Matteo Fumagalli

List of Publications by Year
in descending order

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	Disentangling Signatures of Selection Before and After European Colonization in Latin Americans. Molecular Biology and Evolution, 2022, 39, .	3.5	16
2	Fast and accurate estimation of multidimensional site frequency spectra from low-coverage high-throughput sequencing data. GigaScience, 2022, 11, .	3.3	4
3	Distinguishing between recent balancing selection and incomplete sweep using deep neural networks. Molecular Ecology Resources, 2021, 21, 2706-2718.	2.2	30
4	Detecting adaptive introgression in human evolution using convolutional neural networks. ELife, 2021, 10, .	2.8	59
5	Inference of natural selection from ancient DNA. Evolution Letters, 2020, 4, 94-108.	1.6	58
6	A GWAS in Latin Americans highlights the convergent evolution of lighter skin pigmentation in Eurasia. Nature Communications, 2019, 10, 358.	5.8	130
7	Phenotypic sexual dimorphism is associated with genomic signatures of resolved sexual conflict. Molecular Ecology, 2019, 28, 2860-2871.	2.0	28
8	<i>ngsLD</i>: evaluating linkage disequilibrium using genotype likelihoods. Bioinformatics, 2019, 35, 3855-3856.	1.8	66
9	ImaGene: a convolutional neural network to quantify natural selection from genomic data. BMC Bioinformatics, 2019, 20, 337.	1.2	61
10	Genetic diversity of CHC22 clathrin impacts its function in glucose metabolism. ELife, 2019, 8, .	2.8	22
11	Male-biased gene expression resolves sexual conflict through the evolution of sex-specific genetic architecture. Evolution Letters, 2018, 2, 52-61.	1.6	66
12	Oral microbiomes from hunterâ€gatherers and traditional farmers reveal shifts in commensal balance and pathogen load linked to diet. Molecular Ecology, 2018, 27, 182-195.	2.0	85
13	Recent Asian origin of chytrid fungi causing global amphibian declines. Science, 2018, 360, 621-627.	6.0	389
14	Genome-wide analyses of the Bemisia tabaci species complex reveal contrasting patterns of admixture and complex demographic histories. PLoS ONE, 2018, 13, e0190555.	1.1	46
15	Archaic adaptive introgression in <i>TBX15/WARS2</i>. Molecular Biology and Evolution, 2017, 34, msw283.	3.5	101
16	Survival and divergence in a small group: The extraordinary genomic history of the endangered Apennine brown bear stragglers. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9589-E9597.	3.3	140
17	Natural Selection Associated With Infectious Diseases. , 2017, , 177-191.		2
18	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. Nature Communications, 2016, 7, 11693.	5.8	222

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19	Improving the estimation of genetic distances from Next-Generation Sequencing data. Biological Journal of the Linnean Society, 2016, 117, 139-149.	0.7	102
20	The origin and evolution of maize in the Southwestern United States. Nature Plants, 2015, 1, 14003.	4.7	138
21	Uncovering the Genetic History of the Present-Day Greenlandic Population. American Journal of Human Genetics, 2015, 96, 54-69.	2.6	85
22	Evolutionary Genomics and Conservation of the Endangered Przewalski's Horse. Current Biology, 2015, 25, 2577-2583.	1.8	161
23	Greenlandic Inuit show genetic signatures of diet and climate adaptation. Science, 2015, 349, 1343-1347.	6.0	397
24	Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6889-97.	3.3	139
25	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5661-9.	3.3	260
26	Speciation with gene flow in equids despite extensive chromosomal plasticity. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18655-18660.	3.3	183
27	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. Cell, 2014, 157, 785-794.	13.5	363
28	*ngsTools*: methods for population genetics analyses from next-generation sequencing data. Bioinformatics, 2014, 30, 1486-1487.	1.8	227
29	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. Nature, 2014, 512, 190-193.	13.7	338
30	Human genome variability, natural selection and infectious diseases. Current Opinion in Immunology, 2014, 30, 9-16.	2.4	57
31	Crohn's Disease Loci Are Common Targets of Protozoa-Driven Selection. Molecular Biology and Evolution, 2013, 30, 1077-1087.	3.5	28
32	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. Nature, 2013, 499, 74-78.	13.7	717
33	Quantifying Population Genetic Differentiation from Next-Generation Sequencing Data. Genetics, 2013, 195, 979-992.	1.2	187
34	Estimating inbreeding coefficients from NGS data: Impact on genotype calling and allele frequency estimation. Genome Research, 2013, 23, 1852-1861.	2.4	89
35	A Scan for Human-Specific Relaxation of Negative Selection Reveals Unexpected Polymorphism in Proteasome Genes. Molecular Biology and Evolution, 2013, 30, 1808-1815.	3.5	23
36	Long-Standing Balancing Selection in the *THBS4* Gene: Influence on Sex-Specific Brain Expression and Gray Matter Volumes in Alzheimer Disease. Human Mutation, 2013, 34, 743-753.	1.1	7

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37	Assessing the Effect of Sequencing Depth and Sample Size in Population Genetics Inferences. PLoS ONE, 2013, 8, e79667.	1.1	132
38	Variants in SNAP25 are targets of natural selection and influence verbal performances in women. Cellular and Molecular Life Sciences, 2012, 69, 1705-1715.	2.4	10
39	Identification of a new susceptibility variant for multiple sclerosis in OAS1 by population genetics analysis. Human Genetics, 2012, 131, 87-97.	1.8	20
40	A POSITIVELY SELECTED APOBEC3H HAPLOTYPE IS ASSOCIATED WITH NATURAL RESISTANCE TO HIV-1 INFECTION. Evolution; International Journal of Organic Evolution, 2011, 65, 3311-3322.	1.1	31
41	Balancing selection is common in the extended MHC region but most alleles with opposite risk profile for autoimmune diseases are neutrally evolving. BMC Evolutionary Biology, 2011, 11, 171.	3.2	23
42	Evolutionary genetic dissection of human interferons. Journal of Experimental Medicine, 2011, 208, 2747-2759.	4.2	170
43	An Evolutionary Analysis of RAC2 Identifies Haplotypes Associated with Human Autoimmune Diseases. Molecular Biology and Evolution, 2011, 28, 3319-3329.	3.5	19
44	Signatures of Environmental Genetic Adaptation Pinpoint Pathogens as the Main Selective Pressure through Human Evolution. PLoS Genetics, 2011, 7, e1002355.	1.5	464
45	Genetic variability in the ACE gene region surrounding the Alu I/D polymorphism is maintained by balancing selection in human populations. Pharmacogenetics and Genomics, 2010, 20, 131-134.	0.7	7
46	Response to Wilson etÂal.. American Journal of Human Genetics, 2010, 86, 493-495.	2.6	0
47	The role of protozoa-driven selection in shaping human genetic variability. Trends in Genetics, 2010, 26, 95-99.	2.9	30
48	The landscape of human genes involved in the immune response to parasitic worms. BMC Evolutionary Biology, 2010, 10, 264.	3.2	59
49	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
50	Fine mapping of <i>AHI1</i> as a schizophrenia susceptibility gene: from association to evolutionary evidence. FASEB Journal, 2010, 24, 3066-3082.	0.2	39
51	Polymorphisms in the CPB2 Gene Are Maintained by Balancing Selection and Result in Haplotype-Preferential Splicing of Exon 7. Molecular Biology and Evolution, 2010, 27, 1945-1954.	3.5	13
52	Genome-Wide Identification of Susceptibility Alleles for Viral Infections through a Population Genetics Approach. PLoS Genetics, 2010, 6, e1000849.	1.5	67
53	Balancing selection in the extended MHC region maintains a subset of alleles with opposite risk profile for different autoimmune diseases. Genome Biology, 2010, 11, P38.	13.9	1
54	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

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55	Widespread balancing selection and pathogen-driven selection at blood group antigen genes. Genome Research, 2009, 19, 199-212.	2.4	147
56	Parasites represent a major selective force for interleukin genes and shape the genetic predisposition to autoimmune conditions. Journal of Experimental Medicine, 2009, 206, 1395-1408.	4.2	230
57	A complex selection signature at the human AVPR1B gene. BMC Evolutionary Biology, 2009, 9, 123.	3.2	12
58	Diverse Evolutionary Histories for Î²-adrenoreceptor Genes in Humans. American Journal of Human Genetics, 2009, 85, 64-75.	2.6	34
59	Both selective and neutral processes drive GC content evolution in the human genome. BMC Evolutionary Biology, 2008, 8, 99.	3.2	50
60	The signature of long-standing balancing selection at the human defensin Î²-1 promoter. Genome Biology, 2008, 9, R143.	13.9	60
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. Peer Community in Evolutionary Biology, 0, , .	0.0	0
63	Detecting loci under natural selection from temporal genomic data of selfing populations. Peer Community in Ecology, 0, , .	0.0	0
64	Detecting loci under natural selection from temporal genomic data of selfing populations. Peer Community in Evolutionary Biology, 0, , .	0.0	0
65	ngsJulia: population genetic analysis of next-generation DNA sequencing data with Julia language. F1000Research, 0, 11, 126.	0.8	0