

Gilean McVean

List of Publications by Year in descending order

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Version: 2024-02-01

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	A unified genealogy of modern and ancient genomes. <i>Science</i> , 2022, 375, eabi8264.	6.0	59
2	Identification of host–pathogen-disease relationships using a scalable multiplex serology platform in UK Biobank. <i>Nature Communications</i> , 2022, 13, 1818.	5.8	28
3	Recommendations for improving statistical inference in population genomics. <i>PLoS Biology</i> , 2022, 20, e3001669.	2.6	60
4	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> , 2021, 148, 157-164.	0.7	48
5	The impact of age on genetic risk for common diseases. <i>PLoS Genetics</i> , 2021, 17, e1009723.	1.5	53
6	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> , 2021, 17, e1009287.	1.5	14
7	Genome-wide analysis of 53,400 people with irritable bowel syndrome highlights shared genetic pathways with mood and anxiety disorders. <i>Nature Genetics</i> , 2021, 53, 1543-1552.	9.4	96
8	Identifying cross-disease components of genetic risk across hospital data in the UK Biobank. <i>Nature Genetics</i> , 2020, 52, 126-134.	9.4	35
9	Detection of simple and complex de novo mutations with multiple reference sequences. <i>Genome Research</i> , 2020, 30, 1154-1169.	2.4	7
10	Accounting for long-range correlations in genome-wide simulations of large cohorts. <i>PLoS Genetics</i> , 2020, 16, e1008619.	1.5	43
11	Dating genomic variants and shared ancestry in population-scale sequencing data. <i>PLoS Biology</i> , 2020, 18, e3000586.	2.6	127
12	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
13	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
14	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
15	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
16	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
17	Accounting for long-range correlations in genome-wide simulations of large cohorts. , 2020, 16, e1008619.		0
18	Mapping the drivers of within-host pathogen evolution using massive data sets. <i>Nature Communications</i> , 2019, 10, 3017.	5.8	6

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19	Inferring whole-genome histories in large population datasets. <i>Nature Genetics</i> , 2019, 51, 1330-1338.	9.4	187
20	Genomic Analysis of <i>Plasmodium vivax</i> in Southern Ethiopia Reveals Selective Pressures in Multiple Parasite Mechanisms. <i>Journal of Infectious Diseases</i> , 2019, 220, 1738-1749.	1.9	50
21	Bayesian meta-analysis across genome-wide association studies of diverse phenotypes. <i>Genetic Epidemiology</i> , 2019, 43, 532-547.	0.6	27
22	HLA*LA”HLA typing from linearly projected graph alignments. <i>Bioinformatics</i> , 2019, 35, 4394-4396.	1.8	88
23	Low-Bias RNA Sequencing of the HIV-2 Genome from Blood Plasma. <i>Journal of Virology</i> , 2019, 93, .	1.5	11
24	Graphical Model Selection for Gaussian Conditional Random Fields in the Presence of Latent Variables. <i>Journal of the American Statistical Association</i> , 2019, 114, 723-734.	1.8	6
25	Ultrafast search of all deposited bacterial and viral genomic data. <i>Nature Biotechnology</i> , 2019, 37, 152-159.	9.4	123
26	The origins and relatedness structure of mixed infections vary with local prevalence of <i>P. falciparum</i> malaria. <i>ELife</i> , 2019, 8, .	2.8	52
27	Integrating long-range connectivity information into de Bruijn graphs. <i>Bioinformatics</i> , 2018, 34, 2556-2565.	1.8	61
28	Deconvolution of multiple infections in <i>Plasmodium falciparum</i> from high throughput sequencing data. <i>Bioinformatics</i> , 2018, 34, 9-15.	1.8	64
29	The UK Biobank resource with deep phenotyping and genomic data. <i>Nature</i> , 2018, 562, 203-209.	13.7	5,221
30	Selfish mutations dysregulating RAS-MAPK signaling are pervasive in aged human testes. <i>Genome Research</i> , 2018, 28, 1779-1790.	2.4	56
31	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. <i>Nature Genetics</i> , 2017, 49, 666-673.	9.4	129
32	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	0.3	47
33	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> , 2017, 27, 157-164.	2.4	338
34	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> , 2017, 26, 3869-3882.	1.4	35
35	Characterisation of the changing genomic landscape of metastatic melanoma using cell free DNA. <i>Npj Genomic Medicine</i> , 2017, 2, 25.	1.7	12
36	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank. <i>Nature Genetics</i> , 2017, 49, 1311-1318.	9.4	56

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37	Structural and regulatory diversity shape HLA-C protein expression levels. Nature Communications, 2017, 8, 15924.	5.8	98
38	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
39	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
40	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
41	Indels, structural variation, and recombination drive genomic diversity in <i>Plasmodium falciparum</i> . Genome Research, 2016, 26, 1288-1299.	2.4	180
42	Premalignant SOX2 overexpression in the fallopian tubes of ovarian cancer patients: Discovery and validation studies. EBioMedicine, 2016, 10, 137-149.	2.7	34
43	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. Nature Microbiology, 2016, 1, 16041.	5.9	247
44	Neuroinflammation " using big data to inform clinical practice. Nature Reviews Neurology, 2016, 12, 685-698.	4.9	29
45	Resolving <i>TYK2</i> locus genotype-to-phenotype differences in autoimmunity. Science Translational Medicine, 2016, 8, 363ra149.	5.8	186
46	Trinculo: Bayesian and frequentist multinomial logistic regression for genome-wide association studies of multi-category phenotypes. Bioinformatics, 2016, 32, 1898-1900.	1.8	26
47	Efficient Coalescent Simulation and Genealogical Analysis for Large Sample Sizes. PLoS Computational Biology, 2016, 12, e1004842.	1.5	547
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	Recombination Rate Heterogeneity within Arabidopsis Disease Resistance Genes. PLoS Genetics, 2016, 12, e1006179.	1.5	94
50	Where Next for Genetics and Genomics?. PLoS Biology, 2015, 13, e1002216.	2.6	9
51	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. Nature Communications, 2015, 6, 10063.	5.8	479
52	Genetic architecture of artemisinin-resistant Plasmodium falciparum. Nature Genetics, 2015, 47, 226-234.	9.4	515
53	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
54	Improved genome inference in the MHC using a population reference graph. Nature Genetics, 2015, 47, 682-688.	9.4	197

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55	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. <i>Nature Genetics</i> , 2015, 47, 717-726.	9.4	310
56	Imputation of KIR Types from SNP Variation Data. <i>American Journal of Human Genetics</i> , 2015, 97, 593-607.	2.6	73
57	Class II HLA interactions modulate genetic risk for multiple sclerosis. <i>Nature Genetics</i> , 2015, 47, 1107-1113.	9.4	312
58	Stable recombination hotspots in birds. <i>Science</i> , 2015, 350, 928-932.	6.0	280
59	Demography and the Age of Rare Variants. <i>PLoS Genetics</i> , 2014, 10, e1004528.	1.5	98
60	Genetic characterization of Greek population isolates reveals strong genetic drift at missense and trait-associated variants. <i>Nature Communications</i> , 2014, 5, 5345.	5.8	60
61	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. <i>Human Molecular Genetics</i> , 2014, 23, 3200-3211.	1.4	222
62	Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. <i>Nature Genetics</i> , 2014, 46, 912-918.	9.4	937
63	Strong male bias drives germline mutation in chimpanzees. <i>Science</i> , 2014, 344, 1272-1275.	6.0	146
64	Hypervariable antigen genes in malaria have ancient roots. <i>BMC Evolutionary Biology</i> , 2013, 13, 110.	3.2	47
65	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. <i>Nature Genetics</i> , 2013, 45, 1353-1360.	9.4	1,213
66	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. <i>Nature Genetics</i> , 2013, 45, 648-655.	9.4	424
67	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. <i>Nature Communications</i> , 2013, 4, 2872.	5.8	77
68	Multi-Population Classical HLA Type Imputation. <i>PLoS Computational Biology</i> , 2013, 9, e1002877.	1.5	157
69	Integrating genealogical and dynamical modelling to infer escape and reversion rates in HIV epitopes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20130696.	1.2	14
70	Contributions of intrinsic mutation rate and selfish selection to levels of de novo <i>HRAS</i> mutations in the paternal germline. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20152-20157.	3.3	70
71	High-throughput microbial population genomics using the Cortex variation assembler. <i>Bioinformatics</i> , 2013, 29, 275-276.	1.8	37
72	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. <i>Science</i> , 2012, 336, 193-198.	6.0	273

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73	TNF receptor 1 genetic risk mirrors outcome of anti-TNF therapy in multiple sclerosis. <i>Nature</i> , 2012, 488, 508-511.	13.7	323
74	Estimating Recombination Rates from Genetic Variation in Humans. <i>Methods in Molecular Biology</i> , 2012, 856, 217-237.	0.4	21
75	De novo assembly and genotyping of variants using colored de Bruijn graphs. <i>Nature Genetics</i> , 2012, 44, 226-232.	9.4	564
76	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , 2011, 476, 214-219.	13.7	2,400
77	The variant call format and VCFtools. <i>Bioinformatics</i> , 2011, 27, 2156-2158.	1.8	11,326
78	Multiple Hodgkin lymphoma-associated loci within the HLA region at chromosome 6p21.3. <i>Blood</i> , 2011, 118, 670-674.	0.6	37
79	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> , 2011, 43, 761-767.	9.4	778
80	HLA*IMP an integrated framework for imputing classical HLA alleles from SNP genotypes. <i>Bioinformatics</i> , 2011, 27, 968-972.	1.8	151
81	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. <i>Nature Genetics</i> , 2010, 42, 985-990.	9.4	918
82	What drives recombination hotspots to repeat DNA in humans?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 1213-1218.	1.8	54
83	Drive Against Hotspot Motifs in Primates Implicates the <i>PRDM9</i> Gene in Meiotic Recombination. <i>Science</i> , 2010, 327, 876-879.	6.0	607
84	A Genealogical Interpretation of Principal Components Analysis. <i>PLoS Genetics</i> , 2009, 5, e1000686.	1.5	462
85	A Statistical Method for Predicting Classical HLA Alleles from SNP Data. <i>American Journal of Human Genetics</i> , 2008, 82, 48-56.	2.6	159
86	The Structure of Linkage Disequilibrium Around a Selective Sweep. <i>Genetics</i> , 2007, 175, 1395-1406.	1.2	138
87	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007, 449, 913-918.	13.7	1,788
88	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007, 449, 851-861.	13.7	4,137
89	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. <i>Nature Genetics</i> , 2006, 38, 1166-1172.	9.4	686
90	Estimating Diversifying Selection and Functional Constraint in the Presence of Recombination. <i>Genetics</i> , 2006, 172, 1411-1425.	1.2	269

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91	Perspectives on Human Genetic Variation from the HapMap Project. PLoS Genetics, 2005, 1, e54.	1.5	93
92	A Coalescent-Based Method for Detecting and Estimating Recombination From Gene Sequences. Genetics, 2002, 160, 1231-1241.	1.2	624