

# Matteo Fumagalli

## List of Publications by Year in descending order

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Version: 2024-02-01

65  
papers

6,809  
citations

101496

36  
h-index

138417

58  
g-index

73  
all docs

73  
docs citations

73  
times ranked

12443  
citing authors

#	ARTICLE	IF	CITATIONS
1	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.	13.7	717
2	Signatures of Environmental Genetic Adaptation Pinpoint Pathogens as the Main Selective Pressure through Human Evolution. <i>PLoS Genetics</i> , 2011, 7, e1002355.	1.5	464
3	Greenlandic Inuit show genetic signatures of diet and climate adaptation. <i>Science</i> , 2015, 349, 1343-1347.	6.0	397
4	Recent Asian origin of chytrid fungi causing global amphibian declines. <i>Science</i> , 2018, 360, 621-627.	6.0	389
5	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. <i>Cell</i> , 2014, 157, 785-794.	13.5	363
6	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. <i>Nature</i> , 2014, 512, 190-193.	13.7	338
7	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5661-9.	3.3	260
8	Parasites represent a major selective force for interleukin genes and shape the genetic predisposition to autoimmune conditions. <i>Journal of Experimental Medicine</i> , 2009, 206, 1395-1408.	4.2	230
9	<i>i&gt;ngsTools</i> : methods for population genetics analyses from next-generation sequencing data. <i>Bioinformatics</i> , 2014, 30, 1486-1487.	1.8	227
10	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , 2016, 7, 11693.	5.8	222
11	Quantifying Population Genetic Differentiation from Next-Generation Sequencing Data. <i>Genetics</i> , 2013, 195, 979-992.	1.2	187
12	Speciation with gene flow in equids despite extensive chromosomal plasticity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18655-18660.	3.3	183
13	Evolutionary genetic dissection of human interferons. <i>Journal of Experimental Medicine</i> , 2011, 208, 2747-2759.	4.2	170
14	Evolutionary Genomics and Conservation of the Endangered Przewalski's Horse. <i>Current Biology</i> , 2015, 25, 2577-2583.	1.8	161
15	Widespread balancing selection and pathogen-driven selection at blood group antigen genes. <i>Genome Research</i> , 2009, 19, 199-212.	2.4	147
16	Survival and divergence in a small group: The extraordinary genomic history of the endangered Apennine brown bear stragglers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9589-E9597.	3.3	140
17	Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E6889-97.	3.3	139
18	The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , 2015, 1, 14003.	4.7	138

#	ARTICLE	IF	CITATIONS
19	Assessing the Effect of Sequencing Depth and Sample Size in Population Genetics Inferences. PLoS ONE, 2013, 8, e79667.	1.1	132
20	A GWAS in Latin Americans highlights the convergent evolution of lighter skin pigmentation in Eurasia. Nature Communications, 2019, 10, 358.	5.8	130
21	Improving the estimation of genetic distances from Next-Generation Sequencing data. Biological Journal of the Linnean Society, 2016, 117, 139-149.	0.7	102
22	Archaic adaptive introgression in <i>TBX15/WARS2</i> . Molecular Biology and Evolution, 2017, 34, msw283.	3.5	101
23	Estimating inbreeding coefficients from NGS data: Impact on genotype calling and allele frequency estimation. Genome Research, 2013, 23, 1852-1861.	2.4	89
24	Uncovering the Genetic History of the Present-Day Greenlandic Population. American Journal of Human Genetics, 2015, 96, 54-69.	2.6	85
25	Oral microbiomes from hunter-gatherers and traditional farmers reveal shifts in commensal balance and pathogen load linked to diet. Molecular Ecology, 2018, 27, 182-195.	2.0	85
26	Genetic diversity at endoplasmic reticulum aminopeptidases is maintained by balancing selection and is associated with natural resistance to HIV-1 infection. Human Molecular Genetics, 2010, 19, 4705-4714.	1.4	84
27	Genome-Wide Identification of Susceptibility Alleles for Viral Infections through a Population Genetics Approach. PLoS Genetics, 2010, 6, e1000849.	1.5	67
28	Male-biased gene expression resolves sexual conflict through the evolution of sex-specific genetic architecture. Evolution Letters, 2018, 2, 52-61.	1.6	66
29	<i>ngsLD</i> : evaluating linkage disequilibrium using genotype likelihoods. Bioinformatics, 2019, 35, 3855-3856.	1.8	66
30	lmaGene: a convolutional neural network to quantify natural selection from genomic data. BMC Bioinformatics, 2019, 20, 337.	1.2	61
31	The signature of long-standing balancing selection at the human defensin $\beta$ -1 promoter. Genome Biology, 2008, 9, R143.	13.9	60
32	The landscape of human genes involved in the immune response to parasitic worms. BMC Evolutionary Biology, 2010, 10, 264.	3.2	59
33	Detecting adaptive introgression in human evolution using convolutional neural networks. ELife, 2021, 10, .	2.8	59
34	Population Genetics of IFIH1: Ancient Population Structure, Local Selection, and Implications for Susceptibility to Type 1 Diabetes. Molecular Biology and Evolution, 2010, 27, 2555-2566.	3.5	58
35	Inference of natural selection from ancient DNA. Evolution Letters, 2020, 4, 94-108.	1.6	58
36	Human genome variability, natural selection and infectious diseases. Current Opinion in Immunology, 2014, 30, 9-16.	2.4	57

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37	Both selective and neutral processes drive GC content evolution in the human genome. <i>BMC Evolutionary Biology</i> , 2008, 8, 99.	3.2	50
38	Genome-wide analyses of the <i>Bemisia tabaci</i> species complex reveal contrasting patterns of admixture and complex demographic histories. <i>PLoS ONE</i> , 2018, 13, e0190555.	1.1	46
39	Fine mapping of <i>AHI1</i> as a schizophrenia susceptibility gene: from association to evolutionary evidence. <i>FASEB Journal</i> , 2010, 24, 3066-3082.	0.2	39
40	Diverse Evolutionary Histories for $\beta$ -adrenoreceptor Genes in Humans. <i>American Journal of Human Genetics</i> , 2009, 85, 64-75.	2.6	34
41	A POSITIVELY SELECTED APOBEC3H HAPLOTYPE IS ASSOCIATED WITH NATURAL RESISTANCE TO HIV-1 INFECTION. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 3311-3322.	1.1	31
42	The role of protozoa-driven selection in shaping human genetic variability. <i>Trends in Genetics</i> , 2010, 26, 95-99.	2.9	30
43	Distinguishing between recent balancing selection and incomplete sweep using deep neural networks. <i>Molecular Ecology Resources</i> , 2021, 21, 2706-2718.	2.2	30
44	Crohn's Disease Loci Are Common Targets of Protozoa-Driven Selection. <i>Molecular Biology and Evolution</i> , 2013, 30, 1077-1087.	3.5	28
45	Phenotypic sexual dimorphism is associated with genomic signatures of resolved sexual conflict. <i>Molecular Ecology</i> , 2019, 28, 2860-2871.	2.0	28
46	Balancing selection is common in the extended MHC region but most alleles with opposite risk profile for autoimmune diseases are neutrally evolving. <i>BMC Evolutionary Biology</i> , 2011, 11, 171.	3.2	23
47	A Scan for Human-Specific Relaxation of Negative Selection Reveals Unexpected Polymorphism in Proteasome Genes. <i>Molecular Biology and Evolution</i> , 2013, 30, 1808-1815.	3.5	23
48	Genetic diversity of CHC22 clathrin impacts its function in glucose metabolism. <i>ELife</i> , 2019, 8, .	2.8	22
49	Identification of a new susceptibility variant for multiple sclerosis in OAS1 by population genetics analysis. <i>Human Genetics</i> , 2012, 131, 87-97.	1.8	20
50	An Evolutionary Analysis of RAC2 Identifies Haplotypes Associated with Human Autoimmune Diseases. <i>Molecular Biology and Evolution</i> , 2011, 28, 3319-3329.	3.5	19
51	Disentangling Signatures of Selection Before and After European Colonization in Latin Americans. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	16
52	Polymorphisms in the CPB2 Gene Are Maintained by Balancing Selection and Result in Haplotype-Preferential Splicing of Exon 7. <i>Molecular Biology and Evolution</i> , 2010, 27, 1945-1954.	3.5	13
53	A complex selection signature at the human AVPR1B gene. <i>BMC Evolutionary Biology</i> , 2009, 9, 123.	3.2	12
54	Variants in SNAP25 are targets of natural selection and influence verbal performances in women. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 1705-1715.	2.4	10

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55	Genetic variability in the ACE gene region surrounding the Alu I/D polymorphism is maintained by balancing selection in human populations. <i>Pharmacogenetics and Genomics</i> , 2010, 20, 131-134.	0.7	7
56	Long-Standing Balancing Selection in the <i>THBS4</i> Gene: Influence on Sex-Specific Brain Expression and Gray Matter Volumes in Alzheimer Disease. <i>Human Mutation</i> , 2013, 34, 743-753.	1.1	7
57	Fast and accurate estimation of multidimensional site frequency spectra from low-coverage high-throughput sequencing data. <i>GigaScience</i> , 2022, 11, .	3.3	4
58	Natural Selection Associated With Infectious Diseases. , 2017, , 177-191.		2
59	Balancing selection in the extended MHC region maintains a subset of alleles with opposite risk profile for different autoimmune diseases. <i>Genome Biology</i> , 2010, 11, P38.	13.9	1
60	Response to Wilson etÂal.. <i>American Journal of Human Genetics</i> , 2010, 86, 493-495.	2.6	0
61	An efficient implementation of legofit software to infer demographic histories from population genetic data. , 0, , .		0
62	Determinants of population genetic structure in co-occurring freshwater snails. <i>Peer Community in Evolutionary Biology</i> , 0, , .	0.0	0
63	Detecting loci under natural selection from temporal genomic data of selfing populations. <i>Peer Community in Ecology</i> , 0, , .	0.0	0
64	Detecting loci under natural selection from temporal genomic data of selfing populations. <i>Peer Community in Evolutionary Biology</i> , 0, , .	0.0	0
65	ngsjulia: population genetic analysis of next-generation DNA sequencing data with Julia language. <i>F1000Research</i> , 0, 11, 126.	0.8	0