

# Mathieu Gautier

## List of Publications by Year in descending order

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113  
papers

7,203  
citations

81900  
39  
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69250  
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131  
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131  
docs citations

131  
times ranked

9712  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Statistics estimation and admixture graph construction with Poolâ€Seq or allele count data using the R package <i>poolfstat</i></i> . <i>Molecular Ecology Resources</i> , 2022, 22, 1394-1416.	4.8	32
2	Detecting selection using extended haplotype homozygosity (EHH)-based statistics in unphased or unpolarized data. <i>PLoS ONE</i> , 2022, 17, e0262024.	2.5	16
3	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
4	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
5	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
6	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
7	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
8	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
9	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
10	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
11	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
12	Genomic Footprints of Recovery in the European Bison. <i>Journal of Heredity</i> , 2020, 111, 194-203.	2.4	13
13	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
14	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
15	Title is missing!. , 2020, 16, e1008794.		0
16	Title is missing!. , 2020, 16, e1008794.		0
17	Title is missing!. , 2020, 16, e1008794.		0
18	Title is missing!. , 2020, 16, e1008794.		0

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19	Oviposition Preference and Larval Performance of <i>Drosophila suzukii</i> (Diptera: Drosophilidae), Spotted-Wing Drosophila: Effects of Fruit Identity and Composition. <i>Environmental Entomology</i> , 2019, 48, 867-881.	1.4	43
20	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
21	A genomic map of climate adaptation in Mediterranean cattle breeds. <i>Molecular Ecology</i> , 2019, 28, 1009-1029.	3.9	46
22	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
23	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
24	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
25	The Evolution and Population Diversity of Bison in Pleistocene and Holocene Eurasia: Sex Matters. <i>Diversity</i> , 2018, 10, 65.	1.7	19
26	Measuring Genetic Differentiation from Pool-seq Data. <i>Genetics</i> , 2018, 210, 315-330.	2.9	147
27	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
28	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
29	The Genomic Basis of Color Pattern Polymorphism in the Harlequin Ladybird. <i>Current Biology</i> , 2018, 28, 3296-3302.e7.	3.9	92
30	Inferring sex-specific demographic history from SNP data. <i>PLoS Genetics</i> , 2018, 14, e1007191.	3.5	26
31	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
32	rehh 2.0: a reimplementation of the R package rehh to detect positive selection from haplotype structure. <i>Molecular Ecology Resources</i> , 2017, 17, 78-90.	4.8	243
33	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
34	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
35	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
36	Species composition and environmental adaptation of indigenous Chinese cattle. <i>Scientific Reports</i> , 2017, 7, 16196.	3.3	83

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37	Age-based partitioning of individual genomic inbreeding levels in Belgian Blue cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 92.	3.0	30
38	Taming the late Quaternary phylogeography of the Eurasian wild ass through ancient and modern DNA. <i>PLoS ONE</i> , 2017, 12, e0174216.	2.5	40
39	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
40	<i>i&gt;RADIS:</i> analysis of <i>i&gt;RAD</i> -seq data for interspecific phylogeny. <i>Bioinformatics</i> , 2016, 32, 3027-3028.	4.1	15
41	Deciphering the Wient Demographic and Adaptive Histories from Individual Whole-Genome Sequences. <i>Molecular Biology and Evolution</i> , 2016, 33, 2801-2814.	8.9	41
42	Is There a Genetic Paradox of Biological Invasion?. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2016, 47, 51-72.	8.3	225
43	Reliable ABC model choice via random forests. <i>Bioinformatics</i> , 2016, 32, 859-866.	4.1	272
44	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
45	Genome-Wide Scan for Adaptive Divergence and Association with Population-Specific Covariates. <i>Genetics</i> , 2015, 201, 1555-1579.	2.9	374
46	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
47	Genetic analysis of Thai cattle reveals a Southeast Asian indicine ancestry. <i>PeerJ</i> , 2015, 3, e1318.	2.0	20
48	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
49	Empirical Assessment of RAD Sequencing for Interspecific Phylogeny. <i>Molecular Biology and Evolution</i> , 2014, 31, 1272-1274.	8.9	124
50	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
51	Detecting and Measuring Selection from Gene Frequency Data. <i>Genetics</i> , 2014, 196, 799-817.	2.9	64
52	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
53	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
54	Identification of large selective sweeps associated with major genes in cattle. <i>Animal Genetics</i> , 2013, 44, 758-762.	1.7	36

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55	Inferring Population Histories Using Genome-Wide Allele Frequency Data. <i>Molecular Biology and Evolution</i> , 2013, 30, 654-668.	8.9	34
56	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
57	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
58	The effect of RAD allele dropout on the estimation of genetic variation within and between populations. <i>Molecular Ecology</i> , 2013, 22, 3165-3178.	3.9	259
59	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
60	rehh: 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
61	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
62	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
63	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
64	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
65	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
66	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
67	On the Breeds of Cattle – Historic and Current Classifications. <i>Diversity</i> , 2011, 3, 660-692.	1.7	73
68	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
69	A Bayesian Outlier Criterion to Detect SNPs under Selection in Large Data Sets. <i>PLoS ONE</i> , 2010, 5, e11913.	2.5	19
70	A whole genome Bayesian scan for adaptive genetic divergence in West African cattle. <i>BMC Genomics</i> , 2009, 10, 550.	2.8	186
71	The scurs inheritance: new insights from the French Charolais breed. <i>BMC Genetics</i> , 2009, 10, 33.	2.7	24
72	Detection of selection signatures within candidate regions underlying trypanotolerance in outbred cattle populations. <i>Molecular Ecology</i> , 2009, 18, 1801-1813.	3.9	41

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73	The Genome Response to Artificial Selection: A Case Study in Dairy Cattle. PLoS ONE, 2009, 4, e6595.	2.5	219
74	Comparative gene mapping in cattle, Indian muntjac, and Chinese muntjac by fluorescence in situ hybridization. Genetica, 2008, 134, 345-351.	1.1	10
75	Detection of quantitative trait loci affecting nonâ€return rate in French dairy cattle. Journal of Animal Breeding and Genetics, 2008, 125, 280-288.	2.0	18
76	A Generalized Caprine-like Hypoplasia Syndrome is localized within a 6-cM interval on bovine chromosome 13 in the MontbÃ©liarde breed. Animal Genetics, 2008, 39, 112-120.	1.7	1
77	Fine Mapping of Quantitative Trait Loci Affecting Female Fertility in Dairy Cattle on BTA03 Using a Dense Single-Nucleotide Polymorphism Map. Genetics, 2008, 178, 2227-2235.	2.9	55
78	Atypical structure and phylogenomic evolution of the new eutherian oocyte- and embryo-expressed KHDC1/DPPA5/ECAT1/OOEP gene family. Genomics, 2007, 90, 583-594.	2.9	63
79	Characterization of the DGAT1 K232A and Variable Number of Tandem Repeat Polymorphisms in French Dairy Cattle. Journal of Dairy Science, 2007, 90, 2980-2988.	3.4	61
80	A physical map of the bovine genome. Genome Biology, 2007, 8, R165.	9.6	73
81	Genetic and Haplotypic Structure in 14 European and African Cattle Breeds. Genetics, 2007, 177, 1059-1070.	2.9	133
82	Refinement of two female fertility QTL using alternative phenotypes in French Holstein dairy cattle. Animal Genetics, 2007, 38, 72-74.	1.7	19
83	The extent of linkage disequilibrium in a large cattle population of western Africa and its consequences for association studies. Animal Genetics, 2007, 38, 277-286.	1.7	23
84	Identification of a doublet missense substitution in the bovine LRP4 gene as a candidate causal mutation for syndactyly in Holstein cattle. Genomics, 2006, 88, 610-621.	2.9	43
85	High resolution physical map of porcine chromosome 7 QTL region and comparative mapping of this region among vertebrate genomes. BMC Genomics, 2006, 7, 13.	2.8	21
86	Fine Mapping and Physical Characterization of Two Linked Quantitative Trait Loci Affecting Milk Fat Yield in Dairy Cattle on BTA26. Genetics, 2006, 172, 425-436.	2.9	37
87	Mapping of a Milk Production Quantitative Trait Locus to a 420-kb Region on Bovine Chromosome 6. Genetics, 2005, 169, 275-283.	2.9	104
88	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). Animal Biotechnology, 2005, 16, 1-9.	1.5	19
89	Local gene density predicts the spatial position of genetic loci in the interphase nucleus. Experimental Cell Research, 2005, 311, 14-26.	2.6	55
90	Mapping of the bovine genes of the de novo AMP synthesis pathway. Animal Genetics, 2004, 35, 438-444.	1.7	14

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91	A first generation bovine BAC-based physical map. Genetics Selection Evolution, 2004, 36, 105-22.	3.0	29
92	Integrating linkage and radiation hybrid mapping data for bovine chromosome 15. BMC Genomics, 2004, 5, 77.	2.8	14
93	Identification by R-banding and FISH of chromosome arms involved in Robertsonian translocations in several deer species. Chromosome Research, 2003, 11, 649-663.	2.2	21
94	A comprehensive radiation hybrid map of bovine Chromosome 26 (BTA26): comparative chromosomal organization between HSA10q and BTA26 and BTA28. Mammalian Genome, 2003, 14, 711-721.	2.2	8
95	Chromosome localization of the 31 type I Texas bovine markers in sheep and goat chromosomes by comparative FISH mapping and R-banding. Animal Genetics, 2003, 34, 294-296.	1.7	13
96	Identification and physical mapping of genes expressed in the corpus luteum in cattle1. Animal Genetics, 2003, 34, 325-333.	1.7	5
97	Assignment of monoglyceride lipase (MGLL) gene to bovine chromosome 22q24 by in situ hybridization and confirmation by radiation hybrid mapping. Cytogenetic and Genome Research, 2003, 101, 92A-92A.	1.1	0
98	Development of a comprehensive comparative radiation hybrid map of bovine chromosome 7 (BTA7) versus human chromosomes 1 (HSA1), 5 (HSA5) and 19 (HSA19). Cytogenetic and Genome Research, 2003, 102, 25-31.	1.1	9
99	Mapping of 195 genes in cattle and updated comparative map with man, mouse, rat and pig. Cytogenetic and Genome Research, 2003, 102, 16-24.	1.1	39
100	Assignment of maltase glucoamylase (MGAM) gene to bovine chromosome 4q34 by in situ hybridization and confirmation by radiation hybrid mapping. Cytogenetic and Genome Research, 2002, 98, 311C-311C.	1.1	2
101	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. Cytogenetic and Genome Research, 2002, 97, 276F-276F.	1.1	7
102	An extensive and comprehensive radiation hybrid map of bovine Chromosome 15: comparison with human Chromosome 11. Mammalian Genome, 2002, 13, 316-319.	2.2	18
103	A bovine whole-genome radiation hybrid panel and outline map. Mammalian Genome, 2002, 13, 469-474.	2.2	115
104	Development and assignment of bovine-specific PCR systems for the Texas nomenclature marker genes and isolation of homologous BAC probes. Genetics Selection Evolution, 2001, 33, 191-200.	3.0	13
105	Characterization of the caprine stearoyl-CoA desaturase gene and its mRNA showing an unusually long 3'-UTR sequence arising from a single exon. Gene, 2001, 281, 53-61.	2.2	59
106	FISH-mapping of 31 type I loci (Texas markers) to river buffalo chromosomes. Chromosome Research, 2001, 9, 339-342.	2.2	6
107	Cytogenetic comparison between Vietnamese sika deer and cattle: R-banded karyotypes and FISH mapping. Chromosome Research, 2001, 9, 673-687.	2.2	23
108	Syntenic assignment of sixteen genes from the long arm of human chromosome 10 to bovine chromosomes 26 and 28: refinement of the comparative map. Chromosome Research, 2001, 9, 617-621.	2.2	3

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109	Construction and characterization of a bovine BAC library with four genome-equivalent coverage. Genetics Selection Evolution, 2001, 33, 543-8.	3.0	72
110	Assignment of eight additional genes from human chromosome 11 to bovine chromosomes 15 and 29: refinement of the comparative map. Cytogenetic and Genome Research, 2001, 93, 60-64.	1.1	4
111	Assignment<sup>1</sup> of the fatty acid synthase (FASN) gene to bovine chromosome 19 (19q22) by in situ hybridization and confirmation by somatic cell hybrid mapping. Cytogenetic and Genome Research, 2001, 93, 141-142.	1.1	27
112	Localization by FISH of the 31 Texas nomenclature type I markers to both Q- and R-banded bovine chromosomes. Cytogenetic and Genome Research, 2000, 90, 315-320.	1.1	28
113	Syntenic assignment of the selectin P gene (SELP) to bovine chromosome 16. Animal Genetics, 2000, 31, 344-344.	1.7	0