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	Altering the Binding Properties of PRDM9 Partially Restores Fertility across the Species Boundary. Molecular Biology and Evolution, 2021, 38, 5555-5562.	8.9	9
2	Platypus and echidna genomes reveal mammalian biology and evolution. Nature, 2021, 592, 756-762.	27.8	85
3	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
4	ZCWPW1 is recruited to recombination hotspots by PRDM9 and is essential for meiotic double strand break repair. ELife, 2020, 9, .	6.0	31
5	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. Nature Communications, 2019, 10, 551.	12.8	63
6	Sequencing of human genomes with nanopore technology. Nature Communications, 2019, 10, 1869.	12.8	140
7	Factors influencing meiotic recombination revealed by whole-genome sequencing of single sperm. Science, 2019, 363, .	12.6	98
8	Insights into Platypus Population Structure and History from Whole-Genome Sequencing. Molecular Biology and Evolution, 2018, 35, 1238-1252.	8.9	27
9	The UK Biobank resource with deep phenotyping and genomic data. Nature, 2018, 562, 203-209.	27.8	5,221
10	Identifying loci affecting trait variability and detecting interactions in genome-wide association studies. Nature Genetics, 2018, 50, 1608-1614.	21.4	68
11	Phenome-wide association studies across large population cohorts support drug target validation. Nature Communications, 2018, 9, 4285.	12.8	134
12	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
13	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
14	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
15	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank. Nature Genetics, 2017, 49, 1311-1318.	21.4	56
16	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
17	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
18	Multiple novel gene-by-environment interactions modify the effect of FTO variants on body mass index. Nature Communications, 2016, 7, 12724.	12.8	132

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19	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
20	Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice. Nature, 2016, 530, 171-176.	27.8	194
21	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
22	Where Next for Genetics and Genomics?. PLoS Biology, 2015, 13, e1002216.	5.6	9
23	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
24	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	21.4	310
25	The fine-scale genetic structure of the British population. Nature, 2015, 519, 309-314.	27.8	416
26	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	12.6	252
27	Assessing allele-specific expression across multiple tissues from RNA-seq read data. Bioinformatics, 2015, 31, 2497-2504.	4.1	90
28	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
29	Multicohort analysis of the maternal age effect on recombination. Nature Communications, 2015, 6, 7846.	12.8	29
30	Class II HLA interactions modulate genetic risk for multiple sclerosis. Nature Genetics, 2015, 47, 1107-1113.	21.4	312
31	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	581
32	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
33	Recombination in the Human Pseudoautosomal Region PAR1. PLoS Genetics, 2014, 10, e1004503.	3.5	66
34	Choice of transcripts and software has a large effect on variant annotation. Genome Medicine, 2014, 6, 26.	8.2	158
35	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
36	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. Nature Communications, 2014, 5, 4204.	12.8	72

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37	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
38	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
39	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. Nature Genetics, 2012, 44, 328-333.	21.4	375
40	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	27.8	2,400
41	Making Sense of the Data. Science, 2011, 331, 1024-1025.	12.6	5
42	Drive Against Hotspot Motifs in Primates Implicates the PRDM9 Gene in Meiotic Recombination. Science, 2010, 327, 876-879.	12.6	607
43	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
44	Progress and challenges in genome-wide association studies in humans. Nature, 2008, 456, 728-731.	27.8	335
45	Genome-wide strategies for detecting multiple loci that influence complex diseases. Nature Genetics, 2005, 37, 413-417.	21.4	831
46	Appealing statistics. Significance, 2005, 2, 46-48.	0.4	18
47	Reply to "Genomic Control to the extreme". Nature Genetics, 2004, 36, 1131-1131.	21.4	8
48	Likelihoods and Simulation Methods for a Class of Nonneutral Population Genetics Models. Genetics, 2001, 159, 853-867.	2.9	34
49	Estimating Recombination Rates From Population Genetic Data. Genetics, 2001, 159, 1299-1318.	2.9	272
50	Microsatellite Mutations and Inferences About Human Demography. Genetics, 2000, 154, 1793-1807.	2.9	39
51	Inference of Population Structure Using Multilocus Genotype Data. Genetics, 2000, 155, 945-959.	2.9	28,015
52	Discussion: Recent Common Ancestors of all Present-Day Individuals. Advances in Applied Probability, 1999, 31, 1027-1035.	0.7	6
53	Discussion: Recent Common Ancestors of all Present-Day Individuals. Advances in Applied Probability, 1999, 31, 1027-1035.	0.7	9
54	Heterogeneity of Microsatellite Mutations Within and Between Loci, and Implications for Human Demographic Histories. Genetics, 1998, 148, 1269-1284.	2.9	154

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55	The Coalescent Process With Selfing. Genetics, 1997, 146, 1185-1195.	2.9	175
56	The correlation structure of epidemic models. Mathematical Biosciences, 1993, 117, 49-75.	1.9	19