

Etienne Patin

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

84
papers

4,873
citations

40
h-index

69
g-index

101
ext. papers

6,282
ext. citations

12.1
avg, IF

5.02
L-index

#	Paper	IF	Citations
84	Natural selection has driven population differentiation in modern humans. <i>Nature Genetics</i> , 2008 , 40, 340-5	36.3	436
83	Evolutionary dynamics of human Toll-like receptors and their different contributions to host defense. <i>PLoS Genetics</i> , 2009 , 5, e1000562	6	272
82	Genetic Adaptation and Neandertal Admixture Shaped the Immune System of Human Populations. <i>Cell</i> , 2016 , 167, 643-656.e17	56.2	224
81	The human gene damage index as a gene-level approach to prioritizing exome variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 13615-20	11.5	152
80	Genomic Signatures of Selective Pressures and Introgression from Archaic Hominins at Human Innate Immunity Genes. <i>American Journal of Human Genetics</i> , 2016 , 98, 5-21	11	149
79	Ribosomal protein SA haploinsufficiency in humans with isolated congenital asplenia. <i>Science</i> , 2013 , 340, 976-8	33.3	145
78	Dispersals and genetic adaptation of Bantu-speaking populations in Africa and North America. <i>Science</i> , 2017 , 356, 543-546	33.3	128
77	Maternal traces of deep common ancestry and asymmetric gene flow between Pygmy hunter-gatherers and Bantu-speaking farmers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 1596-601	11.5	126
76	IL28B alleles associated with poor hepatitis C virus (HCV) clearance protect against inflammation and fibrosis in patients infected with non-1 HCV genotypes. <i>Hepatology</i> , 2012 , 55, 384-94	11.2	124
75	Positively selected G6PD-Mahidol mutation reduces Plasmodium vivax density in Southeast Asians. <i>Science</i> , 2009 , 326, 1546-9	33.3	124
74	Evolutionary genetic dissection of human interferons. <i>Journal of Experimental Medicine</i> , 2011 , 208, 2747-2756	13.6	118
73	Inferring the demographic history of African farmers and pygmy hunter-gatherers using a multilocus resequencing data set. <i>PLoS Genetics</i> , 2009 , 5, e1000448	6	117
72	Natural variation in the parameters of innate immune cells is preferentially driven by genetic factors. <i>Nature Immunology</i> , 2018 , 19, 302-314	19.1	112
71	Genome-wide association study identifies variants associated with progression of liver fibrosis from HCV infection. <i>Gastroenterology</i> , 2012 , 143, 1244-1252.e12	13.3	111
70	Human RHOH deficiency causes T cell defects and susceptibility to EV-HPV infections. <i>Journal of Clinical Investigation</i> , 2012 , 122, 3239-47	15.9	109
69	Distinctive roles of age, sex, and genetics in shaping transcriptional variation of human immune responses to microbial challenges. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E488-E497	11.5	107
68	Inherited MST1 deficiency underlies susceptibility to EV-HPV infections. <i>PLoS ONE</i> , 2012 , 7, e44010	3.7	101

67	Deciphering the ancient and complex evolutionary history of human arylamine N-acetyltransferase genes. <i>American Journal of Human Genetics</i> , 2006 , 78, 423-36	11	100
66	Evolutionary insights into the high worldwide prevalence of MBL2 deficiency alleles. <i>Human Molecular Genetics</i> , 2006 , 15, 2650-8	5.6	91
65	Tuberculosis and impaired IL-23-dependent IFN- γ immunity in humans homozygous for a common missense variant. <i>Science Immunology</i> , 2018 , 3,	28	88
64	Human IFN- γ immunity to mycobacteria is governed by both IL-12 and IL-23. <i>Science Immunology</i> , 2018 , 3,	28	83
63	The heritage of pathogen pressures and ancient demography in the human innate-immunity CD209/CD209L region. <i>American Journal of Human Genetics</i> , 2005 , 77, 869-86	11	79
62	Dual T cell- and B cell-intrinsic deficiency in humans with biallelic RLTPR mutations. <i>Journal of Experimental Medicine</i> , 2016 , 213, 2413-2435	16.6	75
61	The impact of agricultural emergence on the genetic history of African rainforest hunter-gatherers and agriculturalists. <i>Nature Communications</i> , 2014 , 5, 3163	17.4	73
60	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	11.5	70
59	Formulating a historical and demographic model of recent human evolution based on resequencing data from noncoding regions. <i>PLoS ONE</i> , 2010 , 5, e10284	3.7	70
58	Signatures of purifying and local positive selection in human miRNAs. <i>American Journal of Human Genetics</i> , 2009 , 84, 316-27	11	68
57	Human genetic variants and age are the strongest predictors of humoral immune responses to common pathogens and vaccines. <i>Genome Medicine</i> , 2018 , 10, 59	14.4	64
56	Exploring the occurrence of classic selective sweeps in humans using whole-genome sequencing data sets. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1850-68	8.3	57
55	The human CIB1-EVER1-EVER2 complex governs keratinocyte-intrinsic immunity to β papillomaviruses. <i>Journal of Experimental Medicine</i> , 2018 , 215, 2289-2310	16.6	56
54	The epigenomic landscape of African rainforest hunter-gatherers and farmers. <i>Nature Communications</i> , 2015 , 6, 10047	17.4	55
53	Population genetic diversity of the NAT2 gene supports a role of acetylation in human adaptation to farming in Central Asia. <i>European Journal of Human Genetics</i> , 2008 , 16, 243-51	5.3	54
52	A comprehensive assessment of demographic, environmental, and host genetic associations with gut microbiome diversity in healthy individuals. <i>Microbiome</i> , 2019 , 7, 130	16.6	52
51	Sub-Saharan African coding sequence variation and haplotype diversity at the NAT2 gene. <i>Human Mutation</i> , 2006 , 27, 720	4.7	52
50	A genomic portrait of the genetic architecture and regulatory impact of microRNA expression in response to infection. <i>Genome Research</i> , 2014 , 24, 850-9	9.7	49

49	Homozygosity for P1104A underlies tuberculosis in about 1% of patients in a cohort of European ancestry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 10430-10434	11.5	46
48	Evolutionary trajectories of primate genes involved in HIV pathogenesis. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2865-75	8.3	46
47	Trends in DNA Methylation with Age Replicate Across Diverse Human Populations. <i>Genetics</i> , 2017 , 206, 1659-1674	4	44
46	Exploring the genetic basis of human population differences in DNA methylation and their causal impact on immune gene regulation. <i>Genome Biology</i> , 2018 , 19, 222	18.3	44
45	Extensive Admixture and Selective Pressure Across the Sahel Belt. <i>Genome Biology and Evolution</i> , 2015 , 7, 3484-95	3.9	42
44	Mutations involving the SRY-related gene SOX8 are associated with a spectrum of human reproductive anomalies. <i>Human Molecular Genetics</i> , 2018 , 27, 1228-1240	5.6	40
43	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
42	Different selective pressures shape the evolution of Toll-like receptors in human and African great ape populations. <i>Human Molecular Genetics</i> , 2013 , 22, 4829-40	5.6	38
41	Parkinson's disease-related LRRK2 G2019S mutation results from independent mutational events in humans. <i>Human Molecular Genetics</i> , 2010 , 19, 1998-2004	5.6	38
40	The selective footprints of viral pressures at the human RIG-I-like receptor family. <i>Human Molecular Genetics</i> , 2011 , 20, 4462-74	5.6	38
39	The Milieu Intérieur study - an integrative approach for study of human immunological variance. <i>Clinical Immunology</i> , 2015 , 157, 277-93	9	35
38	The Genomic Impact of European Colonization of the Americas. <i>Current Biology</i> , 2019 , 29, 3974-3986.e4	6.3	33
37	The demographic history and mutational load of African hunter-gatherers and farmers. <i>Nature Ecology and Evolution</i> , 2018 , 2, 721-730	12.3	29
36	Human genetic data reveal contrasting demographic patterns between sedentary and nomadic populations that predate the emergence of farming. <i>Molecular Biology and Evolution</i> , 2013 , 30, 2629-44	8.3	28
35	The evolutionary landscape of cytosolic microbial sensors in humans. <i>American Journal of Human Genetics</i> , 2012 , 91, 27-37	11	26
34	Genomic insights into population history and biological adaptation in Oceania. <i>Nature</i> , 2021 , 592, 583-589	9.4	26
33	Blacklisting variants common in private cohorts but not in public databases optimizes human exome analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 950-959	11.5	26
32	Genomic Evidence for Local Adaptation of Hunter-Gatherers to the African Rainforest. <i>Current Biology</i> , 2019 , 29, 2926-2935.e4	6.3	25

31	IRF4 haploinsufficiency in a family with Whipple's disease. <i>ELife</i> , 2018 , 7,	8.9	25
30	Associations between consumption of dietary fibers and the risk of cardiovascular diseases, cancers, type 2 diabetes, and mortality in the prospective NutriNet-Santé cohort. <i>American Journal of Clinical Nutrition</i> , 2020 , 112, 195-207	7	21
29	Recent Adaptive Acquisition by African Rainforest Hunter-Gatherers of the Late Pleistocene Sickle-Cell Mutation Suggests Past Differences in Malaria Exposure. <i>American Journal of Human Genetics</i> , 2019 , 104, 553-561	11	21
28	Polygenic adaptation and convergent evolution on growth and cardiac genetic pathways in African and Asian rainforest hunter-gatherers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E11256-E11263	11.5	21
27	Automated flow cytometric analysis across large numbers of samples and cell types. <i>Clinical Immunology</i> , 2015 , 157, 249-60	9	20
26	Evolutionary genetics evidence of an essential, nonredundant role of the IFN- γ pathway in protective immunity. <i>Human Mutation</i> , 2011 , 32, 633-42	4.7	20
25	The Genetic Legacy of the Indian Ocean Slave Trade: Recent Admixture and Post-admixture Selection in the Makranis of Pakistan. <i>American Journal of Human Genetics</i> , 2017 , 101, 977-984	11	19
24	Human thymopoiesis is influenced by a common genetic variant within the locus. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	19
23	Human ancient DNA analyses reveal the high burden of tuberculosis in Europeans over the last 2,000 years. <i>American Journal of Human Genetics</i> , 2021 , 108, 517-524	11	18
22	Demeter's legacy: rapid changes to our genome imposed by diet. <i>Trends in Ecology and Evolution</i> , 2008 , 23, 56-9	10.9	17
21	The demographic and adaptive history of central African hunter-gatherers and farmers. <i>Current Opinion in Genetics and Development</i> , 2018 , 53, 90-97	4.9	15
20	Interferon gamma receptor 2 gene variants are associated with liver fibrosis in patients with chronic hepatitis C infection. <i>Gut</i> , 2010 , 59, 1120-6	19.2	15
19	Negative selection on human genes underlying inborn errors depends on disease outcome and both the mode and mechanism of inheritance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	14
18	Two common disease-associated TYK2 variants impact exon splicing and TYK2 dosage. <i>PLoS ONE</i> , 2020 , 15, e0225289	3.7	13
17	Gut microbiome stability and dynamics in healthy donors and patients with non-gastrointestinal cancers. <i>Journal of Experimental Medicine</i> , 2021 , 218,	16.6	13
16	A 1,100-year-old founder effect mutation in IL12B gene is responsible for Mendelian susceptibility to mycobacterial disease in Tunisian patients. <i>Immunogenetics</i> , 2014 , 66, 67-71	3.2	10
15	Common homozygosity for predicted loss-of-function variants reveals both redundant and advantageous effects of dispensable human genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 13626-13636	11.5	9
14	Heterogeneous pattern of selective pressure for PRRT2 in human populations, but no association with autism spectrum disorders. <i>PLoS ONE</i> , 2014 , 9, e88600	3.7	9

13	Positive selection in the chromosome 16 VKORC1 genomic region has contributed to the variability of anticoagulant response in humans. <i>PLoS ONE</i> , 2012 , 7, e53049	3.7	8
12	Plague as a cause for familial Mediterranean fever. <i>Nature Immunology</i> , 2020 , 21, 833-834	19.1	5
11	New insights into human immunity from ancient genomics. <i>Current Opinion in Immunology</i> , 2021 , 72, 116-125	7.8	5
10	Immune Profiling Enables Stratification of Patients With Active Tuberculosis Disease or Mycobacterium tuberculosis Infection. <i>Clinical Infectious Diseases</i> , 2021 , 73, e3398-e3408	11.6	4
9	Genome-wide data from the Bubi of Bioko Island clarifies the Atlantic fringe of the Bantu dispersal. <i>BMC Genomics</i> , 2019 , 20, 179	4.5	3
8	Quantitative genetic analysis deciphers the impact of cis and trans regulation on cell-to-cell variability in protein expression levels. <i>PLoS Genetics</i> , 2020 , 16, e1008686	6	2
7	Factors Driving DNA Methylation Variation in Human Blood		2
6	Negative selection on human genes causing severe inborn errors depends on disease outcome and both the mode and mechanism of inheritance		1
5	Exploring the Genetic Basis of Human Population Differences in DNA Methylation and their Causal Impact on Immune Gene Regulation		1
4	The genomic impact of European colonization of the Americas		1
3	Integrative genetic and immune cell analysis of plasma proteins in healthy donors identifies novel associations involving primary immune deficiency genes.. <i>Genome Medicine</i> , 2022 , 14, 28	14.4	1
2	Associations between untargeted plasma metabolomic signatures and gut microbiota composition in the population of healthy adults. <i>British Journal of Nutrition</i> , 2021 , 126, 982-992	3.6	0
1	Human evolution: The unsealed fates of foragers and farmers.. <i>Current Biology</i> , 2022 , 32, R362-R365	6.3	