Gilean McVean

List of Publications by Year
in descending order

92 papers	41,977 citations	34016 52 h-index	49773 87 g-index
124 all docs	124 docs citations	124 times ranked	58768 citing authors

#	Article	IF	Citations
1	The variant call format and VCFtools. Bioinformatics, 2011, 27, 2156-2158.	1.8	11,326
2	The UK Biobank resource with deep phenotyping and genomic data. Nature, 2018, 562, 203-209.	13.7	5,221
3	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	13.7	4,137
4	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	13.7	2,400
5	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	13.7	1,788
6	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	9.4	1,213
7	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
8	Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. Nature Genetics, 2014, 46, 912-918.	9.4	937
9	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. Nature Genetics, 2010, 42, 985-990.	9.4	918
10	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. Nature Genetics, 2011, 43, 761-767.	9.4	778
11	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. Nature Genetics, 2006, 38, 1166-1172.	9.4	686
12	A Coalescent-Based Method for Detecting and Estimating Recombination From Gene Sequences. Genetics, 2002, 160, 1231-1241.	1.2	624
13	Drive Against Hotspot Motifs in Primates Implicates the PRDM9 Gene in Meiotic Recombination. Science, 2010, 327, 876-879.	6.0	607
14	De novo assembly and genotyping of variants using colored de Bruijn graphs. Nature Genetics, 2012, 44, 226-232.	9.4	564
15	Efficient Coalescent Simulation and Genealogical Analysis for Large Sample Sizes. PLoS Computational Biology, 2016, 12, e1004842.	1.5	547
16	Genetic architecture of artemisinin-resistant Plasmodium falciparum. Nature Genetics, 2015, 47, 226-234.	9.4	515
17	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. Nature Communications, 2015, 6, 10063.	5.8	479
18	A Genealogical Interpretation of Principal Components Analysis. PLoS Genetics, 2009, 5, e1000686.	1.5	462

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19	Multiple populations of artemisinin-resistant Plasmodium falciparum in Cambodia. Nature Genetics, 2013, 45, 648-655.	9.4	424
20	A reference data set of 5.4 million phased human variants validated by genetic inheritance from sequencing a three-generation 17-member pedigree. Genome Research, 2017, 27, 157-164.	2.4	338
21	TNF receptor 1 genetic risk mirrors outcome of anti-TNF therapy in multiple sclerosis. Nature, 2012, 488, 508-511.	13.7	323
22	Class II HLA interactions modulate genetic risk for multiple sclerosis. Nature Genetics, 2015, 47, 1107-1113.	9.4	312
23	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	9.4	310
24	Stable recombination hotspots in birds. Science, 2015, 350, 928-932.	6.0	280
25	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. Science, 2012, 336, 193-198.	6.0	273
26	Estimating Diversifying Selection and Functional Constraint in the Presence of Recombination. Genetics, 2006, 172, 1411-1425.	1.2	269
27	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. Nature Microbiology, 2016, 1, 16041.	5.9	247
28	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. Human Molecular Genetics, 2014, 23, 3200-3211.	1.4	222
29	Improved genome inference in the MHC using a population reference graph. Nature Genetics, 2015, 47, 682-688.	9.4	197
30	Inferring whole-genome histories in large population datasets. Nature Genetics, 2019, 51, 1330-1338.	9.4	187
31	Resolving TYK2 locus genotype-to-phenotype differences in autoimmunity. Science Translational Medicine, 2016, 8, 363ra149.	5.8	186
32	Indels, structural variation, and recombination drive genomic diversity in Plasmodium falciparum. Genome Research, 2016, 26, 1288-1299.	2.4	180
33	A Statistical Method for Predicting Classical HLA Alleles from SNP Data. American Journal of Human Genetics, 2008, 82, 48-56.	2.6	159
34	Multi-Population Classical HLA Type Imputation. PLoS Computational Biology, 2013, 9, e1002877.	1.5	157
35	HLA*IMPâ€”an integrated framework for imputing classical HLA alleles from SNP genotypes. Bioinformatics, 2011, 27, 968-972.	1.8	151
36	Strong male bias drives germline mutation in chimpanzees. Science, 2014, 344, 1272-1275.	6.0	146

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37	The Structure of Linkage Disequilibrium Around a Selective Sweep. Genetics, 2007, 175, 1395-1406.	1.2	138
38	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. Nature Genetics, 2017, 49, 666-673.	9.4	129
39	Dating genomic variants and shared ancestry in population-scale sequencing data. PLoS Biology, 2020, 18, e3000586.	2.6	127
40	The Power of Gene-Based Rare Variant Methods to Detect Disease-Associated Variation and Test Hypotheses About Complex Disease. PLoS Genetics, 2015, 11, e1005165.	1.5	124
41	Ultrafast search of all deposited bacterial and viral genomic data. Nature Biotechnology, 2019, 37, 152-159.	9.4	123
42	Demography and the Age of Rare Variants. PLoS Genetics, 2014, 10, e1004528.	1.5	98
43	Structural and regulatory diversity shape HLA-C protein expression levels. Nature Communications, 2017, 8, 15924.	5.8	98
44	Genome-wide analysis of 53,400 people with irritable bowel syndrome highlights shared genetic pathways with mood and anxiety disorders. Nature Genetics, 2021, 53, 1543-1552.	9.4	96
45	Recombination Rate Heterogeneity within Arabidopsis Disease Resistance Genes. PLoS Genetics, 2016, 12, e1006179.	1.5	94
46	Perspectives on Human Genetic Variation from the HapMap Project. PLoS Genetics, 2005, 1, e54.	1.5	93
47	HLA*LAâ€”HLA typing from linearly projected graph alignments. Bioinformatics, 2019, 35, 4394-4396.	1.8	88
48	High-Accuracy HLA Type Inference from Whole-Genome Sequencing Data Using Population Reference Graphs. PLoS Computational Biology, 2016, 12, e1005151.	1.5	87
49	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. Nature Communications, 2013, 4, 2872.	5.8	77
50	Imputation of KIR Types from SNP Variation Data. American Journal of Human Genetics, 2015, 97, 593-607.	2.6	73
51	Contributions of intrinsic mutation rate and selfish selection to levels of de novo HRAS mutations in the paternal germline. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20152-20157.	3.3	70
52	Deconvolution of multiple infections in Plasmodium falciparum from high throughput sequencing data. Bioinformatics, 2018, 34, 9-15.	1.8	64
53	Integrating long-range connectivity information into de Bruijn graphs. Bioinformatics, 2018, 34, 2556-2565.	1.8	61
54	Genetic characterization of Greek population isolates reveals strong genetic drift at missense and trait-associated variants. Nature Communications, 2014, 5, 5345.	5.8	60

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55	Recommendations for improving statistical inference in population genomics. PLoS Biology, 2022, 20, e3001669.	2.6	60
56	A unified genealogy of modern and ancient genomes. Science, 2022, 375, eabi8264.	6.0	59
57	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank. Nature Genetics, 2017, 49, 1311-1318.	9.4	56
58	Selfish mutations dysregulating RAS-MAPK signaling are pervasive in aged human testes. Genome Research, 2018, 28, 1779-1790.	2.4	56
59	What drives recombination hotspots to repeat DNA in humans?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 1213-1218.	1.8	54
60	The impact of age on genetic risk for common diseases. PLoS Genetics, 2021, 17, e1009723.	1.5	53
61	The origins and relatedness structure of mixed infections vary with local prevalence of P. falciparum malaria. ELife, 2019, 8, .	2.8	52
62	Genomic Analysis of Plasmodium vivax in Southern Ethiopia Reveals Selective Pressures in Multiple Parasite Mechanisms. Journal of Infectious Diseases, 2019, 220, 1738-1749.	1.9	50
63	Validation of an Integrated Risk Tool, Including Polygenic Risk Score, for Atherosclerotic Cardiovascular Disease in Multiple Ethnicities and Ancestries. American Journal of Cardiology, 2021, 148, 157-164.	0.7	48
64	Hypervariable antigen genes in malaria have ancient roots. BMC Evolutionary Biology, 2013, 13, 110.	3.2	47
65	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
66	Accounting for long-range correlations in genome-wide simulations of large cohorts. PLoS Genetics, 2020, 16, e1008619.	1.5	43
67	Multiple Hodgkin lymphomaâ€“associated loci within the HLA region at chromosome 6p21.3. Blood, 2011, 118, 670-674.	0.6	37
68	High-throughput microbial population genomics using the Cortex variation assembler. Bioinformatics, 2013, 29, 275-276.	1.8	37
69	Whole-genome sequencing of spermatocytic tumors provides insights into the mutational processes operating in the male germline. PLoS ONE, 2017, 12, e0178169.	1.1	36
70	A point mutation in the ion conduction pore of AMPA receptor GRIA3 causes dramatically perturbed sleep patterns as well as intellectual disability. Human Molecular Genetics, 2017, 26, 3869-3882.	1.4	35
71	Identifying cross-disease components of genetic risk across hospital data in the UK Biobank. Nature Genetics, 2020, 52, 126-134.	9.4	35
72	Premalignant SOX2 overexpression in the fallopian tubes of ovarian cancer patients: Discovery and validation studies. EBioMedicine, 2016, 10, 137-149.	2.7	34

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73	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
74	Neuroinflammation â€" using big data to inform clinical practice. Nature Reviews Neurology, 2016, 12, 685-698.	4.9	29
75	Identification of hostâ€"pathogen-disease relationships using a scalable multiplex serology platform in UK Biobank. Nature Communications, 2022, 13, 1818.	5.8	28
76	Bayesian metaâ€analysis across genomeâ€wide association studies of diverse phenotypes. Genetic Epidemiology, 2019, 43, 532-547.	0.6	27
77	Trinculo: Bayesian and frequentist multinomial logistic regression for genome-wide association studies of multi-category phenotypes. Bioinformatics, 2016, 32, 1898-1900.	1.8	26
78	Estimating Recombination Rates from Genetic Variation in Humans. Methods in Molecular Biology, 2012, 856, 217-237.	0.4	21
79	Integrating genealogical and dynamical modelling to infer escape and reversion rates in HIV epitopes. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20130696.	1.2	14
80	Elucidating relationships between P.falciparum prevalence and measures of genetic diversity with a combined genetic-epidemiological model of malaria. PLoS Computational Biology, 2021, 17, e1009287.	1.5	14
81	Characterisation of the changing genomic landscape of metastatic melanoma using cell free DNA. Npj Genomic Medicine, 2017, 2, 25.	1.7	12
82	Low-Bias RNA Sequencing of the HIV-2 Genome from Blood Plasma. Journal of Virology, 2019, 93, .	1.5	11
83	Where Next for Genetics and Genomics?. PLoS Biology, 2015, 13, e1002216.	2.6	9
84	Detection of simple and complex de novo mutations with multiple reference sequences. Genome Research, 2020, 30, 1154-1169.	2.4	7
85	Mapping the drivers of within-host pathogen evolution using massive data sets. Nature Communications, 2019, 10, 3017.	5.8	6
86	Graphical Model Selection for Gaussian Conditional Random Fields in the Presence of Latent Variables. Journal of the American Statistical Association, 2019, 114, 723-734.	1.8	6
87	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
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89	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
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91	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
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