Peter Donnelly

List of Publications by Year
in descending order

56 papers	62,290 citations	94433 37 h-index	149698 56 g-index
61 all docs	61 docs citations	61 times ranked	82906 citing authors

#	Article	IF	Citations
1	Inference of Population Structure Using Multilocus Genotype Data. Genetics, 2000, 155, 945-959.	2.9	28,015
2	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
3	The UK Biobank resource with deep phenotyping and genomic data. Nature, 2018, 562, 203-209.	27.8	5,221
4	A Flexible and Accurate Genotype Imputation Method for the Next Generation of Genome-Wide Association Studies. PLoS Genetics, 2009, 5, e1000529.	3.5	3,526
5	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	27.8	2,400
6	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
7	Genome-wide strategies for detecting multiple loci that influence complex diseases. Nature Genetics, 2005, 37, 413-417.	21.4	831
8	Identification of multiple risk variants for ankylosing spondylitis through high-density genotyping of immune-related loci. Nature Genetics, 2013, 45, 730-738.	21.4	699
9	Drive Against Hotspot Motifs in Primates Implicates the PRDM9 Gene in Meiotic Recombination. Science, 2010, 327, 876-879.	12.6	607
10	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	581
11	The fine-scale genetic structure of the British population. Nature, 2015, 519, 309-314.	27.8	416
12	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. Nature Genetics, 2012, 44, 328-333.	21.4	375
13	Progress and challenges in genome-wide association studies in humans. Nature, 2008, 456, 728-731.	27.8	335
14	Class II HLA interactions modulate genetic risk for multiple sclerosis. Nature Genetics, 2015, 47, 1107-1113.	21.4	312
15	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	21.4	310
16	Estimating Recombination Rates From Population Genetic Data. Genetics, 2001, 159, 1299-1318.	2.9	272
17	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	12.6	252
18	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. Human Molecular Genetics, 2014, 23, 3200-3211.	2.9	222

#	Article	IF	Citations
19	Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice. Nature, 2016, 530, 171-176.	27.8	194
20	The Coalescent Process With Selfing. Genetics, 1997, 146, 1185-1195.	2.9	175
21	Choice of transcripts and software has a large effect on variant annotation. Genome Medicine, 2014, 6, 26.	8.2	158
22	Heterogeneity of Microsatellite Mutations Within and Between Loci, and Implications for Human Demographic Histories. Genetics, 1998, 148, 1269-1284.	2.9	154
23	Progress and promise in understanding the genetic basis of common diseases. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20151684.	2.6	147
24	Sequencing of human genomes with nanopore technology. Nature Communications, 2019, 10, 1869.	12.8	140
25	Phenome-wide association studies across large population cohorts support drug target validation. Nature Communications, 2018, 9, 4285.	12.8	134
26	Multiple novel gene-by-environment interactions modify the effect of FTO variants on body mass index. Nature Communications, 2016, 7, 12724.	12.8	132
27	Factors influencing meiotic recombination revealed by whole-genome sequencing of single sperm. Science, 2019, 363, .	12.6	98
28	Assessing allele-specific expression across multiple tissues from RNA-seq read data. Bioinformatics, 2015, 31, 2497-2504.	4.1	90
29	The Configuration of RPA, RAD51, and DMC1 Binding in Meiosis Reveals the Nature of Critical Recombination Intermediates. Molecular Cell, 2020, 79, 689-701.e10.	9.7	87
30	Common variants in the HLA-DRB1â€“HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. Nature Genetics, 2013, 45, 208-213.	21.4	86
31	Platypus and echidna genomes reveal mammalian biology and evolution. Nature, 2021, 592, 756-762.	27.8	85
32	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. Nature Communications, 2014, 5, 4204.	12.8	72
33	Identifying loci affecting trait variability and detecting interactions in genome-wide association studies. Nature Genetics, 2018, 50, 1608-1614.	21.4	68
34	Recombination in the Human Pseudoautosomal Region PAR1. PLoS Genetics, 2014, 10, e1004503.	3.5	66
35	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. Nature Communications, 2019, 10, 551.	12.8	63
36	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank. Nature Genetics, 2017, 49, 1311-1318.	21.4	56

#	Article	IF	Citations
37	Long-read whole genome sequencing and comparative analysis of six strains of the human pathogen Orientia tsutsugamushi. PLoS Neglected Tropical Diseases, 2018, 12, e0006566.	3.0	50
38	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. American Journal of Human Genetics, 2016, 98, 1092-1100.	6.2	39
39	Microsatellite Mutations and Inferences About Human Demography. Genetics, 2000, 154, 1793-1807.	2.9	39
40	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.	2.9	35
41	Likelihoods and Simulation Methods for a Class of Nonneutral Population Genetics Models. Genetics, 2001, 159, 853-867.	2.9	34
42	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
43	ZCWPW1 is recruited to recombination hotspots by PRDM9 and is essential for meiotic double strand break repair. ELife, 2020, 9, .	6.0	31
44	Multicohort analysis of the maternal age effect on recombination. Nature Communications, 2015, 6, 7846.	12.8	29
45	Homozygous microdeletion of exon 5 in ZNF277 in a girl with specific language impairment. European Journal of Human Genetics, 2014, 22, 1165-1171.	2.8	27
46	Insights into Platypus Population Structure and History from Whole-Genome Sequencing. Molecular Biology and Evolution, 2018, 35, 1238-1252.	8.9	27
47	The correlation structure of epidemic models. Mathematical Biosciences, 1993, 117, 49-75.	1.9	19
48	Appealing statistics. Significance, 2005, 2, 46-48.	0.4	18
49	Where Next for Genetics and Genomics?. PLoS Biology, 2015, 13, e1002216.	5.6	9
50	Altering the Binding Properties of PRDM9 Partially Restores Fertility across the Species Boundary. Molecular Biology and Evolution, 2021, 38, 5555-5562.	8.9	9
51	Discussion: Recent Common Ancestors of all Present-Day Individuals. Advances in Applied Probability, 1999, 31, 1027-1035.	0.7	9
52	Reply to "Genomic Control to the extreme". Nature Genetics, 2004, 36, 1131-1131.	21.4	8
53	Discussion: Recent Common Ancestors of all Present-Day Individuals. Advances in Applied Probability, 1999, 31, 1027-1035.	0.7	6
54	Making Sense of the Data. Science, 2011, 331, 1024-1025.	12.6	5

#	Article	IF	Citations
55	Reply to â€œComment on â€˜Nodal infection in Markovian susceptible-infected-susceptible and susceptible-infected-removed epidemics on networks are non-negatively correlated'Ââ€• Physical Review E, 2018, 98, 026302.	2.1	3
56	Reply to Pembrey et al: â€˜ZNF277 microdeletions, specific language impairment and the meiotic mismatch methylation (3M) hypothesisâ€™. European Journal of Human Genetics, 2015, 23, 1113-1115.	2.8	2