

Mathieu Gautier

List of Publications by Year in descending order

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113
papers

7,203
citations

81900

39
h-index

69250

77
g-index

131
all docs

131
docs citations

131
times ranked

9712
citing authors

#	ARTICLE	IF	CITATIONS
1	DIYABC v2.0: a software to make approximate Bayesian computation inferences about population history using single nucleotide polymorphism, DNA sequence and microsatellite data. <i>Bioinformatics</i> , 2014, 30, 1187-1189.	4.1	983
2	<i>rehh</i> : an R package to detect footprints of selection in genome-wide SNP data from haplotype structure. <i>Bioinformatics</i> , 2012, 28, 1176-1177.	4.1	434
3	Genome-Wide Scan for Adaptive Divergence and Association with Population-Specific Covariates. <i>Genetics</i> , 2015, 201, 1555-1579.	2.9	374
4	Reliable ABC model choice via random forests. <i>Bioinformatics</i> , 2016, 32, 859-866.	4.1	272
5	The effect of <i>RAD</i> allele dropout on the estimation of genetic variation within and between populations. <i>Molecular Ecology</i> , 2013, 22, 3165-3178.	3.9	259
6	<i>rehh</i> 2.0: a reimplementation of the R package <i>rehh</i> to detect positive selection from haplotype structure. <i>Molecular Ecology Resources</i> , 2017, 17, 78-90.	4.8	243
7	Is There a Genetic Paradox of Biological Invasion?. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2016, 47, 51-72.	8.3	225
8	The Genome Response to Artificial Selection: A Case Study in Dairy Cattle. <i>PLoS ONE</i> , 2009, 4, e6595.	2.5	219
9	Estimation of population allele frequencies from next-generation sequencing data: pool versus individual-based genotyping. <i>Molecular Ecology</i> , 2013, 22, 3766-3779.	3.9	195
10	A whole genome Bayesian scan for adaptive genetic divergence in West African cattle. <i>BMC Genomics</i> , 2009, 10, 550.	2.8	186
11	Insights into the Genetic History of French Cattle from Dense SNP Data on 47 Worldwide Breeds. <i>PLoS ONE</i> , 2010, 5, e13038.	2.5	167
12	Measuring Genetic Differentiation from Pool-seq Data. <i>Genetics</i> , 2018, 210, 315-330.	2.9	147
13	Genetic and Haplotypic Structure in 14 European and African Cattle Breeds. <i>Genetics</i> , 2007, 177, 1059-1070.	2.9	133
14	Footprints of selection in the ancestral admixture of a New World Creole cattle breed. <i>Molecular Ecology</i> , 2011, 20, 3128-3143.	3.9	130
15	Empirical Assessment of RAD Sequencing for Interspecific Phylogeny. <i>Molecular Biology and Evolution</i> , 2014, 31, 1272-1274.	8.9	124
16	A bovine whole-genome radiation hybrid panel and outline map. <i>Mammalian Genome</i> , 2002, 13, 469-474.	2.2	115
17	Mapping of a Milk Production Quantitative Trait Locus to a 420-kb Region on Bovine Chromosome 6. <i>Genetics</i> , 2005, 169, 275-283.	2.9	104
18	LARGE-SCALE CANDIDATE GENE SCAN REVEALS THE ROLE OF CHEMORECEPTOR GENES IN HOST PLANT SPECIALIZATION AND SPECIATION IN THE PEA APHID. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 2723-2738.	2.3	99

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19	The Genomic Basis of Color Pattern Polymorphism in the Harlequin Ladybird. <i>Current Biology</i> , 2018, 28, 3296-3302.e7.	3.9	92
20	Species composition and environmental adaptation of indigenous Chinese cattle. <i>Scientific Reports</i> , 2017, 7, 16196.	3.3	83
21	Dual Origins of Dairy Cattle Farming – Evidence from a Comprehensive Survey of European Y-Chromosomal Variation. <i>PLoS ONE</i> , 2011, 6, e15922.	2.5	79
22	A physical map of the bovine genome. <i>Genome Biology</i> , 2007, 8, R165.	9.6	73
23	On the Breeds of Cattle – Historic and Current Classifications. <i>Diversity</i> , 2011, 3, 660-692.	1.7	73
24	Construction and characterization of a bovine BAC library with four genome-equivalent coverage. <i>Genetics Selection Evolution</i> , 2001, 33, 543-8.	3.0	72
25	A model-based approach to characterize individual inbreeding at both global and local genomic scales. <i>Molecular Ecology</i> , 2017, 26, 5820-5841.	3.9	72
26	A Genomic Map of Climate Adaptation in <i>Arabidopsis thaliana</i> at a Micro-Geographic Scale. <i>Frontiers in Plant Science</i> , 2018, 9, 967.	3.6	65
27	Detecting and Measuring Selection from Gene Frequency Data. <i>Genetics</i> , 2014, 196, 799-817.	2.9	64
28	Atypical structure and phylogenomic evolution of the new eutherian oocyte- and embryo-expressed KHDC1/DPPA5/ECAT1/OOEP gene family. <i>Genomics</i> , 2007, 90, 583-594.	2.9	63
29	Extending approximate Bayesian computation with supervised machine learning to infer demographic history from genetic polymorphisms using DIYABC Random Forest. <i>Molecular Ecology Resources</i> , 2021, 21, 2598-2613.	4.8	63
30	Characterization of the DGAT1 K232A and Variable Number of Tandem Repeat Polymorphisms in French Dairy Cattle. <i>Journal of Dairy Science</i> , 2007, 90, 2980-2988.	3.4	61
31	Adaptive admixture in the West African bovine hybrid zone: insight from the Borgou population. <i>Molecular Ecology</i> , 2014, 23, 3241-3257.	3.9	60
32	Characterization of the caprine stearoyl-CoA desaturase gene and its mRNA showing an unusually long 5'-UTR sequence arising from a single exon. <i>Gene</i> , 2001, 281, 53-61.	2.2	59
33	A Whole-Genome Scan for Association with Invasion Success in the Fruit Fly <i>Drosophila suzukii</i> Using Contrasts of Allele Frequencies Corrected for Population Structure. <i>Molecular Biology and Evolution</i> , 2020, 37, 2369-2385.	8.9	57
34	WIDDE: a Web-Interfaced next generation database for genetic diversity exploration, with a first application in cattle. <i>BMC Genomics</i> , 2015, 16, 940.	2.8	56
35	Local gene density predicts the spatial position of genetic loci in the interphase nucleus. <i>Experimental Cell Research</i> , 2005, 311, 14-26.	2.6	55
36	Fine Mapping of Quantitative Trait Loci Affecting Female Fertility in Dairy Cattle on BTA03 Using a Dense Single-Nucleotide Polymorphism Map. <i>Genetics</i> , 2008, 178, 2227-2235.	2.9	55

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37	Detecting correlation between allele frequencies and environmental variables as a signature of selection. A fast computational approach for genome-wide studies. <i>Spatial Statistics</i> , 2014, 8, 145-155.	1.9	52
38	RZooRoH: An R package to characterize individual genomic autozygosity and identify homozygous-by-descent segments. <i>Methods in Ecology and Evolution</i> , 2019, 10, 860-866.	5.2	52
39	A Quasi-Exclusive European Ancestry in the Senepol Tropical Cattle Breed Highlights the Importance of the slick Locus in Tropical Adaptation. <i>PLoS ONE</i> , 2012, 7, e36133.	2.5	48
40	A genomic map of climate adaptation in Mediterranean cattle breeds. <i>Molecular Ecology</i> , 2019, 28, 1009-1029.	3.9	46
41	Identification of a doublet missense substitution in the bovine LRP4 gene as a candidate causal mutation for syndactyly in Holstein cattle. <i>Genomics</i> , 2006, 88, 610-621.	2.9	43
42	Oviposition Preference and Larval Performance of <i>Drosophila suzukii</i> (Diptera: Drosophilidae), Spotted-Wing <i>Drosophila</i> : Effects of Fruit Identity and Composition. <i>Environmental Entomology</i> , 2019, 48, 867-881.	1.4	43
43	Near-chromosome level genome assembly of the fruit pest <i>Drosophila suzukii</i> using long-read sequencing. <i>Scientific Reports</i> , 2020, 10, 11227.	3.3	42
44	Detection of selection signatures within candidate regions underlying trypanotolerance in outbred cattle populations. <i>Molecular Ecology</i> , 2009, 18, 1801-1813.	3.9	41
45	Deciphering the Wisent Demographic and Adaptive Histories from Individual Whole-Genome Sequences. <i>Molecular Biology and Evolution</i> , 2016, 33, 2801-2814.	8.9	41
46	Taming the late Quaternary phylogeography of the Eurasiatic wild ass through ancient and modern DNA. <i>PLoS ONE</i> , 2017, 12, e0174216.	2.5	40
47	Mapping of 195 genes in cattle and updated comparative map with man, mouse, rat and pig. <i>Cytogenetic and Genome Research</i> , 2003, 102, 16-24.	1.1	39
48	Fine Mapping and Physical Characterization of Two Linked Quantitative Trait Loci Affecting Milk Fat Yield in Dairy Cattle on BTA26. <i>Genetics</i> , 2006, 172, 425-436.	2.9	37
49	Identification of large selective sweeps associated with major genes in cattle. <i>Animal Genetics</i> , 2013, 44, 758-762.	1.7	36
50	Positive selection of protective variants for type 2 diabetes from the Neolithic onward: a case study in Central Asia. <i>European Journal of Human Genetics</i> , 2013, 21, 1146-1151.	2.8	35
51	Inferring Population Histories Using Genome-Wide Allele Frequency Data. <i>Molecular Biology and Evolution</i> , 2013, 30, 654-668.	8.9	34
52	C-Nap1 mutation affects centriole cohesion and is associated with a Seckel-like syndrome in cattle. <i>Nature Communications</i> , 2015, 6, 6894.	12.8	34
53	Identifying genomic hotspots of differentiation and candidate genes involved in the adaptive divergence of pea aphid host races. <i>Molecular Ecology</i> , 2018, 27, 3287-3300.	3.9	34
54	ES-Statistics estimation and admixture graph construction with Pool-Seq or allele count data using the R package <i>poolstat</i> . <i>Molecular Ecology Resources</i> , 2022, 22, 1394-1416.	4.8	32

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55	Age-based partitioning of individual genomic inbreeding levels in Belgian Blue cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 92.	3.0	30
56	A first generation bovine BAC-based physical map. <i>Genetics Selection Evolution</i> , 2004, 36, 105-22.	3.0	29
57	A novel locus on chromosome 1 underlies the evolution of a melanic plumage polymorphism in a wild songbird. <i>Royal Society Open Science</i> , 2017, 4, 160805.	2.4	29
58	Localization by FISH of the 31 Texas nomenclature type I markers to both Q- and R-banded bovine chromosomes. <i>Cytogenetic and Genome Research</i> , 2000, 90, 315-320.	1.1	28
59	Assignment¹ of the fatty acid synthase (FASN) gene to bovine chromosome 19 (19q22) by in situ hybridization and confirmation by somatic cell hybrid mapping. <i>Cytogenetic and Genome Research</i> , 2001, 93, 141-142.	1.1	27
60	Inferring sex-specific demographic history from SNP data. <i>PLoS Genetics</i> , 2018, 14, e1007191.	3.5	26
61	The scurs inheritance: new insights from the French Charolais breed. <i>BMC Genetics</i> , 2009, 10, 33.	2.7	24
62	Cytogenetic comparison between Vietnamese sika deer and cattle: R-banded karyotypes and FISH mapping. <i>Chromosome Research</i> , 2001, 9, 673-687.	2.2	23
63	The extent of linkage disequilibrium in a large cattle population of western Africa and its consequences for association studies. <i>Animal Genetics</i> , 2007, 38, 277-286.	1.7	23
64	Using genotyping data to assign markers to their chromosome type and to infer the sex of individuals: a Bayesian model-based classifier. <i>Molecular Ecology Resources</i> , 2014, 14, 1141-1159.	4.8	23
65	Draft genome and reference transcriptomic resources for the urticating pine defoliator <i>Thaumetopoea pityocampa</i> (Lepidoptera: Notodontidae). <i>Molecular Ecology Resources</i> , 2018, 18, 602-619.	4.8	23
66	An ABC estimate of pedigree error rate: application in dog, sheep and cattle breeds. <i>Animal Genetics</i> , 2012, 43, 309-314.	1.7	22
67	Deciphering the demographic history of allochronic differentiation in the pine processionary moth <i>Thaumetopoea pityocampa</i> . <i>Molecular Ecology</i> , 2018, 27, 264-278.	3.9	22
68	Identification by R-banding and FISH of chromosome arms involved in Robertsonian translocations in several deer species. <i>Chromosome Research</i> , 2003, 11, 649-663.	2.2	21
69	High resolution physical map of porcine chromosome 7 QTL region and comparative mapping of this region among vertebrate genomes. <i>BMC Genomics</i> , 2006, 7, 13.	2.8	21
70	Private Selective Sweeps Identified from Next-Generation Pool-Sequencing Reveal Convergent Pathways under Selection in Two Inbred <i>Schistosoma mansoni</i> Strains. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2591.	3.0	20
71	Genome scans on experimentally evolved populations reveal candidate regions for adaptation to plant resistance in the potato cyst nematode <i>Globodera pallida</i> . <i>Molecular Ecology</i> , 2017, 26, 4700-4711.	3.9	20
72	Genetic analysis of Thai cattle reveals a Southeast Asian indicine ancestry. <i>PeerJ</i> , 2015, 3, e1318.	2.0	20

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73	RADIATION HYBRID AND GENETIC LINKAGE MAPPING OF TWO GENES RELATED TO FAT METABOLISM IN CATTLE: FATTY ACID SYNTHASE (FASN) AND GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE MITOCHONDRIAL (GPAM). <i>Animal Biotechnology</i> , 2005, 16, 1-9.	1.5	19
74	Refinement of two female fertility QTL using alternative phenotypes in French Holstein dairy cattle. <i>Animal Genetics</i> , 2007, 38, 72-74.	1.7	19
75	The Evolution and Population Diversity of Bison in Pleistocene and Holocene Eurasia: Sex Matters. <i>Diversity</i> , 2018, 10, 65.	1.7	19
76	The Worldwide Invasion of <i>Drosophila suzukii</i> Is Accompanied by a Large Increase of Transposable Element Load and a Small Number of Putatively Adaptive Insertions. <i>Molecular Biology and Evolution</i> , 2021, 38, 4252-4267.	8.9	19
77	A Bayesian Outlier Criterion to Detect SNPs under Selection in Large Data Sets. <i>PLoS ONE</i> , 2010, 5, e11913.	2.5	19
78	An extensive and comprehensive radiation hybrid map of bovine Chromosome 15: comparison with human Chromosome 11. <i>Mammalian Genome</i> , 2002, 13, 316-319.	2.2	18
79	Detection of quantitative trait loci affecting non-return rate in French dairy cattle. <i>Journal of Animal Breeding and Genetics</i> , 2008, 125, 280-288.	2.0	18
80	Association studies in QTL regions linked to bovine trypanotolerance in a West African crossbred population. <i>Animal Genetics</i> , 2012, 43, 123-132.	1.7	17
81	Detecting selection using extended haplotype homozygosity (EHH)-based statistics in unphased or unpolarized data. <i>PLoS ONE</i> , 2022, 17, e0262024.	2.5	16
82	Evidence for low-level hybridization between two allochronic populations of the pine processionary moth, <i>Thaumetopoea pityocampa</i> (Lepidoptera: Notodontidae). <i>Biological Journal of the Linnean Society</i> , 2016, 119, 311-328.	1.6	15
83	<i>RADIS</i> : analysis of <i>RAD</i> -seq data for interspecific phylogeny. <i>Bioinformatics</i> , 2016, 32, 3027-3028.	4.1	15
84	Temperature, rainfall and wind variables underlie environmental adaptation in natural populations of <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2021, 30, 938-954.	3.9	15
85	Mapping of the bovine genes of the de novo AMP synthesis pathway. <i>Animal Genetics</i> , 2004, 35, 438-444.	1.7	14
86	Integrating linkage and radiation hybrid mapping data for bovine chromosome 15. <i>BMC Genomics</i> , 2004, 5, 77.	2.8	14
87	Development and assignment of bovine-specific PCR systems for the Texas nomenclature marker genes and isolation of homologous BAC probes. <i>Genetics Selection Evolution</i> , 2001, 33, 191-200.	3.0	13
88	Chromosome localization of the 31 type I Texas bovine markers in sheep and goat chromosomes by comparative FISH mapping and R-banding. <i>Animal Genetics</i> , 2003, 34, 294-296.	1.7	13
89	Exome-wide association study reveals largely distinct gene sets underlying specific resistance to dengue virus types 1 and 3 in <i>Aedes aegypti</i> . <i>PLoS Genetics</i> , 2020, 16, e1008794.	3.5	13
90	Genomic Footprints of Recovery in the European Bison. <i>Journal of Heredity</i> , 2020, 111, 194-203.	2.4	13

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91	Exploring systematic biases, rooting methods and morphological evidence to unravel the evolutionary history of the genus <i>Ficus</i> (Moraceae). <i>Cladistics</i> , 2021, 37, 402-422.	3.3	11
92	Comparative gene mapping in cattle, Indian muntjac, and Chinese muntjac by fluorescence in situ hybridization. <i>Genetica</i> , 2008, 134, 345-351.	1.1	10
93	Development of a comprehensive comparative radiation hybrid map of bovine chromosome 7 (BTA7) versus human chromosomes 1 (HSA1), 5 (HSA5) and 19 (HSA19). <i>Cytogenetic and Genome Research</i> , 2003, 102, 25-31.	1.1	9
94	Effect of genetic European taurine ancestry on milk yield of Ankole-Holstein crossbred dairy cattle in mixed smallholders system of Burundi highlands. <i>Animal Genetics</i> , 2017, 48, 544-550.	1.7	9
95	Preliminary insights into the genetics of bank vole tolerance to Puumala hantavirus in Sweden. <i>Ecology and Evolution</i> , 2018, 8, 11273-11292.	1.9	9
96	A comprehensive radiation hybrid map of bovine Chromosome 26 (BTA26): comparative chromosomal organization between HSA10q and BTA26 and BTA28. <i>Mammalian Genome</i> , 2003, 14, 711-721.	2.2	8
97	Adaptation and correlated fitness responses over two time scales in <i>Drosophila suzukii</i> populations evolving in different environments. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1225-1240.	1.7	8
98	Assignment of mitochondrial glycerol-3-phosphate acyltransferase (GPAM) gene to bovine chromosome 26 (26q22) by in situ hybridization and confirmation by somatic cell hybrid mapping. <i>Cytogenetic and Genome Research</i> , 2002, 97, 276F-276F.	1.1	7
99	FISH-mapping of 31 type I loci (Texas markers) to river buffalo chromosomes. <i>Chromosome Research</i> , 2001, 9, 339-342.	2.2	6
100	The genetic history of Mayotte and Madagascar cattle breeds mirrors the complex pattern of human exchanges in Western Indian Ocean. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	6
101	A hidden Markov model to estimate homozygous-by-descent probabilities associated with nested layers of ancestors. <i>Theoretical Population Biology</i> , 2022, 145, 38-51.	1.1	6
102	Identification and physical mapping of genes expressed in the corpus luteum in cattle1. <i>Animal Genetics</i> , 2003, 34, 325-333.	1.7	5
103	Assignment of eight additional genes from human chromosome 11 to bovine chromosomes 15 and 29: refinement of the comparative map. <i>Cytogenetic and Genome Research</i> , 2001, 93, 60-64.	1.1	4
104	Simulation-Based Evaluation of Three Methods for Local Ancestry Deconvolution of Non-model Crop Species Genomes. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 569-579.	1.8	4
105	Syntenic assignment of sixteen genes from the long arm of human chromosome 10 to bovine chromosomes 26 and 28: refinement of the comparative map. <i>Chromosome Research</i> , 2001, 9, 617-621.	2.2	3
106	Assignment of maltase glucoamylase (MGAM) gene to bovine chromosome 4q34 by in situ hybridization and confirmation by radiation hybrid mapping. <i>Cytogenetic and Genome Research</i> , 2002, 98, 311C-311C.	1.1	2
107	A Generalized Caprine-like Hypoplasia Syndrome is localized within a 6-cM interval on bovine chromosome 13 in the Montbéliarde breed. <i>Animal Genetics</i> , 2008, 39, 112-120.	1.7	1
108	Assignment of monoglyceride lipase (MGLL) gene to bovine chromosome 22q24 by in situ hybridization and confirmation by radiation hybrid mapping. <i>Cytogenetic and Genome Research</i> , 2003, 101, 92A-92A.	1.1	0

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109	Syntenic assignment of the selectin P gene (SELP) to bovine chromosome 16. Animal Genetics, 2000, 31, 344-344.	1.7	0
110	Title is missing!., 2020, 16, e1008794.		0
111	Title is missing!., 2020, 16, e1008794.		0
112	Title is missing!., 2020, 16, e1008794.		0
113	Title is missing!., 2020, 16, e1008794.		0