

# Peter Donnelly

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Altering the Binding Properties of PRDM9 Partially Restores Fertility across the Species Boundary. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 5555-5562	8.3	0
58	Platypus and echidna genomes reveal mammalian biology and evolution. <i>Nature</i> , <b>2021</b> , 592, 756-762	50.4	28
57	The Configuration of RPA, RAD51, and DMC1 Binding in Meiosis Reveals the Nature of Critical Recombination Intermediates. <i>Molecular Cell</i> , <b>2020</b> , 79, 689-701.e10	17.6	27
56	ZCWPW1 is recruited to recombination hotspots by PRDM9 and is essential for meiotic double strand break repair. <i>ELife</i> , <b>2020</b> , 9,	8.9	10
55	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. <i>Nature Communications</i> , <b>2019</b> , 10, 551	17.4	34
54	Sequencing of human genomes with nanopore technology. <i>Nature Communications</i> , <b>2019</b> , 10, 1869	17.4	89
53	Factors influencing meiotic recombination revealed by whole-genome sequencing of single sperm. <i>Science</i> , <b>2019</b> , 363,	33.3	54
52	Insights into Platypus Population Structure and History from Whole-Genome Sequencing. <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 1238-1252	8.3	15
51	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> , <b>2018</b> , 98, 026302	2.4	2
50	The UK Biobank resource with deep phenotyping and genomic data. <i>Nature</i> , <b>2018</b> , 562, 203-209	50.4	2108
49	Identifying loci affecting trait variability and detecting interactions in genome-wide association studies. <i>Nature Genetics</i> , <b>2018</b> , 50, 1608-1614	36.3	34
48	Phenome-wide association studies across large population cohorts support drug target validation. <i>Nature Communications</i> , <b>2018</b> , 9, 4285	17.4	76
47	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> , <b>2018</b> , 12, e0006566	4.8	18
46	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
45	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
44	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , <b>2017</b> , 4, 170179	8.2	22
43	Multiple novel gene-by-environment interactions modify the effect of FTO variants on body mass index. <i>Nature Communications</i> , <b>2016</b> , 7, 12724	17.4	94

42	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. <i>American Journal of Human Genetics</i> , <b>2016</b> , 98, 1092-1100	11	30
41	Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice. <i>Nature</i> , <b>2016</b> , 530, 171-176	50.4	135
40	The genetic architecture of type 2 diabetes. <i>Nature</i> , <b>2016</b> , 536, 41-47	50.4	704
39	Reply to Pembrey et al: ZNF277 microdeletions, specific language impairment and the meiotic mismatch methylation (3M) hypothesis <i>European Journal of Human Genetics</i> , <b>2015</b> , 23, 1113-5	5.3	2
38	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. <i>Nature Genetics</i> , <b>2015</b> , 47, 717-726	36.3	244
37	The fine-scale genetic structure of the British population. <i>Nature</i> , <b>2015</b> , 519, 309-314	50.4	298
36	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , <b>2015</b> , 348, 666-9	33.3	170
35	Assessing allele-specific expression across multiple tissues from RNA-seq read data. <i>Bioinformatics</i> , <b>2015</b> , 31, 2497-504	7.2	48
34	A global reference for human genetic variation. <i>Nature</i> , <b>2015</b> , 526, 68-74	50.4	8599
33	Multicohort analysis of the maternal age effect on recombination. <i>Nature Communications</i> , <b>2015</b> , 6, 7846	17.4	21
32	Class II HLA interactions modulate genetic risk for multiple sclerosis. <i>Nature Genetics</i> , <b>2015</b> , 47, 1107-1113	36.3	215
31	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. <i>Nature</i> , <b>2015</b> , 518, 102-6	50.4	463
30	Progress and promise in understanding the genetic basis of common diseases. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2015</b> , 282, 20151684	4.4	98
29	Where Next for Genetics and Genomics?. <i>PLoS Biology</i> , <b>2015</b> , 13, e1002216	9.7	8
28	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
27	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. <i>Nature Communications</i> , <b>2014</b> , 5, 4204	17.4	54
26	Homozygous microdeletion of exon 5 in ZNF277 in a girl with specific language impairment. <i>European Journal of Human Genetics</i> , <b>2014</b> , 22, 1165-71	5.3	22
25	Recombination in the human Pseudoautosomal region PAR1. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004503	6	47

24	Choice of transcripts and software has a large effect on variant annotation. <i>Genome Medicine</i> , <b>2014</b> , 6, 26	14.4	125
23	Common variants in the HLA-DRB1-HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. <i>Nature Genetics</i> , <b>2013</b> , 45, 208-13	36.3	76
22	Identification of multiple risk variants for ankylosing spondylitis through high-density genotyping of immune-related loci. <i>Nature Genetics</i> , <b>2013</b> , 45, 730-8	36.3	551
21	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. <i>Nature Genetics</i> , <b>2012</b> , 44, 328-33	36.3	314
20	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
19	Genome-sequencing anniversary. Making sense of the data. <i>Science</i> , <b>2011</b> , 331, 1024-5	33.3	5
18	Drive against hotspot motifs in primates implicates the PRDM9 gene in meiotic recombination. <i>Science</i> , <b>2010</b> , 327, 876-9	33.3	465
17	A flexible and accurate genotype imputation method for the next generation of genome-wide association studies. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000529	6	2866
16	Progress and challenges in genome-wide association studies in humans. <i>Nature</i> , <b>2008</b> , 456, 728-31	50.4	286
15	Genome-wide strategies for detecting multiple loci that influence complex diseases. <i>Nature Genetics</i> , <b>2005</b> , 37, 413-7	36.3	730
14	Appealing statistics. <i>Significance</i> , <b>2005</b> , 2, 46-48	0.5	14
13	Reply to "Genomic Control to the extreme". <i>Nature Genetics</i> , <b>2004</b> , 36, 1131-1131	36.3	6
12	Likelihoods and simulation methods for a class of nonneutral population genetics models. <i>Genetics</i> , <b>2001</b> , 159, 853-67	4	28
11	Estimating recombination rates from population genetic data. <i>Genetics</i> , <b>2001</b> , 159, 1299-318	4	222
10	Microsatellite mutations and inferences about human demography. <i>Genetics</i> , <b>2000</b> , 154, 1793-807	4	27
9	Inference of population structure using multilocus genotype data. <i>Genetics</i> , <b>2000</b> , 155, 945-59	4	22315
8	Discussion: Recent Common Ancestors of all Present-Day Individuals. <i>Advances in Applied Probability</i> , <b>1999</b> , 31, 1027-1035	0.7	6
7	Discussion: Recent Common Ancestors of all Present-Day Individuals. <i>Advances in Applied Probability</i> , <b>1999</b> , 31, 1027-1035	0.7	7

6	Heterogeneity of microsatellite mutations within and between loci, and implications for human demographic histories. <i>Genetics</i> , <b>1998</b> , 148, 1269-84	4	107
5	The coalescent process with selfing. <i>Genetics</i> , <b>1997</b> , 146, 1185-95	4	130
4	The correlation structure of epidemic models. <i>Mathematical Biosciences</i> , <b>1993</b> , 117, 49-75	3.9	16
3	ZCWPW1 is recruited to recombination hotspots by PRDM9, and is essential for meiotic double strand break repair		3
2	Genome-wide genetic data on ~500,000 UK Biobank participants		320
1	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula		4