Synthetic Allopolyploids of <i>Nicotiana tabacum</i> . <i>PLoS ONE</i> , 2012, 7, e36963.	2.5	77
32	The role of vicariance vs. dispersal in shaping genetic patterns in ocellated lizard species in the western Mediterranean. <i>Molecular Ecology</i> , 2008, 17, 1535-1551.	3.9	75
33	Reconstructing the emergence of a lethal infectious disease of wildlife supports a key role for spread through translocations by humans. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20160952.	2.6	74
34	Ribosomal DNA in the Grasshopper <i>Podisma pedestris</i> : Escape From Concerted Evolution. <i>Genetics</i> , 2006, 174, 863-874.	2.9	72
35	Genomic Prediction of Testcross Performance in Canola (<i>Brassica napus</i>). <i>PLoS ONE</i> , 2016, 11, e0147769.	2.5	72
36	Genetic differentiation of a European caddisfly: past and present gene flow among fragmented larval habitats. <i>Molecular Ecology</i> , 2001, 10, 1821-1834.	3.9	71

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37	Molecular phylogeny and morphological change in the <i>Psittacula</i> parakeets. <i>Molecular Phylogenetics and Evolution</i> , 2004, 31, 96-108.	2.7	69
38	Effects of population structure on DNA fingerprint analysis in forensic science. <i>Heredity</i> , 1991, 66, 297-302.	2.6	67
39	The origin and evolution of geminivirus-related DNA sequences in <i>Nicotiana</i> . <i>Heredity</i> , 2004, 92, 352-358.	2.6	65
40	The fire ant social chromosome supergene variant <i>Sb</i> shows low diversity but high divergence from <i>SB</i> . <i>Molecular Ecology</i> , 2017, 26, 2864-2879.	3.9	65
41	Significant genetic correlations among Caucasians at forensic DNA loci. <i>Heredity</i> , 1997, 78, 583-589.	2.6	63
42	Sustaining genetic variation in a small population: evidence from the Mauritius kestrel. <i>Molecular Ecology</i> , 2008, 10, 593-602.	3.9	63
43	Next generation sequencing analysis reveals a relationship between rDNA unit diversity and locus number in <i>Nicotiana</i> diploids. <i>BMC Genomics</i> , 2012, 13, 722.	2.8	60
44	Landscape, habitat characteristics and the genetic population structure of two caddisflies. <i>Freshwater Biology</i> , 2007, 52, 1907-1929.	2.4	57
45	European phylogeography of the common frog (<i>Rana temporaria</i>): routes of postglacial colonization into the British Isles, and evidence for an Irish glacial refugium. <i>Heredity</i> , 2009, 102, 490-496.	2.6	54
46	Severe Inbreeding Depression and Rapid Fitness Rebound in the Butterfly <i>Bicyclus anynana</i> (Satyridae). <i>Evolution; International Journal of Organic Evolution</i> , 1996, 50, 2000.	2.3	52
47	Genetic population structure and neighbourhood population size estimates of the caddisfly <i>Plectrocnemia conspersa</i> . <i>Freshwater Biology</i> , 2003, 48, 1813-1824.	2.4	51
48	Inbreeding of Bottlenecked Butterfly Populations: Estimation Using the Likelihood of Changes in Marker Allele Frequencies. <i>Genetics</i> , 1999, 151, 1053-1063.	2.9	51
49	Natural selection for rash-forming genotypes of the varicella-zoster vaccine virus detected within immunized human hosts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 208-212.	7.1	49
50	A molecular phylogeny of African kestrels with reference to divergence across the Indian Ocean. <i>Molecular Phylogenetics and Evolution</i> , 2002, 25, 267-277.	2.7	48
51	Using nested clade analysis to assess the history of colonization and the persistence of populations of an Iberian Lizard. <i>Molecular Ecology</i> , 2002, 11, 809-819.	3.9	48
52	Population genetics of STR loci in Caucasians. <i>International Journal of Legal Medicine</i> , 1996, 108, 300-305.	2.2	46
53	A Method for Distinguishing Consanguinity and Population Substructure Using Multilocus Genotype Data. <i>Molecular Biology and Evolution</i> , 2001, 18, 2048-2056.	8.9	45
54	Molecular footprints of the <i>H</i> -olocene retreat of dwarf birch in <i>B</i> -ritain. <i>Molecular Ecology</i> , 2014, 23, 2771-2782.	3.9	45

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55	What is genetic differentiation, and how should we measure it? <i>Molecular Ecology</i> , 2014, 23, 4216-4225.	3.9	44
56	The double origin of Iberian peninsular chameleons. <i>Biological Journal of the Linnean Society</i> , 2002, 75, 1-7.	1.6	43
57	Effects of historic and projected climate change on the range and impacts of an emerging wildlife disease. <i>Global Change Biology</i> , 2019, 25, 2648-2660.	9.5	43
58	Does runaway sexual selection work in finite populations?. <i>Journal of Evolutionary Biology</i> , 1989, 2, 299-313.	1.7	42
59	Minisatellite mutational processes reduce F_{st} estimates. <i>Human Genetics</i> , 1999, 105, 567-576.	3.8	41
60	Population structure and the shape of a chromosomal cline between two races of <i>Podisma pedestris</i> (Orthoptera: Acrididae). <i>Biological Journal of the Linnean Society</i> , 1986, 29, 301-316.	1.6	37
61	Genomic assessment of local adaptation in dwarf birch to inform assisted gene flow. <i>Evolutionary Applications</i> , 2020, 13, 161-175.	3.1	37
62	Effects of bottlenecks on quantitative genetic variation in the butterfly <i>Bicyclus anynana</i> . <i>Genetical Research</i> , 2001, 77, 167-181.	0.9	36
63	Range expansion and hybridization in Round Island petrels (<i>Pterodroma</i> spp.): evidence from microsatellite genotypes. <i>Molecular Ecology</i> , 2010, 19, 3157-3170.	3.9	36
64	Detecting gene conversion: primate visual pigment genes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1992, 249, 275-280.	2.6	32
65	Household size is critical to varicella-zoster virus transmission in the tropics despite lower viral infectivity. <i>Epidemics</i> , 2011, 3, 12-18.	3.0	32
66	Conservation Genetic Resources for Effective Species Survival (ConGRESS): Bridging the divide between conservation research and practice. <i>Journal for Nature Conservation</i> , 2013, 21, 433-437.	1.8	32
67	Rates of Vaccine Evolution Show Strong Effects of Latency: Implications for Varicella Zoster Virus Epidemiology. <i>Molecular Biology and Evolution</i> , 2015, 32, 1020-1028.	8.9	32
68	Population genetic patterns suggest a behavioural change in wild common frogs (<i>Rana</i>). <i>Evolutionary Ecology</i> , 2010, 24, 222-231.	3.9	31
69	Spatial targeting of infectious disease control: identifying multiple, unknown sources. <i>Methods in Ecology and Evolution</i> , 2014, 5, 647-655.	5.2	30
70	Homogamy in a hybrid zone in the alpine grasshopper <i>Podisma pedestris</i> . <i>Heredity</i> , 1987, 59, 457-466.	2.6	29
71	Heterochromatin readjusting chiasma distribution in two species of the genus <i>Arcyptera</i> : The effect among individuals and populations. <i>Heredity</i> , 1986, 56, 177-184.	2.6	28
72	Using molecular markers with high mutation rates to obtain estimates of relative population size and to distinguish the effects of gene flow and mutation: a demonstration using data from endemic Mauritian skinks. <i>Molecular Ecology</i> , 2004, 13, 775-787.	3.9	27

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73	Vaccine Oka Varicellaâ€Zoster Virus Genotypes Are Monomorphic in Single Vesicles and Polymorphic in Respiratory Tract Secretions. <i>Journal of Infectious Diseases</i> , 2006, 193, 927-930.	4.0	27
74	Genome-wide haplotype analysis improves trait predictions in <i>Brassica napus</i> hybrids. <i>Plant Science</i> , 2019, 283, 157-164.	3.6	26
75	Testing single-sample estimators of effective population size in genetically structured populations. <i>Conservation Genetics</i> , 2014, 15, 23-35.	1.5	25
76	Evaluating the severity of the population bottleneck in the Mauritius kestrel <i>Falco punctatus</i> from ringing records using MCMC estimation. <i>Journal of Animal Ecology</i> , 2001, 70, 401-409.	2.8	23
77	An Analysis of Consanguinity and Social Structure Within the UK Asian Population Using Microsatellite Data. <i>Annals of Human Genetics</i> , 2003, 67, 525-537.	0.8	22
78	Genetic diversity maintained among fragmented populations of a tree undergoing range contraction. <i>Heredity</i> , 2018, 121, 304-318.	2.6	22
79	The Inexorable Spread of a Newly Arisen Neo-Y Chromosome. <i>PLoS Genetics</i> , 2008, 4, e1000082.	3.5	21
80	Philopatry in the alpine grasshopper, <i>Podisma pedestris</i> : a novel experimental and analytical method. <i>Ecological Entomology</i> , 1995, 20, 137-145.	2.2	20
81	THE FREQUENCY OF rDNA VARIANTS WITHIN INDIVIDUALS PROVIDES EVIDENCE OF POPULATION HISTORY AND GENE FLOW ACROSS A GRASSHOPPER HYBRID ZONE. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 833-844.	2.3	20
82	Genetic differentiation between and within strains of the saw-toothed grain beetle, <i>Oryzaephilus surinamensis</i> (Coleoptera: Silvanidae) at RAPD loci. <i>Insect Molecular Biology</i> , 1997, 6, 285-289.	2.0	19
83	The effect of reproductive compensation on recessive disorders within consanguineous human populations. <i>Heredity</i> , 2002, 88, 474-479.	2.6	19
84	Genome-wide characterisation of Hepatitis B mutations involved in clinical outcome. <i>Heredity</i> , 2006, 97, 389-397.	2.6	18
85	Genetical and ecological differentiation across a hybrid zone. <i>Ecological Entomology</i> , 1988, 13, 39-49.	2.2	17
86	The Fragmentation of Tension Zones in Sparsely Populated Areas. <i>American Naturalist</i> , 1989, 134, 969-977.	2.1	17
87	Recruitment, kin and the spatial genetic structure of a caddisfly <i>Plectrocnemia conspersa</i> in a southern English stream. <i>Freshwater Biology</i> , 2005, 50, 1499-1514.	2.4	16
88	Geographically localised bursts of ribosomal DNA mobility in the grasshopper <i>Podisma pedestris</i> . <i>Heredity</i> , 2009, 103, 54-61.	2.6	16
89	Interactions between plant genome size, nutrients and herbivory by rabbits, molluscs and insects on a temperate grassland. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182619.	2.6	16
90	A method for quantifying differentiation between populations at multi-allelic loci and its implications for investigating identity and paternity. <i>Contemporary Issues in Genetics and Evolution</i> , 1995, , 3-12.	0.9	16

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91	Genomic architecture and evolutionary antagonism drive allelic expression bias in the social supergene of red fire ants. <i>ELife</i> , 2020, 9, .	6.0	16
92	Minisatellite mutational processes reduce F_{st} estimates. <i>Human Genetics</i> , 1999, 105, 567-576.	3.8	15
93	Predictions of single-nucleotide polymorphism differentiation between two populations in terms of mutual information. <i>Molecular Ecology</i> , 2011, 20, 3156-3166.	3.9	15
94	Inside the Melanoplineae: New molecular evidence for the evolutionary history of the Eurasian Podismini (Orthoptera: Acrididae). <i>Molecular Phylogenetics and Evolution</i> , 2014, 71, 224-233.	2.7	15
95	Significant genetic correlations among Caucasians at forensic DNA loci. <i>Heredity</i> , 1997, 78, 583-589.	2.6	15
96	Phylogenetic Relationships in Pterodroma Petrels Are Obscured by Recent Secondary Contact and Hybridization. <i>PLoS ONE</i> , 2011, 6, e20350.	2.5	15
97	[DNA Fingerprinting: A Review of the Controversy]: Comment: Some Causes for Concern about DNA Profiles. <i>Statistical Science</i> , 1994, 9, .	2.8	14
98	Experimental evidence in support of single host maintenance of a multihost pathogen. <i>Ecosphere</i> , 2014, 5, art142.	2.2	13
99	Population diversity in batches of the varicella Oka vaccine. <i>Vaccine</i> , 2011, 29, 3293-3298.	3.8	12
100	A novel approach to characterise pathogen candidate genetic polymorphisms involved in clinical outcome. <i>Infection, Genetics and Evolution</i> , 2006, 6, 38-45.	2.3	11
101	Stops making sense: translational trade-offs and stop codon reassignment. <i>BMC Evolutionary Biology</i> , 2011, 11, 227.	3.2	10
102	Purifying Selection in Deeply Conserved Human Enhancers Is More Consistent than in Coding Sequences. <i>PLoS ONE</i> , 2014, 9, e103357.	2.5	9
103	DNA Sequence Variability in Oka Vaccine Isolates. <i>Journal of Infectious Diseases</i> , 2007, 196, 801-802.	4.0	8
104	Morphological differentiation following experimental bottlenecks in the butterfly <i>Bicyclus fanyana</i> (Nymphalidae). <i>Biological Journal of the Linnean Society</i> , 2006, 89, 107-115.	1.6	7
105	Modelling Ranavirus Transmission in Populations of Common Frogs (<i>Rana temporaria</i>) in the United Kingdom. <i>Viruses</i> , 2019, 11, 556.	3.3	7
106	Whi3 mnemonic association with endoplasmic reticulum membranes confines the memory of deceptive courtship to the yeast mother cell. <i>Current Biology</i> , 2022, 32, 963-974.e7.	3.9	7
107	Microsatellites for the net-spinning caddisfly <i>Plectrocnemia conspersa</i> (Polycentropodidae). <i>Molecular Ecology Notes</i> , 2001, 1, 318-319.	1.7	6
108	Sexual preference and genetic correlations. <i>Trends in Ecology and Evolution</i> , 1992, 7, 29-30.	8.7	5

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109	Induced dispersal in wildlife management: experimental evaluation of the risk of hybrid breakdown and the benefit of hybrid vigor in the F1 generation. <i>Conservation Genetics</i> , 2011, 12, 31-40.	1.5	5
110	Phylogentic Analysis of 24 Ranavirus Isolates from English Amphibians using 2 Partial Loci. <i>Journal of Emerging Diseases and Virology</i> , 2017, 3, .	0.2	4
111	Population Structure and Insecticidal Control of the Sawtoothed Grain Beetle (Coleoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.8	3
112	1868 and all that for Magicicada. <i>Nature</i> , 1988, 336, 206-207.	27.8	2
113	Quantitative genetics focus issue. <i>Heredity</i> , 2005, 94, 273-274.	2.6	2
114	Mitocho drial DNA clues to Gopher tortoise dispersal. <i>Trends in Ecology and Evolution</i> , 1989, 4, 192-193.	8.7	1
115	Godfrey M Hewitt (1940â€“2013): highlights in <i>Heredity</i> from a career in evolutionary genetics. <i>Heredity</i> , 2013, 110, 405-406.	2.6	1
116	Spatially clustered count data provide more efficient search strategies in invasion biology and disease control. <i>Ecological Applications</i> , 2021, 31, e02329.	3.8	1
117	Evolution at a snail's pace. <i>Trends in Ecology and Evolution</i> , 1988, 3, 94-95.	8.7	0