Matthieu Foll

List of Publications by Year
in descending order

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	Differential Orthopedia Homeobox expression in pulmonary carcinoids is associated with changes in <scp>DNA</scp> methylation. International Journal of Cancer, 2022, 150, 1987-1997.	2.3	4
2	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
3	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
4	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
5	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
6	EURACAN/IASLC Proposals for Updating the Histologic Classification of Pleural Mesothelioma: Towards a More Multidisciplinary Approach. Journal of Thoracic Oncology, 2020, 15, 29-49.	0.5	106
7	Detecting Selection from Linked Sites Using an F-Model. Genetics, 2020, 216, 1205-1215.	1.2	6
8	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
9	A molecular map of lung neuroendocrine neoplasms. GigaScience, 2020, 9, .	3.3	17
10	Needlestack: an ultra-sensitive variant caller for multi-sample next generation sequencing data. NAR Genomics and Bioinformatics, 2020, 2, lqaa021.	1.5	5
11	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
12	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
13	Integrative and comparative genomic analyses identify clinicallyÂrelevant pulmonary carcinoidÂgroups and unveil the supra-carcinoids. Nature Communications, 2019, 10, 3407.	5.8	132
14	Sex specific associations in genome wide association analysis of renal cell carcinoma. European Journal of Human Genetics, 2019, 27, 1589-1598.	1.4	27
15	Linking a mutation to survival in wild mice. Science, 2019, 363, 499-504.	6.0	126
16	Urinary TERT promoter mutations as non-invasive biomarkers for the comprehensive detection of urothelial cancer. EBioMedicine, 2019, 44, 431-438.	2.7	41
17	Exome sequencing identifies germline variants in DIS3 in familial multiple myeloma. Leukemia, 2019, 33, 2324-2330.	3.3	33
18	Molecular studies of lung neuroendocrine neoplasms uncover new concepts and entities. Translational Lung Cancer Research, 2019, 8, S430-S434.	1.3	25

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19	Redefining malignant pleural mesothelioma types as a continuum uncovers immune-vascular interactions. EBioMedicine, 2019, 48, 191-202.	2.7	55
20	The influence of obesity-related factors in the etiology of renal cell carcinomaâ€"A mendelian randomization study. PLoS Medicine, 2019, 16, e1002724.	3.9	59
21	The Evolutionary History of Nebraska Deer Mice: Local Adaptation in the Face of Strong Gene Flow. Molecular Biology and Evolution, 2018, 35, 792-806.	3.5	76
22	Integrative genomic profiling of large-cell neuroendocrine carcinomas reveals distinct subtypes of high-grade neuroendocrine lung tumors. Nature Communications, 2018, 9, 1048.	5.8	254
23	Molecular Subtypes of Pulmonary Large-cell Neuroendocrine Carcinoma Predict Chemotherapy Treatment Outcome. Clinical Cancer Research, 2018, 24, 33-42.	3.2	164
24	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	13.7	617
25	Genomic analysis of head and neck cancer cases from two high incidence regions. PLoS ONE, 2018, 13, e0191701.	1.1	18
26	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. Nature Communications, 2017, 8, 15724.	5.8	106
27	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
28	BAP1 Is Altered by Copy Number Loss, Mutation, and/or Loss of Protein Expression in More Than 70% ofÂMalignant Peritoneal Mesotheliomas. Journal of Thoracic Oncology, 2017, 12, 724-733.	0.5	67
29	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
30	Long-distance dispersal suppresses introgression of local alleles during range expansions. Heredity, 2017, 118, 135-142.	1.2	24
31	Circulating tumor DNA detection in head and neck cancer: evaluation of two different detection approaches. Oncotarget, 2017, 8, 72621-72632.	0.8	51
32	Identification of Circulating Tumor DNA for the Early Detection of Small-cell Lung Cancer. EBioMedicine, 2016, 10, 117-123.	2.7	153
33	Inferring the age of a fixed beneficial allele. Molecular Ecology, 2016, 25, 157-169.	2.0	23
34	Likelihood-Free Inference in High-Dimensional Models. Genetics, 2016, 203, 893-904.	1.2	29
35	An experimental evaluation of drugâ€induced mutational meltdown as an antiviral treatment strategy. Evolution; International Journal of Organic Evolution, 2016, 70, 2470-2484.	1.1	36
36	Detecting and Quantifying Changing Selection Intensities from Time-Sampled Polymorphism Data. G3: Genes, Genomes, Genetics, 2016, 6, 893-904.	0.8	27

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37	The past, present and future of genomic scans for selection. Molecular Ecology, 2016, 25, 1-4.	2.0	80
38	KRASmutations in blood circulating cell-free DNA: a pancreatic cancer case-control. Oncotarget, 2016, 7, 78827-78840.	0.8	70
39	Alterations in the NF2/LATS1/LATS2/YAP Pathway in Schwannomas. Journal of Neuropathology and Experimental Neurology, 2015, 74, 952-959.	0.9	52
40	<scp>WFABC</scp>: a <scp>W</scp>rightâ€“<scp>F</scp>isher <scp>ABC</scp>â€based approach for inferring effective population sizes and selection coefficients from timeâ€sampled data. Molecular Ecology Resources, 2015, 15, 87-98.	2.2	126
41	Quantifying polymorphism and divergence from epigenetic data: a framework for inferring the action of selection. Frontiers in Genetics, 2015, 6, 190.	1.1	0
42	A Novel Risk Locus at 6p21.3 for Epsteinâ€“Barr Virus-Positive Hodgkin Lymphoma. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1838-1843.	1.1	20
43	Positive Selection Drives Preferred Segment Combinations during Influenza Virus Reassortment. Molecular Biology and Evolution, 2015, 32, 1519-1532.	3.5	16
44	Neutral and Adaptive Drivers of Microgeographic Genetic Divergence within Continuous Populations: The Case of the Neotropical Tree Eperua falcata (Aubl.). PLoS ONE, 2015, 10, e0121394.	1.1	53
45	Worldwide Population Structure, Long-Term Demography, and Local Adaptation of Helicobacter pylori. Genetics, 2015, 200, 947-963.	1.2	65
46	Detection of Convergent Genome-Wide Signals of Adaptation to Tropical Forests in Humans. PLoS ONE, 2015, 10, e0121557.	1.1	32
47	Rare Circulating Cells in Familial WaldenstrÃ¶m Macroglobulinemia Displaying the MYD88 L265P Mutation Are Enriched by Epstein-Barr Virus Immortalization. PLoS ONE, 2015, 10, e0136505.	1.1	6
48	Influenza Virus Drug Resistance: A Time-Sampled Population Genetics Perspective. PLoS Genetics, 2014, 10, e1004185.	1.5	126
49	Thinking too positive? Revisiting current methods of population genetic selection inference. Trends in Genetics, 2014, 30, 540-546.	2.9	121
50	Adaptive, convergent origins of the pygmy phenotype in African rainforest hunter-gatherers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3596-603.	3.3	91
51	Widespread Signals of Convergent Adaptation to High Altitude in Asia and America. American Journal of Human Genetics, 2014, 95, 394-407.	2.6	131
52	Continental-Scale Footprint of Balancing and Positive Selection in a Small Rodent (Microtus arvalis). PLoS ONE, 2014, 9, e112332.	1.1	16
53	Robust Demographic Inference from Genomic and SNP Data. PLoS Genetics, 2013, 9, e1003905.	1.5	1,185
54	Approximate Bayesian Computation. PLoS Computational Biology, 2013, 9, e1002803.	1.5	449

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55	Genomic Data Reveal a Complex Making of Humans. PLoS Genetics, 2012, 8, e1002837.	1.5	43
56	Evolutionary forces shaping genomic islands of population differentiation in humans. BMC Genomics, 2012, 13, 107.	1.2	51
57	Enhanced AFLP genome scans detect local adaptation in highâ€altitude populations of a small rodent (Microtus arvalis). Molecular Ecology, 2011, 20, 1450-1462.	2.0	126
58	fastsimcoal: a continuous-time coalescent simulator of genomic diversity under arbitrarily complex evolutionary scenarios. Bioinformatics, 2011, 27, 1332-1334.	1.8	401
59	In defence of model-based inference in phylogeography. Molecular Ecology, 2010, 19, 436-446.	2.0	141
60	Estimating population structure from AFLP amplification intensity. Molecular Ecology, 2010, 19, 4638-4647.	2.0	66
61	SPLATCHE2: a spatially explicit simulation framework for complex demography, genetic admixture and recombination. Bioinformatics, 2010, 26, 2993-2994.	1.8	113
62	Quantifying population structure using the Fâ€model. Molecular Ecology Resources, 2010, 10, 821-830.	2.2	91
63	Correcting for ascertainment bias in the inference of population structure. Bioinformatics, 2009, 25, 552-554.	1.8	31
64	Detecting loci under selection in a hierarchically structured population. Heredity, 2009, 103, 285-298.	1.2	718
65	DISENTANGLING THE EFFECTS OF EVOLUTIONARY, DEMOGRAPHIC, AND ENVIRONMENTAL FACTORS INFLUENCING GENETIC STRUCTURE OF NATURAL POPULATIONS: ATLANTIC HERRING AS A CASE STUDY. Evolution; International Journal of Organic Evolution, 2009, 63, 2939-2951.	1.1	183
66	Genetic Consequences of Range Expansions. Annual Review of Ecology, Evolution, and Systematics, 2009, 40, 481-501.	3.8	1,072
67	A Genome-Scan Method to Identify Selected Loci Appropriate for Both Dominant and Codominant Markers: A Bayesian Perspective. Genetics, 2008, 180, 977-993.	1.2	2,366
68	An Approximate Bayesian Computation Approach to Overcome Biases That Arise When Using Amplified Fragment Length Polymorphism Markers to Study Population Structure. Genetics, 2008, 179, 927-939.	1.2	82
69	Identifying the Environmental Factors That Determine the Genetic Structure of Populations. Genetics, 2006, 174, 875-891.	1.2	295
70	colonise: a computer program to study colonization processes in metapopulations. Molecular Ecology Notes, 2005, 5, 705-707.	1.7	6