

# Gil Mcvean

## List of Publications by Citations

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56  
papers

17,211  
citations

36  
h-index

58  
g-index

58  
ext. papers

21,613  
ext. citations

22.5  
avg, IF

6.02  
L-index

#	Paper	IF	Citations
56	Integrating common and rare genetic variation in diverse human populations. <i>Nature</i> , <b>2010</b> , 467, 52-8	50.4	2135
55	The UK Biobank resource with deep phenotyping and genomic data. <i>Nature</i> , <b>2018</b> , 562, 203-209	50.4	2108
54	A new multipoint method for genome-wide association studies by imputation of genotypes. <i>Nature Genetics</i> , <b>2007</b> , 39, 906-13	36.3	2040
53	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
52	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
51	A fine-scale map of recombination rates and hotspots across the human genome. <i>Science</i> , <b>2005</b> , 310, 321-4	33.3	836
50	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , <b>2011</b> , 470, 59-65	50.4	833
49	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
48	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. <i>Nature</i> , <b>2010</b> , 464, 713-20	50.4	639
47	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
46	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
45	A common sequence motif associated with recombination hot spots and genome instability in humans. <i>Nature Genetics</i> , <b>2008</b> , 40, 1124-9	36.3	335
44	Genome-wide genetic data on ~500,000 UK Biobank participants		320
43	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
42	Arabidopsis meiotic crossover hot spots overlap with H2A.Z nucleosomes at gene promoters. <i>Nature Genetics</i> , <b>2013</b> , 45, 1327-36	36.3	234
41	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
40	A fine-scale chimpanzee genetic map from population sequencing. <i>Science</i> , <b>2012</b> , 336, 193-8	33.3	218

39	Class II HLA interactions modulate genetic risk for multiple sclerosis. <i>Nature Genetics</i> , <b>2015</b> , 47, 1107-1113	36.3	215
38	The influence of recombination on human genetic diversity. <i>PLoS Genetics</i> , <b>2006</b> , 2, e148	6	185
37	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
36	Recombination rate estimation in the presence of hotspots. <i>Genome Research</i> , <b>2007</b> , 17, 1219-27	9.7	172
35	The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes. <i>Genome Research</i> , <b>2013</b> , 23, 749-61	9.7	150
34	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
33	Improved genome inference in the MHC using a population reference graph. <i>Nature Genetics</i> , <b>2015</b> , 47, 682-8	36.3	144
32	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
31	Multi-population classical HLA type imputation. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1002877	5	129
30	Resolving TYK2 locus genotype-to-phenotype differences in autoimmunity. <i>Science Translational Medicine</i> , <b>2016</b> , 8, 363ra149	17.5	118
29	The structure of linkage disequilibrium around a selective sweep. <i>Genetics</i> , <b>2007</b> , 175, 1395-406	4	109
28	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
27	Inferring whole-genome histories in large population datasets. <i>Nature Genetics</i> , <b>2019</b> , 51, 1330-1338	36.3	80
26	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
25	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
24	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
23	Imputation of KIR Types from SNP Variation Data. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 593-607	11	44
22	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

21	Integrating long-range connectivity information into de Bruijn graphs. <i>Bioinformatics</i> , <b>2018</b> , 34, 2556-2565	36
20	Genome Graphs	34
19	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
18	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
17	Scanning the human genome for signals of selection. <i>Current Opinion in Genetics and Development</i> , <b>2006</b> , 16, 624-9	4.9 23
16	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
15	Neuroinflammation - using big data to inform clinical practice. <i>Nature Reviews Neurology</i> , <b>2016</b> , 12, 685-698	6.9 20
14	Estimating recombination rates from genetic variation in humans. <i>Methods in Molecular Biology</i> , <b>2012</b> , 856, 217-37	1.4 17
13	Practical Use of Methods for Imputation of HLA Alleles from SNP Genotype Data	15
12	A reference dataset of 5.4 million phased human variants validated by genetic inheritance from sequencing a three-generation 17-member pedigree	12
11	Identification of host-pathogen-disease relationships using a scalable Multiplex Serology platform in UK Biobank	11
10	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
9	The impact of age on genetic risk for common diseases. <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009723	6 7
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- 3 A unified genealogy of modern and ancient genomes.. *Science*, **2022**, 375, eabi8264 33.3 1
- 2 Identification of host-pathogen-disease relationships using a scalable multiplex serology platform in UK Biobank.. *Nature Communications*, **2022**, 13, 1818 17.4 1
- 1 Linkage Disequilibrium, Recombination and Haplotype Structure **2019**, 51-86