

# Gilean McVean

## 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.

114  
papers

27,613  
citations

48  
h-index

124  
g-index

124  
ext. papers

36,542  
ext. citations

17.6  
avg, IF

6.5  
L-index

#	Paper	IF	Citations
114	The variant call format and VCFtools. <i>Bioinformatics</i> , <b>2011</b> , 27, 2156-8	7.2	6200
113	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , <b>2007</b> , 449, 851-61	50.4	3647
112	The UK Biobank resource with deep phenotyping and genomic data. <i>Nature</i> , <b>2018</b> , 562, 203-209	50.4	2108
111	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , <b>2011</b> , 476, 214-9	50.4	1948
110	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , <b>2007</b> , 449, 913-8	50.4	1367
109	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. <i>Nature Genetics</i> , <b>2013</b> , 45, 1353-60	36.3	934
108	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. <i>Nature Genetics</i> , <b>2010</b> , 42, 985-90	36.3	773
107	The genetic architecture of type 2 diabetes. <i>Nature</i> , <b>2016</b> , 536, 41-47	50.4	704
106	Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. <i>Nature Genetics</i> , <b>2014</b> , 46, 912-918	36.3	671
105	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. <i>Nature Genetics</i> , <b>2011</b> , 43, 761-7	36.3	646
104	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. <i>Nature Genetics</i> , <b>2006</b> , 38, 1166-72	36.3	618
103	A coalescent-based method for detecting and estimating recombination from gene sequences. <i>Genetics</i> , <b>2002</b> , 160, 1231-41	4	530
102	Drive against hotspot motifs in primates implicates the PRDM9 gene in meiotic recombination. <i>Science</i> , <b>2010</b> , 327, 876-9	33.3	465
101	De novo assembly and genotyping of variants using colored de Bruijn graphs. <i>Nature Genetics</i> , <b>2012</b> , 44, 226-32	36.3	433
100	Genetic architecture of artemisinin-resistant Plasmodium falciparum. <i>Nature Genetics</i> , <b>2015</b> , 47, 226-34	36.3	382
99	Multiple populations of artemisinin-resistant Plasmodium falciparum in Cambodia. <i>Nature Genetics</i> , <b>2013</b> , 45, 648-55	36.3	350
98	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. <i>Nature Communications</i> , <b>2015</b> , 6, 10063	17.4	348

97	Genome-wide genetic data on ~500,000 UK Biobank participants		320
96	A genealogical interpretation of principal components analysis. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000686	6	317
95	Efficient Coalescent Simulation and Genealogical Analysis for Large Sample Sizes. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1004842	5	287
94	TNF receptor 1 genetic risk mirrors outcome of anti-TNF therapy in multiple sclerosis. <i>Nature</i> , <b>2012</b> , 488, 508-511	50.4	269
93	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. <i>Nature Genetics</i> , <b>2015</b> , 47, 717-726	36.3	244
92	A reference data set of 5.4 million phased human variants validated by genetic inheritance from sequencing a three-generation 17-member pedigree. <i>Genome Research</i> , <b>2017</b> , 27, 157-164	9.7	223
91	A fine-scale chimpanzee genetic map from population sequencing. <i>Science</i> , <b>2012</b> , 336, 193-8	33.3	218
90	Class II HLA interactions modulate genetic risk for multiple sclerosis. <i>Nature Genetics</i> , <b>2015</b> , 47, 1107-1113	36.3	215
89	Estimating diversifying selection and functional constraint in the presence of recombination. <i>Genetics</i> , <b>2006</b> , 172, 1411-25	4	210
88	Stable recombination hotspots in birds. <i>Science</i> , <b>2015</b> , 350, 928-32	33.3	187
87	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 3200-11	5.6	179
86	A statistical method for predicting classical HLA alleles from SNP data. <i>American Journal of Human Genetics</i> , <b>2008</b> , 82, 48-56	11	145
85	Improved genome inference in the MHC using a population reference graph. <i>Nature Genetics</i> , <b>2015</b> , 47, 682-8	36.3	144
84	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16041	26.6	143
83	HLA*IMP--an integrated framework for imputing classical HLA alleles from SNP genotypes. <i>Bioinformatics</i> , <b>2011</b> , 27, 968-72	7.2	134
82	Multi-population classical HLA type imputation. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1002877	5	129
81	Resolving TYK2 locus genotype-to-phenotype differences in autoimmunity. <i>Science Translational Medicine</i> , <b>2016</b> , 8, 363ra149	17.5	118
80	The structure of linkage disequilibrium around a selective sweep. <i>Genetics</i> , <b>2007</b> , 175, 1395-406	4	109

79	Nonhuman genetics. Strong male bias drives germline mutation in chimpanzees. <i>Science</i> , <b>2014</b> , 344, 1272-1275	35.3	103
78	Indels, structural variation, and recombination drive genomic diversity in <i>Plasmodium falciparum</i> . <i>Genome Research</i> , <b>2016</b> , 26, 1288-99	9.7	100
77	The power of gene-based rare variant methods to detect disease-associated variation and test hypotheses about complex disease. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005165	6	98
76	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. <i>Nature Genetics</i> , <b>2017</b> , 49, 666-673	36.3	81
75	Inferring whole-genome histories in large population datasets. <i>Nature Genetics</i> , <b>2019</b> , 51, 1330-1338	36.3	80
74	Perspectives on human genetic variation from the HapMap Project. <i>PLoS Genetics</i> , <b>2005</b> , 1, e54	6	77
73	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. <i>Nature Communications</i> , <b>2013</b> , 4, 2872	17.4	70
72	Ultrafast search of all deposited bacterial and viral genomic data. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 152-159	44.5	70
71	Recombination Rate Heterogeneity within Arabidopsis Disease Resistance Genes. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006179	6	69
70	Demography and the age of rare variants. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004528	6	64
69	Structural and regulatory diversity shape HLA-C protein expression levels. <i>Nature Communications</i> , <b>2017</b> , 8, 15924	17.4	62
68	High-Accuracy HLA Type Inference from Whole-Genome Sequencing Data Using Population Reference Graphs. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1005151	5	60
67	Contributions of intrinsic mutation rate and selfish selection to levels of de novo HRAS mutations in the paternal germline. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 20152-7	11.5	51
66	Genetic characterization of Greek population isolates reveals strong genetic drift at missense and trait-associated variants. <i>Nature Communications</i> , <b>2014</b> , 5, 5345	17.4	46
65	What drives recombination hotspots to repeat DNA in humans?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2010</b> , 365, 1213-8	5.8	46
64	Imputation of KIR Types from SNP Variation Data. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 593-607	7.1	44
63	HLA*LA-HLA typing from linearly projected graph alignments. <i>Bioinformatics</i> , <b>2019</b> , 35, 4394-4396	7.2	42
62	Dating genomic variants and shared ancestry in population-scale sequencing data. <i>PLoS Biology</i> , <b>2020</b> , 18, e3000586	9.7	42

61	Deconvolution of multiple infections in Plasmodium falciparum from high throughput sequencing data. <i>Bioinformatics</i> , <b>2018</b> , 34, 9-15	7.2	39
60	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank. <i>Nature Genetics</i> , <b>2017</b> , 49, 1311-1318	36.3	38
59	Integrating long-range connectivity information into de Bruijn graphs. <i>Bioinformatics</i> , <b>2018</b> , 34, 2556-2565	5.2	36
58	Selfish mutations dysregulating RAS-MAPK signaling are pervasive in aged human testes. <i>Genome Research</i> , <b>2018</b> , 28, 1779-1790	9.7	36
57	Hypervariable antigen genes in malaria have ancient roots. <i>BMC Evolutionary Biology</i> , <b>2013</b> , 13, 110	3	34
56	High-throughput microbial population genomics using the Cortex variation assembler. <i>Bioinformatics</i> , <b>2013</b> , 29, 275-6	7.2	32
55	Multiple Hodgkin lymphoma-associated loci within the HLA region at chromosome 6p21.3. <i>Blood</i> , <b>2011</b> , 118, 670-4	2.2	31
54	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , <b>2017</b> , 66, 2019-2032	0.9	29
53	Premalignant SOX2 overexpression in the fallopian tubes of ovarian cancer patients: Discovery and validation studies. <i>EBioMedicine</i> , <b>2016</b> , 10, 137-49	8.8	29
52	Genomic Analysis of Plasmodium vivax in Southern Ethiopia Reveals Selective Pressures in Multiple Parasite Mechanisms. <i>Journal of Infectious Diseases</i> , <b>2019</b> , 220, 1738-1749	7	25
51	The origins and relatedness structure of mixed infections vary with local prevalence of malaria. <i>ELife</i> , <b>2019</b> , 8,	8.9	25
50	A point mutation in the ion conduction pore of AMPA receptor GRIA3 causes dramatically perturbed sleep patterns as well as intellectual disability. <i>Human Molecular Genetics</i> , <b>2017</b> , 26, 3869-3882	5.6	24
49	Whole-genome sequencing of spermatocytic tumors provides insights into the mutational processes operating in the male germline. <i>PLoS ONE</i> , <b>2017</b> , 12, e0178169	3.7	24
48	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , <b>2017</b> , 4, 170179	8.2	22
47	Identifying cross-disease components of genetic risk across hospital data in the UK Biobank. <i>Nature Genetics</i> , <b>2020</b> , 52, 126-134	36.3	22
46	Neuroinflammation - using big data to inform clinical practice. <i>Nature Reviews Neurology</i> , <b>2016</b> , 12, 685-698	6.8	20
45	Trinculo: Bayesian and frequentist multinomial logistic regression for genome-wide association studies of multi-category phenotypes. <i>Bioinformatics</i> , <b>2016</b> , 32, 1898-900	7.2	18
44	Estimating recombination rates from genetic variation in humans. <i>Methods in Molecular Biology</i> , <b>2012</b> , 856, 217-37	1.4	17

43	Practical Use of Methods for Imputation of HLA Alleles from SNP Genotype Data		15
42	Bayesian meta-analysis across genome-wide association studies of diverse phenotypes. <i>Genetic Epidemiology</i> , <b>2019</b> , 43, 532-547	2.6	13
41	Accounting for long-range correlations in genome-wide simulations of large cohorts. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1008619	6	13
40	Real-time search of all bacterial and viral genomic data		13
39	A reference dataset of 5.4 million phased human variants validated by genetic inheritance from sequencing a three-generation 17-member pedigree		12
38	Genome-wide analysis of 53,400 people with irritable bowel syndrome highlights shared genetic pathways with mood and anxiety disorders. <i>Nature Genetics</i> , <b>2021</b> , 53, 1543-1552	36.3	11
37	Identification of host-pathogen-disease relationships using a scalable Multiplex Serology platform in UK Biobank		11
36	Integrating genealogical and dynamical modelling to infer escape and reversion rates in HIV epitopes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2013</b> , 280, 20130696	4.4	10
35	Validation of an Integrated Risk Tool, Including Polygenic Risk Score, for Atherosclerotic Cardiovascular Disease in Multiple Ethnicities and Ancestries. <i>American Journal of Cardiology</i> , <b>2021</b> , 148, 157-164	3	10
34	Where Next for Genetics and Genomics?. <i>PLoS Biology</i> , <b>2015</b> , 13, e1002216	9.7	8
33	Dating genomic variants and shared ancestry in population-scale sequencing data		7
32	The impact of age on genetic risk for common diseases. <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009723	6	7
31	Inferring the ancestry of everyone		6
30	Characterisation of the changing genomic landscape of metastatic melanoma using cell free DNA. <i>Npj Genomic Medicine</i> , <b>2017</b> , 2, 25	6.2	5
29	Detection of simple and complex de novo mutations with multiple reference sequences. <i>Genome Research</i> , <b>2020</b> , 30, 1154-1169	9.7	5
28	Graphical Model Selection for Gaussian Conditional Random Fields in the Presence of Latent Variables. <i>Journal of the American Statistical Association</i> , <b>2019</b> , 114, 723-734	2.8	5
27	Mapping the drivers of within-host pathogen evolution using massive data sets. <i>Nature Communications</i> , <b>2019</b> , 10, 3017	17.4	4
26	Genome variation and meiotic recombination in <i>Plasmodium falciparum</i> : insights from deep sequencing of genetic crosses		4

25	Low-Bias RNA Sequencing of the HIV-2 Genome from Blood Plasma. <i>Journal of Virology</i> , <b>2019</b> , 93,	6.6	4
24	A unified genealogy of modern and ancient genomes		4
23	High trait variability in optimal polygenic prediction strategy within multiple-ancestry cohorts		4
22	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank		3
21	The origins and relatedness structure of mixed infections vary with local prevalence of <i>P. falciparum</i> malaria		3
20	Integrating long-range connectivity information into de Bruijn graphs		3
19	The impact of age on genetic risk for common diseases		1
18	Systematic classification of shared components of genetic risk for common human diseases		1
17	Mapping the drivers of within-host pathogen evolution using massive data sets		1
16	Parental-fetal interplay of immune genes leads to intrauterine growth restriction		1
15	A unified genealogy of modern and ancient genomes.. <i>Science</i> , <b>2022</b> , 375, eabi8264	33.3	1
14	Identification of host-pathogen-disease relationships using a scalable multiplex serology platform in UK Biobank.. <i>Nature Communications</i> , <b>2022</b> , 13, 1818	17.4	1
13	Elucidating relationships between <i>P.falciparum</i> prevalence and measures of genetic diversity with a combined genetic-epidemiological model of malaria. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1009287	5	0
12	Dating genomic variants and shared ancestry in population-scale sequencing data <b>2020</b> , 18, e3000586		
11	Dating genomic variants and shared ancestry in population-scale sequencing data <b>2020</b> , 18, e3000586		
10	Dating genomic variants and shared ancestry in population-scale sequencing data <b>2020</b> , 18, e3000586		
9	Dating genomic variants and shared ancestry in population-scale sequencing data <b>2020</b> , 18, e3000586		
8	Dating genomic variants and shared ancestry in population-scale sequencing data <b>2020</b> , 18, e3000586		

- 7 Dating genomic variants and shared ancestry in population-scale sequencing data **2020**, 18, e3000586
- 6 Accounting for long-range correlations in genome-wide simulations of large cohorts **2020**, 16, e1008619
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- 2 Accounting for long-range correlations in genome-wide simulations of large cohorts **2020**, 16, e1008619
- 1 Accounting for long-range correlations in genome-wide simulations of large cohorts **2020**, 16, e1008619