Gil Mcvean

List of Publications by Year in Descending Order

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	A unified genealogy of modern and ancient genomes.. *Science*, **2022**, 375, eabi8264	33.3	1
55	Identification of host-pathogen-disease relationships using a scalable multiplex serology platform in UK Biobank.. *Nature Communications*, **2022**, 13, 1818	17.4	1
54	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
53	The impact of age on genetic risk for common diseases. *PLoS Genetics*, **2021**, 17, e1009723	6	7
52	Identifying cross-disease components of genetic risk across hospital data in the UK Biobank. *Nature Genetics*, **2020**, 52, 126-134	36.3	22
51	Inferring whole-genome histories in large population datasets. *Nature Genetics*, **2019**, 51, 1330-1338	36.3	80
50	Linkage Disequilibrium, Recombination and Haplotype Structure **2019**, 51-86		
49	Integrating long-range connectivity information into de Bruijn graphs. *Bioinformatics*, **2018**, 34, 2556-2565	7.2	36
48	The UK Biobank resource with deep phenotyping and genomic data. *Nature*, **2018**, 562, 203-209	50.4	2108
47	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
46	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
45	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank. *Nature Genetics*, **2017**, 49, 1311-1318	36.3	38
44	Indels, structural variation, and recombination drive genomic diversity in Plasmodium falciparum. *Genome Research*, **2016**, 26, 1288-99	9.7	100
43	Premalignant SOX2 overexpression in the fallopian tubes of ovarian cancer patients: Discovery and validation studies. *EBioMedicine*, **2016**, 10, 137-49	8.8	29
42	Neuroinflammation - using big data to inform clinical practice. *Nature Reviews Neurology*, **2016**, 12, 685-698	43	20
41	Resolving TYK2 locus genotype-to-phenotype differences in autoimmunity. *Science Translational Medicine*, **2016**, 8, 363ra149	17.5	118
40	High-Accuracy HLA Type Inference from Whole-Genome Sequencing Data Using Population Reference Graphs. *PLoS Computational Biology*, **2016**, 12, e1005151	5	60

39	Improved genome inference in the MHC using a population reference graph. *Nature Genetics*, **2015**, 47, 682-8	36.3	144
38	Imputation of KIR Types from SNP Variation Data. *American Journal of Human Genetics*, **2015**, 97, 593-607	11	44
37	Class II HLA interactions modulate genetic risk for multiple sclerosis. *Nature Genetics*, **2015**, 47, 1107-1113	36.3	215
36	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
35	Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. *Nature Genetics*, **2014**, 46, 912-918	36.3	671
34	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. *Nature Genetics*, **2013**, 45, 1353-60	36.3	934
33	Arabidopsis meiotic crossover hot spots overlap with H2A.Z nucleosomes at gene promoters. *Nature Genetics*, **2013**, 45, 1327-36	36.3	234
32	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. *Nature Communications*, **2013**, 4, 2872	17.4	70
31	The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes. *Genome Research*, **2013**, 23, 749-61	9.7	150
30	Multi-population classical HLA type imputation. *PLoS Computational Biology*, **2013**, 9, e1002877	5	129
29	A fine-scale chimpanzee genetic map from population sequencing. *Science*, **2012**, 336, 193-8	33.3	218
28	TNF receptor 1 genetic risk mirrors outcome of anti-TNF therapy in multiple sclerosis. *Nature*, **2012**, 488, 508-511	50.4	269
27	Estimating recombination rates from genetic variation in humans. *Methods in Molecular Biology*, **2012**, 856, 217-37	1.4	17
26	De novo assembly and genotyping of variants using colored de Bruijn graphs. *Nature Genetics*, **2012** , 44, 226-32	36.3	433
25	Mapping copy number variation by population-scale genome sequencing. *Nature*, **2011**, 470, 59-65	50.4	833
24	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. *Nature*, **2011**, 476, 214-9	50.4	1948
23	HLA*IMP--an integrated framework for imputing classical HLA alleles from SNP genotypes. *Bioinformatics*, **2011**, 27, 968-72	7.2	134
22	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. *Nature*, **2010**, 464, 713-20	50.4	639

21	Integrating common and rare genetic variation in diverse human populations. *Nature*, **2010**, 467, 52-8	50.4	2135
20	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
19	A common sequence motif associated with recombination hot spots and genome instability in humans. *Nature Genetics*, **2008**, 40, 1124-9	36.3	335
18	A statistical method for predicting classical HLA alleles from SNP data. *American Journal of Human Genetics*, **2008**, 82, 48-56	11	145
17	A new multipoint method for genome-wide association studies by imputation of genotypes. *Nature Genetics*, **2007**, 39, 906-13	36.3	2040
16	The structure of linkage disequilibrium around a selective sweep. *Genetics*, **2007**, 175, 1395-406	4	109
15	Recombination rate estimation in the presence of hotspots. *Genome Research*, **2007**, 17, 1219-27	9.7	172
14	The influence of recombination on human genetic diversity. *PLoS Genetics*, **2006**, 2, e148	6	185
13	Scanning the human genome for signals of selection. *Current Opinion in Genetics and Development*, **2006**, 16, 624-9	4.9	23
12	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
11	A fine-scale map of recombination rates and hotspots across the human genome. *Science*, **2005**, 310, 321-4	33.3	836
10	The impact of age on genetic risk for common diseases		1
9	A reference dataset of 5.4 million phased human variants validated by genetic inheritance from sequencing a three-generation 17-member pedigree		12
8	Practical Use of Methods for Imputation of HLA Alleles from SNP Genotype Data		15
7	Genome Graphs		34
6	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank		3
5	Genome-wide genetic data on ~500,000 UK Biobank participants		320
4	Identification of host-pathogen-disease relationships using a scalable Multiplex Serology platform in UK Biobank		11

List of Publications

3	Inferring the ancestry of everyone	6
2	Integrating long-range connectivity information into de Bruijn graphs	3
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