Peter Donnelly

List of Publications by Citations

59 papers	44,583 citations	34 h-index	61 g-index
61 ext. papers	54,203 ext. citations	20.3 avg, IF	7.26 L-index

#	Paper	IF	Citations
59	Inference of population structure using multilocus genotype data. *Genetics*, **2000**, 155, 945-59	4	22315
58	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599
57	A flexible and accurate genotype imputation method for the next generation of genome-wide association studies. *PLoS Genetics*, **2009**, 5, e1000529	6	2866
56	The UK Biobank resource with deep phenotyping and genomic data. *Nature*, **2018**, 562, 203-209	50.4	2108
55	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. *Nature*, **2011**, 476, 214-9	50.4	1948
54	Genome-wide strategies for detecting multiple loci that influence complex diseases. *Nature Genetics*, **2005**, 37, 413-7	36.3	730
53	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
52	Identification of multiple risk variants for ankylosing spondylitis through high-density genotyping of immune-related loci. *Nature Genetics*, **2013**, 45, 730-8	36.3	551
51	Drive against hotspot motifs in primates implicates the PRDM9 gene in meiotic recombination. *Science*, **2010**, 327, 876-9	33.3	465
50	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. *Nature*, **2015**, 518, 102-6	50.4	463
49	Genome-wide genetic data on ~500,000 UK Biobank participants		320
48	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. *Nature Genetics*, **2012**, 44, 328-33	36.3	314
47	The fine-scale genetic structure of the British population. *Nature*, **2015**, 519, 309-314	50.4	298
46	Progress and challenges in genome-wide association studies in humans. *Nature*, **2008**, 456, 728-31	50.4	286
45	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. *Nature Genetics*, **2015**, 47, 717-726	36.3	244
44	Estimating recombination rates from population genetic data. *Genetics*, **2001**, 159, 1299-318	4	222
43	Class II HLA interactions modulate genetic risk for multiple sclerosis. *Nature Genetics*, **2015**, 47, 1107-1113	36.3	215

42	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
41	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. *Science*, **2015**, 348, 666-9	33.3	170
40	Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice. *Nature*, **2016**, 530, 171-176	50.4	135
39	The coalescent process with selfing. *Genetics*, **1997**, 146, 1185-95	4	130
38	Choice of transcripts and software has a large effect on variant annotation. *Genome Medicine*, **2014**, 6, 26	14.4	125
37	Heterogeneity of microsatellite mutations within and between loci, and implications for human demographic histories. *Genetics*, **1998**, 148, 1269-84	4	107
36	Progress and promise in understanding the genetic basis of common diseases. *Proceedings of the Royal Society B: Biological Sciences*, **2015**, 282, 20151684	4.4	98
35	Multiple novel gene-by-environment interactions modify the effect of FTO variants on body mass index. *Nature Communications*, **2016**, 7, 12724	17.4	94
34	Sequencing of human genomes with nanopore technology. *Nature Communications*, **2019**, 10, 1869	17.4	89
33	Common variants in the HLA-DRB1-HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. *Nature Genetics*, **2013**, 45, 208-13	36.3	76
32	Phenome-wide association studies across large population cohorts support drug target validation. *Nature Communications*, **2018**, 9, 4285	17.4	76
31	Factors influencing meiotic recombination revealed by whole-genome sequencing of single sperm. *Science*, **2019**, 363,	33.3	54
30	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. *Nature Communications*, **2014**, 5, 4204	17.4	54
29	Assessing allele-specific expression across multiple tissues from RNA-seq read data. *Bioinformatics*, **2015**, 31, 2497-504	7.2	48
28	Recombination in the human Pseudoautosomal region PAR1. *PLoS Genetics*, **2014**, 10, e1004503	6	47
27	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank. *Nature Genetics*, **2017**, 49, 1311-1318	36.3	38
26	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. *Nature Communications*, **2019**, 10, 551	17.4	34
25	Identifying loci affecting trait variability and detecting interactions in genome-wide association studies. *Nature Genetics*, **2018**, 50, 1608-1614	36.3	34

24	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. *American Journal of Human Genetics*, **2016**, 98, 1092-1100	11	30
23	Likelihoods and simulation methods for a class of nonneutral population genetics models. *Genetics*, **2001**, 159, 853-67	4	28
22	Platypus and echidna genomes reveal mammalian biology and evolution. *Nature*, **2021**, 592, 756-762	50.4	28
21	The Configuration of RPA, RAD51, and DMC1 Binding in Meiosis Reveals the Nature of Critical Recombination Intermediates. *Molecular Cell*, **2020**, 79, 689-701.e10	17.6	27
20	Microsatellite mutations and inferences about human demography. *Genetics*, **2000**, 154, 1793-807	4	27
19	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
18	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
17	Homozygous microdeletion of exon 5 in ZNF277 in a girl with specific language impairment. *European Journal of Human Genetics*, **2014**, 22, 1165-71	5.3	22
16	Multicohort analysis of the maternal age effect on recombination. *Nature Communications*, **2015**, 6, 7846	17.4	21
15	Long-read whole genome sequencing and comparative analysis of six strains of the human pathogen Orientia tsutsugamushi. *PLoS Neglected Tropical Diseases*, **2018**, 12, e0006566	4.8	18
14	The correlation structure of epidemic models. *Mathematical Biosciences*, **1993**, 117, 49-75	3.9	16
13	Insights into Platypus Population Structure and History from Whole-Genome Sequencing. *Molecular Biology and Evolution*, **2018**, 35, 1238-1252	8.3	15
12	Appealing statistics. *Significance*, **2005**, 2, 46-48	0.5	14
11	ZCWPW1 is recruited to recombination hotspots by PRDM9 and is essential for meiotic double strand break repair. *ELife*, **2020**, 9,	8.9	10
10	Where Next for Genetics and Genomics?. *PLoS Biology*, **2015**, 13, e1002216	9.7	8
9	Discussion: Recent Common Ancestors of all Present-Day Individuals. *Advances in Applied Probability*, **1999**, 31, 1027-1035	0.7	7
8	Reply to "Genomic Control to the extreme". *Nature Genetics*, **2004**, 36, 1131-1131	36.3	6
7	Discussion: Recent Common Ancestors of all Present-Day Individuals. *Advances in Applied Probability*, **1999**, 31, 1027-1035	0.7	6

6	Genome-sequencing anniversary. Making sense of the data. *Science*, **2011**, 331, 1024-5	33.3	5
5	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula		4
4	ZCWPW1 is recruited to recombination hotspots by PRDM9, and is essential for meiotic double strand break repair		3
3	Reply to Pembrey et al: ‘ZNF277 microdeletions, specific language impairment and the meiotic mismatch methylation (3M) hypothesis’ *European Journal of Human Genetics*, **2015**, 23, 1113-5	5.3	2
2	Reply to "Comment on ‘Nodal infection in Markovian susceptible-infected-susceptible and susceptible-infected-removed epidemics on networks are non-negatively correlated’". *Physical Review E*, **2018**, 98, 026302	2.4	2
1	Altering the Binding Properties of PRDM9 Partially Restores Fertility across the Species Boundary. *Molecular Biology and Evolution*, **2021**, 38, 5555-5562	8.3	0