

# Peter Donnelly

## List of Publications by Year in descending order

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Version: 2024-02-01

56  
papers

62,290  
citations

94269

37  
h-index

149479

56  
g-index

61  
all docs

61  
docs citations

61  
times ranked

82906  
citing authors

#	ARTICLE	IF	CITATIONS
1	Altering the Binding Properties of PRDM9 Partially Restores Fertility across the Species Boundary. <i>Molecular Biology and Evolution</i> , 2021, 38, 5555-5562.	3.5	9
2	Platypus and echidna genomes reveal mammalian biology and evolution. <i>Nature</i> , 2021, 592, 756-762.	13.7	85
3	The Configuration of RPA, RAD51, and DMC1 Binding in Meiosis Reveals the Nature of Critical Recombination Intermediates. <i>Molecular Cell</i> , 2020, 79, 689-701.e10.	4.5	87
4	ZCWPW1 is recruited to recombination hotspots by PRDM9 and is essential for meiotic double strand break repair. <i>ELife</i> , 2020, 9, .	2.8	31
5	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. <i>Nature Communications</i> , 2019, 10, 551.	5.8	63
6	Sequencing of human genomes with nanopore technology. <i>Nature Communications</i> , 2019, 10, 1869.	5.8	140
7	Factors influencing meiotic recombination revealed by whole-genome sequencing of single sperm. <i>Science</i> , 2019, 363, .	6.0	98
8	Insights into Platypus Population Structure and History from Whole-Genome Sequencing. <i>Molecular Biology and Evolution</i> , 2018, 35, 1238-1252.	3.5	27
9	The UK Biobank resource with deep phenotyping and genomic data. <i>Nature</i> , 2018, 562, 203-209.	13.7	5,221
10	Identifying loci affecting trait variability and detecting interactions in genome-wide association studies. <i>Nature Genetics</i> , 2018, 50, 1608-1614.	9.4	68
11	Phenome-wide association studies across large population cohorts support drug target validation. <i>Nature Communications</i> , 2018, 9, 4285.	5.8	134
12	Long-read whole genome sequencing and comparative analysis of six strains of the human pathogen <i>Orientia tsutsugamushi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006566.	1.3	50
13	Reply to 'Comment on 'Nodal infection in Markovian susceptible-infected-susceptible and susceptible-infected-removed epidemics on networks are non-negatively correlated'' <i>Physical Review E</i> , 2018, 98, 026302.	0.8	3
14	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
15	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
16	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	2.4	31
17	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	13.7	952
18	Multiple novel gene-by-environment interactions modify the effect of FTO variants on body mass index. <i>Nature Communications</i> , 2016, 7, 12724.	5.8	132

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19	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. <i>American Journal of Human Genetics</i> , 2016, 98, 1092-1100.	2.6	39
20	Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice. <i>Nature</i> , 2016, 530, 171-176.	13.7	194
21	Progress and promise in understanding the genetic basis of common diseases. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20151684.	1.2	147
22	Where Next for Genetics and Genomics?. <i>PLoS Biology</i> , 2015, 13, e1002216.	2.6	9
23	Reply to Pembrey et al: "ZNF277 microdeletions, specific language impairment and the meiotic mismatch methylation (3M) hypothesis"™. <i>European Journal of Human Genetics</i> , 2015, 23, 1113-1115.	1.4	2
24	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. <i>Nature Genetics</i> , 2015, 47, 717-726.	9.4	310
25	The fine-scale genetic structure of the British population. <i>Nature</i> , 2015, 519, 309-314.	13.7	416
26	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	6.0	252
27	Assessing allele-specific expression across multiple tissues from RNA-seq read data. <i>Bioinformatics</i> , 2015, 31, 2497-2504.	1.8	90
28	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
29	Multicohort analysis of the maternal age effect on recombination. <i>Nature Communications</i> , 2015, 6, 7846.	5.8	29
30	Class II HLA interactions modulate genetic risk for multiple sclerosis. <i>Nature Genetics</i> , 2015, 47, 1107-1113.	9.4	312
31	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. <i>Nature</i> , 2015, 518, 102-106.	13.7	581
32	Homozygous microdeletion of exon 5 in ZNF277 in a girl with specific language impairment. <i>European Journal of Human Genetics</i> , 2014, 22, 1165-1171.	1.4	27
33	Recombination in the Human Pseudoautosomal Region PAR1. <i>PLoS Genetics</i> , 2014, 10, e1004503.	1.5	66
34	Choice of transcripts and software has a large effect on variant annotation. <i>Genome Medicine</i> , 2014, 6, 26.	3.6	158
35	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
36	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. <i>Nature Communications</i> , 2014, 5, 4204.	5.8	72

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37	Common variants in the HLA-DRB1-HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. <i>Nature Genetics</i> , 2013, 45, 208-213.	9.4	86
38	Identification of multiple risk variants for ankylosing spondylitis through high-density genotyping of immune-related loci. <i>Nature Genetics</i> , 2013, 45, 730-738.	9.4	699
39	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. <i>Nature Genetics</i> , 2012, 44, 328-333.	9.4	375
40	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
41	Making Sense of the Data. <i>Science</i> , 2011, 331, 1024-1025.	6.0	5
42	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
43	A Flexible and Accurate Genotype Imputation Method for the Next Generation of Genome-Wide Association Studies. <i>PLoS Genetics</i> , 2009, 5, e1000529.	1.5	3,526
44	Progress and challenges in genome-wide association studies in humans. <i>Nature</i> , 2008, 456, 728-731.	13.7	335
45	Genome-wide strategies for detecting multiple loci that influence complex diseases. <i>Nature Genetics</i> , 2005, 37, 413-417.	9.4	831
46	Appealing statistics. <i>Significance</i> , 2005, 2, 46-48.	0.3	18
47	Reply to "Genomic Control to the extreme". <i>Nature Genetics</i> , 2004, 36, 1131-1131.	9.4	8
48	Likelihoods and Simulation Methods for a Class of Nonneutral Population Genetics Models. <i>Genetics</i> , 2001, 159, 853-867.	1.2	34
49	Estimating Recombination Rates From Population Genetic Data. <i>Genetics</i> , 2001, 159, 1299-1318.	1.2	272
50	Microsatellite Mutations and Inferences About Human Demography. <i>Genetics</i> , 2000, 154, 1793-1807.	1.2	39
51	Inference of Population Structure Using Multilocus Genotype Data. <i>Genetics</i> , 2000, 155, 945-959.	1.2	28,015
52	Discussion: Recent Common Ancestors of all Present-Day Individuals. <i>Advances in Applied Probability</i> , 1999, 31, 1027-1035.	0.4	6
53	Discussion: Recent Common Ancestors of all Present-Day Individuals. <i>Advances in Applied Probability</i> , 1999, 31, 1027-1035.	0.4	9
54	Heterogeneity of Microsatellite Mutations Within and Between Loci, and Implications for Human Demographic Histories. <i>Genetics</i> , 1998, 148, 1269-1284.	1.2	154

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55	The Coalescent Process With Selfing. <i>Genetics</i> , 1997, 146, 1185-1195.	1.2	175
56	The correlation structure of epidemic models. <i>Mathematical Biosciences</i> , 1993, 117, 49-75.	0.9	19