

Matthieu Foll

List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

10,879
citations

81743

39
h-index

91712

69
g-index

82
all docs

82
docs citations

82
times ranked

16438
citing authors

#	ARTICLE	IF	CITATIONS
1	A Genome-Scan Method to Identify Selected Loci Appropriate for Both Dominant and Codominant Markers: A Bayesian Perspective. <i>Genetics</i> , 2008, 180, 977-993.	1.2	2,366
2	Robust Demographic Inference from Genomic and SNP Data. <i>PLoS Genetics</i> , 2013, 9, e1003905.	1.5	1,185
3	Genetic Consequences of Range Expansions. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2009, 40, 481-501.	3.8	1,072
4	Detecting loci under selection in a hierarchically structured population. <i>Heredity</i> , 2009, 103, 285-298.	1.2	718
5	Prediction of acute myeloid leukaemia risk in healthy individuals. <i>Nature</i> , 2018, 559, 400-404.	13.7	617
6	Approximate Bayesian Computation. <i>PLoS Computational Biology</i> , 2013, 9, e1002803.	1.5	449
7	fastsimcoal: a continuous-time coalescent simulator of genomic diversity under arbitrarily complex evolutionary scenarios. <i>Bioinformatics</i> , 2011, 27, 1332-1334.	1.8	401
8	Identifying the Environmental Factors That Determine the Genetic Structure of Populations. <i>Genetics</i> , 2006, 174, 875-891.	1.2	295
9	Integrative genomic profiling of large-cell neuroendocrine carcinomas reveals distinct subtypes of high-grade neuroendocrine lung tumors. <i>Nature Communications</i> , 2018, 9, 1048.	5.8	254
10	DISENTANGLING THE EFFECTS OF EVOLUTIONARY, DEMOGRAPHIC, AND ENVIRONMENTAL FACTORS INFLUENCING GENETIC STRUCTURE OF NATURAL POPULATIONS: ATLANTIC HERRING AS A CASE STUDY. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 2939-2951.	1.1	183
11	Molecular Subtypes of Pulmonary Large-cell Neuroendocrine Carcinoma Predict Chemotherapy Treatment Outcome. <i>Clinical Cancer Research</i> , 2018, 24, 33-42.	3.2	164
12	Identification of Circulating Tumor DNA for the Early Detection of Small-cell Lung Cancer. <i>EBioMedicine</i> , 2016, 10, 117-123.	2.7	153
13	In defence of model-based inference in phylogeography. <i>Molecular Ecology</i> , 2010, 19, 436-446.	2.0	141
14	Integrative and comparative genomic analyses identify clinically relevant pulmonary carcinoid groups and unveil the supra-carcinoids. <i>Nature Communications</i> , 2019, 10, 3407.	5.8	132
15	Widespread Signals of Convergent Adaptation to High Altitude in Asia and America. <i>American Journal of Human Genetics</i> , 2014, 95, 394-407.	2.6	131
16	Enhanced AFLP genome scans detect local adaptation in high-altitude populations of a small rodent (<i>Microtus arvalis</i>). <i>Molecular Ecology</i> , 2011, 20, 1450-1462.	2.0	126
17	Influenza Virus Drug Resistance: A Time-Sampled Population Genetics Perspective. <i>PLoS Genetics</i> , 2014, 10, e1004185.	1.5	126
18	WFABC: a Wright-Fisher based approach for inferring effective population sizes and selection coefficients from time-sampled data. <i>Molecular Ecology Resources</i> , 2015, 15, 87-98.	2.2	126

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19	Linking a mutation to survival in wild mice. <i>Science</i> , 2019, 363, 499-504.	6.0	126
20	Thinking too positive? Revisiting current methods of population genetic selection inference. <i>Trends in Genetics</i> , 2014, 30, 540-546.	2.9	121
21	SPLATCHE2: a spatially explicit simulation framework for complex demography, genetic admixture and recombination. <i>Bioinformatics</i> , 2010, 26, 2993-2994.	1.8	113
22	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. <i>Nature Communications</i> , 2017, 8, 15724.	5.8	106
23	EURACAN/IASLC Proposals for Updating the Histologic Classification of Pleural Mesothelioma: Towards a More Multidisciplinary Approach. <i>Journal of Thoracic Oncology</i> , 2020, 15, 29-49.	0.5	106
24	Quantifying population structure using the <i>F_{st}</i> model. <i>Molecular Ecology Resources</i> , 2010, 10, 821-830.	2.2	91
25	Adaptive, convergent origins of the pygmy phenotype in African rainforest hunter-gatherers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3596-603.	3.3	91
26	An Approximate Bayesian Computation Approach to Overcome Biases That Arise When Using Amplified Fragment Length Polymorphism Markers to Study Population Structure. <i>Genetics</i> , 2008, 179, 927-939.	1.2	82
27	The past, present and future of genomic scans for selection. <i>Molecular Ecology</i> , 2016, 25, 1-4.	2.0	80
28	The Evolutionary History of Nebraska Deer Mice: Local Adaptation in the Face of Strong Gene Flow. <i>Molecular Biology and Evolution</i> , 2018, 35, 792-806.	3.5	76
29	<i>KRAS</i> mutations in blood circulating cell-free DNA: a pancreatic cancer case-control. <i>Oncotarget</i> , 2016, 7, 78827-78840.	0.8	70
30	BAP1 Is Altered by Copy Number Loss, Mutation, and/or Loss of Protein Expression in More Than 70% of Malignant Peritoneal Mesotheliomas. <i>Journal of Thoracic Oncology</i> , 2017, 12, 724-733.	0.5	67
31	Estimating population structure from AFLP amplification intensity. <i>Molecular Ecology</i> , 2010, 19, 4638-4647.	2.0	66
32	Worldwide Population Structure, Long-Term Demography, and Local Adaptation of <i>Helicobacter pylori</i> . <i>Genetics</i> , 2015, 200, 947-963.	1.2	65
33	The influence of obesity-related factors in the etiology of renal cell carcinoma—A mendelian randomization study. <i>PLoS Medicine</i> , 2019, 16, e1002724.	3.9	59
34	Redefining malignant pleural mesothelioma types as a continuum uncovers immune-vascular interactions. <i>EBioMedicine</i> , 2019, 48, 191-202.	2.7	55
35	Neutral and Adaptive Drivers of Microgeographic Genetic Divergence within Continuous Populations: The Case of the Neotropical Tree <i>Eperua falcata</i> (Aubl.). <i>PLoS ONE</i> , 2015, 10, e0121394.	1.1	53
36	Alterations in the NF2/LATS1/LATS2/YAP Pathway in Schwannomas. <i>Journal of Neuropathology and Experimental Neurology</i> , 2015, 74, 952-959.	0.9	52

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37	Evolutionary forces shaping genomic islands of population differentiation in humans. BMC Genomics, 2012, 13, 107.	1.2	51
38	Circulating tumor DNA detection in head and neck cancer: evaluation of two different detection approaches. Oncotarget, 2017, 8, 72621-72632.	0.8	51
39	Urinary TERT promoter mutations are detectable up to 10 years prior to clinical diagnosis of bladder cancer: Evidence from the Golestan Cohort Study. EBioMedicine, 2020, 53, 102643.	2.7	51
40	Genomic Data Reveal a Complex Making of Humans. PLoS Genetics, 2012, 8, e1002837.	1.5	43
41	Urinary TERT promoter mutations as non-invasive biomarkers for the comprehensive detection of urothelial cancer. EBioMedicine, 2019, 44, 431-438.	2.7	41
42	Genetic Variants Related to Longer Telomere Length are Associated with Increased Risk of Renal Cell Carcinoma. European Urology, 2017, 72, 747-754.	0.9	39
43	An experimental evaluation of drug-induced mutational meltdown as an antiviral treatment strategy. Evolution; International Journal of Organic Evolution, 2016, 70, 2470-2484.	1.1	36
44	Exome sequencing identifies germline variants in DIS3 in familial multiple myeloma. Leukemia, 2019, 33, 2324-2330.	3.3	33
45	Detection of Convergent Genome-Wide Signals of Adaptation to Tropical Forests in Humans. PLoS ONE, 2015, 10, e0121557.	1.1	32
46	Correcting for ascertainment bias in the inference of population structure. Bioinformatics, 2009, 25, 552-554.	1.8	31
47	Likelihood-Free Inference in High-Dimensional Models. Genetics, 2016, 203, 893-904.	1.2	29
48	Detecting and Quantifying Changing Selection Intensities from Time-Sampled Polymorphism Data. G3: Genes, Genomes, Genetics, 2016, 6, 893-904.	0.8	27
49	Sex specific associations in genome wide association analysis of renal cell carcinoma. European Journal of Human Genetics, 2019, 27, 1589-1598.	1.4	27
50	Development of Sensitive Droplet Digital PCR Assays for Detecting Urinary TERT Promoter Mutations as Non-Invasive Biomarkers for Detection of Urothelial Cancer. Cancers, 2020, 12, 3541.	1.7	27
51	Molecular studies of lung neuroendocrine neoplasms uncover new concepts and entities. Translational Lung Cancer Research, 2019, 8, S430-S434.	1.3	25
52	Long-distance dispersal suppresses introgression of local alleles during range expansions. Heredity, 2017, 118, 135-142.	1.2	24
53	Inferring the age of a fixed beneficial allele. Molecular Ecology, 2016, 25, 157-169.	2.0	23
54	A Novel Risk Locus at 6p21.3 for Epstein-Barr Virus-Positive Hodgkin Lymphoma. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1838-1843.	1.1	20

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55	Genomic analysis of head and neck cancer cases from two high incidence regions. PLoS ONE, 2018, 13, e0191701.	1.1	18
56	A molecular map of lung neuroendocrine neoplasms. GigaScience, 2020, 9, .	3.3	17
57	Positive Selection Drives Preferred Segment Combinations during Influenza Virus Reassortment. Molecular Biology and Evolution, 2015, 32, 1519-1532.	3.5	16
58	Continental-Scale Footprint of Balancing and Positive Selection in a Small Rodent (<i>Microtus arvalis</i>). PLoS ONE, 2014, 9, e112332.	1.1	16
59	Circulating tumour-derived KRAS mutations in pancreatic cancer cases are predominantly carried by very short fragments of cell-free DNA. EBioMedicine, 2020, 55, 102462.	2.7	14
60	Challenges in lung and thoracic pathology: molecular advances in the classification of pleural mesotheliomas. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2021, 478, 73-80.	1.4	11
61	Genetic Analysis of Lung Cancer and the Germline Impact on Somatic Mutation Burden. Journal of the National Cancer Institute, 2022, 114, 1159-1166.	3.0	8
62	colonise: a computer program to study colonization processes in metapopulations. Molecular Ecology Notes, 2005, 5, 705-707.	1.7	6
63	Detecting Selection from Linked Sites Using an <i>i</i> -Model. Genetics, 2020, 216, 1205-1215.	1.2	6
64	TP53 Targeted Deep Sequencing of Cell-Free DNA in Esophageal Squamous Cell Carcinoma Using Low-Quality Serum: Concordance with Tumor Mutation. International Journal of Molecular Sciences, 2021, 22, 5627.	1.8	6
65	Rare Circulating Cells in Familial Waldenström Macroglobulinemia Displaying the MYD88 L265P Mutation Are Enriched by Epstein-Barr Virus Immortalization. PLoS ONE, 2015, 10, e0136505.	1.1	6
66	Detection of acquired TERT amplification in addition to predisposing p53 and Rb pathways alterations in EGFR-mutant lung adenocarcinomas transformed into small-cell lung cancers. Lung Cancer, 2022, 167, 98-106.	0.9	6
67	Needlestack: an ultra-sensitive variant caller for multi-sample next generation sequencing data. NAR Genomics and Bioinformatics, 2020, 2, lqaa021.	1.5	5
68	Differential Orthopedia Homeobox expression in pulmonary carcinoids is associated with changes in <i>scp</i> DNA methylation. International Journal of Cancer, 2022, 150, 1987-1997.	2.3	4
69	Quantifying polymorphism and divergence from epigenetic data: a framework for inferring the action of selection. Frontiers in Genetics, 2015, 6, 190.	1.1	0
70	MA11.05 A Case-Control Study to Test the Use of ctDNA in the Early Detection of SCLC Reveals TP53 Mutations in Non-Cancer Controls. Journal of Thoracic Oncology, 2017, 12, S405-S406.	0.5	0