Gilean McVean

List of Publications by Year in Descending Order

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	A unified genealogy of modern and ancient genomes.. *Science*, **2022**, 375, eabi8264	33.3	1
113	Identification of host-pathogen-disease relationships using a scalable multiplex serology platform in UK Biobank.. *Nature Communications*, **2022**, 13, 1818	17.4	1
112	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	36.3	11
111	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	3	10
110	The impact of age on genetic risk for common diseases. *PLoS Genetics*, **2021**, 17, e1009723	6	7
109	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	5	0
108	Accounting for long-range correlations in genome-wide simulations of large cohorts. *PLoS Genetics*, **2020**, 16, e1008619	6	13
107	Dating genomic variants and shared ancestry in population-scale sequencing data. *PLoS Biology*, **2020**, 18, e3000586	9.7	42
106	Identifying cross-disease components of genetic risk across hospital data in the UK Biobank. *Nature Genetics*, **2020**, 52, 126-134	36.3	22
105	Detection of simple and complex de novo mutations with multiple reference sequences. *Genome Research*, **2020**, 30, 1154-1169	9.7	5
104	Dating genomic variants and shared ancestry in population-scale sequencing data **2020**, 18, e3000586		
103	Dating genomic variants and shared ancestry in population-scale sequencing data **2020**, 18, e3000586		
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98	Accounting for long-range correlations in genome-wide simulations of large cohorts **2020**, 16, e1008619		

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93	Accounting for long-range correlations in genome-wide simulations of large cohorts **2020**, 16, e1008619		
92	Inferring whole-genome histories in large population datasets. *Nature Genetics*, **2019**, 51, 1330-1338	36.3	80
91	Genomic Analysis of Plasmodium vivax in Southern Ethiopia Reveals Selective Pressures in Multiple Parasite Mechanisms. *Journal of Infectious Diseases*, **2019**, 220, 1738-1749	7	25
90	Bayesian meta-analysis across genome-wide association studies of diverse phenotypes. *Genetic Epidemiology*, **2019**, 43, 532-547	2.6	13
89	HLA*LA-HLA typing from linearly projected graph alignments. *Bioinformatics*, **2019**, 35, 4394-4396	7.2	42
88	Mapping the drivers of within-host pathogen evolution using massive data sets. *Nature Communications*, **2019**, 10, 3017	17.4	4
87	The origins and relatedness structure of mixed infections vary with local prevalence of malaria. *ELife*, **2019**, 8,	8.9	25
86	Ultrafast search of all deposited bacterial and viral genomic data. *Nature Biotechnology*, **2019**, 37, 152-159	41.5	70
85	Low-Bias RNA Sequencing of the HIV-2 Genome from Blood Plasma. *Journal of Virology*, **2019**, 93,	6.6	4
84	Graphical Model Selection for Gaussian Conditional Random Fields in the Presence of Latent Variables. *Journal of the American Statistical Association*, **2019**, 114, 723-734	2.8	5
83	Integrating long-range connectivity information into de Bruijn graphs. *Bioinformatics*, **2018**, 34, 2556-2565	7.2	36
82	Deconvolution of multiple infections in Plasmodium falciparum from high throughput sequencing data. *Bioinformatics*, **2018**, 34, 9-15	7.2	39
81	The UK Biobank resource with deep phenotyping and genomic data. *Nature*, **2018**, 562, 203-209	50.4	2108
80	Selfish mutations dysregulating RAS-MAPK signaling are pervasive in aged human testes. *Genome Research*, **2018**, 28, 1779-1790	9.7	36

79	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	36.3	81
78	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes*, **2017**, 66, 2019-2032	0.9	29
77	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	9.7	223
76	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	5.6	24
75	Characterisation of the changing genomic landscape of metastatic melanoma using cell free DNA. *Npj Genomic Medicine*, **2017**, 2, 25	6.2	5
74	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank. *Nature Genetics*, **2017**, 49, 1311-1318	36.3	38
73	Structural and regulatory diversity shape HLA-C protein expression levels. *Nature Communications*, **2017**, 8, 15924	17.4	62
72	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
71	Whole-genome sequencing of spermatocytic tumors provides insights into the mutational processes operating in the male germline. *PLoS ONE*, **2017**, 12, e0178169	3.7	24
70	Indels, structural variation, and recombination drive genomic diversity in Plasmodium falciparum. *Genome Research*, **2016**, 26, 1288-99	9.7	100
69	Premalignant SOX2 overexpression in the fallopian tubes of ovarian cancer patients: Discovery and validation studies. *EBioMedicine*, **2016**, 10, 137-49	8.8	29
68	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. *Nature Microbiology*, **2016**, 1, 16041	26.6	143
67	Neuroinflammation - using big data to inform clinical practice. *Nature Reviews Neurology*, **2016**, 12, 685-698	13	20
66	Resolving TYK2 locus genotype-to-phenotype differences in autoimmunity. *Science Translational Medicine*, **2016**, 8, 363ra149	17.5	118
65	Trinculo: Bayesian and frequentist multinomial logistic regression for genome-wide association studies of multi-category phenotypes. *Bioinformatics*, **2016**, 32, 1898-900	7.2	18
64	Efficient Coalescent Simulation and Genealogical Analysis for Large Sample Sizes. *PLoS Computational Biology*, **2016**, 12, e1004842	5	287
63	High-Accuracy HLA Type Inference from Whole-Genome Sequencing Data Using Population Reference Graphs. *PLoS Computational Biology*, **2016**, 12, e1005151	5	60
62	Recombination Rate Heterogeneity within Arabidopsis Disease Resistance Genes. *PLoS Genetics*, **2016**, 12, e1006179	6	69

61	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
60	Genetic architecture of artemisinin-resistant Plasmodium falciparum. *Nature Genetics*, **2015**, 47, 226-34	36.3	382
59	The power of gene-based rare variant methods to detect disease-associated variation and test hypotheses about complex disease. *PLoS Genetics*, **2015**, 11, e1005165	6	98
58	Improved genome inference in the MHC using a population reference graph. *Nature Genetics*, **2015**, 47, 682-8	36.3	144
57	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. *Nature Genetics*, **2015**, 47, 717-726	36.3	244
56	Imputation of KIR Types from SNP Variation Data. *American Journal of Human Genetics*, **2015**, 97, 593-607	11	44
55	Class II HLA interactions modulate genetic risk for multiple sclerosis. *Nature Genetics*, **2015**, 47, 1107-1113	36.3	215
54	Stable recombination hotspots in birds. *Science*, **2015**, 350, 928-32	33.3	187
53	Where Next for Genetics and Genomics?. *PLoS Biology*, **2015**, 13, e1002216	9.7	8
52	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. *Nature Communications*, **2015**, 6, 10063	17.4	348
51	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. *Human Molecular Genetics*, **2014**, 23, 3200-11	5.6	179
50	Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. *Nature Genetics*, **2014**, 46, 912-918	36.3	671
49	Nonhuman genetics. Strong male bias drives germline mutation in chimpanzees. *Science*, **2014**, 344, 1272-5	33.3	103
48	Demography and the age of rare variants. *PLoS Genetics*, **2014**, 10, e1004528	6	64
47	Genetic characterization of Greek population isolates reveals strong genetic drift at missense and trait-associated variants. *Nature Communications*, **2014**, 5, 5345	17.4	46
46	Hypervariable antigen genes in malaria have ancient roots. *BMC Evolutionary Biology*, **2013**, 13, 110	3	34
45	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. *Nature Genetics*, **2013**, 45, 1353-60	36.3	934
44	Multiple populations of artemisinin-resistant Plasmodium falciparum in Cambodia. *Nature Genetics*, **2013**, 45, 648-55	36.3	350

43	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. *Nature Communications*, **2013**, 4, 2872	17.4	70
42	Multi-population classical HLA type imputation. *PLoS Computational Biology*, **2013**, 9, e1002877	5	129
41	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	4.4	10
40	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, 20152-7	11.5	51
39	High-throughput microbial population genomics using the Cortex variation assembler. *Bioinformatics*, **2013**, 29, 275-6	7.2	32
38	A fine-scale chimpanzee genetic map from population sequencing. *Science*, **2012**, 336, 193-8	33.3	218
37	TNF receptor 1 genetic risk mirrors outcome of anti-TNF therapy in multiple sclerosis. *Nature*, **2012**, 488, 508-511	50.4	269
36	Estimating recombination rates from genetic variation in humans. *Methods in Molecular Biology*, **2012**, 856, 217-37	1.4	17
35	De novo assembly and genotyping of variants using colored de Bruijn graphs. *Nature Genetics*, **2012** , 44, 226-32	36.3	433
34	Multiple Hodgkin lymphoma-associated loci within the HLA region at chromosome 6p21.3. *Blood*, **2011**, 118, 670-4	2.2	31
33	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, 761-7	36.3	646
32	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. *Nature*, **2011**, 476, 214-9	50.4	1948
31	The variant call format and VCFtools. *Bioinformatics*, **2011**, 27, 2156-8	7.2	6200
30	HLA*IMP--an integrated framework for imputing classical HLA alleles from SNP genotypes. *Bioinformatics*, **2011**, 27, 968-72	7.2	134
29	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. *Nature Genetics*, **2010**, 42, 985-90	36.3	773
28	What drives recombination hotspots to repeat DNA in humans?. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2010**, 365, 1213-8	5.8	46
27	Drive against hotspot motifs in primates implicates the PRDM9 gene in meiotic recombination. *Science*, **2010**, 327, 876-9	33.3	465
26	A genealogical interpretation of principal components analysis. *PLoS Genetics*, **2009**, 5, e1000686	6	317

25	A statistical method for predicting classical HLA alleles from SNP data. *American Journal of Human Genetics*, **2008**, 82, 48-56	11	145
24	Genome-wide detection and characterization of positive selection in human populations. *Nature*, **2007**, 449, 913-8	50.4	1367
23	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
22	The structure of linkage disequilibrium around a selective sweep. *Genetics*, **2007**, 175, 1395-406	4	109
21	Estimating diversifying selection and functional constraint in the presence of recombination. *Genetics*, **2006**, 172, 1411-25	4	210
20	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. *Nature Genetics*, **2006**, 38, 1166-72	36.3	618
19	Perspectives on human genetic variation from the HapMap Project. *PLoS Genetics*, **2005**, 1, e54	6	77
18	A coalescent-based method for detecting and estimating recombination from gene sequences. *Genetics*, **2002**, 160, 1231-41	4	530
17	The impact of age on genetic risk for common diseases		1
16	Genome variation and meiotic recombination in Plasmodium falciparum: insights from deep sequencing of genetic crosses		4
15	A reference dataset of 5.4 million phased human variants validated by genetic inheritance from sequencing a three-generation 17-member pedigree		12
14	Practical Use of Methods for Imputation of HLA Alleles from SNP Genotype Data		15
13	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank		3
12	Genome-wide genetic data on ~500,000 UK Biobank participants		320
11	Identification of host-pathogen-disease relationships using a scalable Multiplex Serology platform in UK Biobank		11
10	Real-time search of all bacterial and viral genomic data		13
9	Systematic classification of shared components of genetic risk for common human diseases		1
8	The origins and relatedness structure of mixed infections vary with local prevalence of P. falciparum malaria		3

7	Dating genomic variants and shared ancestry in population-scale sequencing data	7
6	Inferring the ancestry of everyone	6
5	Mapping the drivers of within-host pathogen evolution using massive data sets	1
4	Integrating long-range connectivity information into de Bruijn graphs	3
3	Parental-fetal interplay of immune genes leads to intrauterine growth restriction	1
2	A unified genealogy of modern and ancient genomes	4
1	High trait variability in optimal polygenic prediction strategy within multiple-ancestry cohorts	4