

Molly Przeworski

List of Publications by Citations

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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.

90
papers

9,151
citations

48
h-index

95
g-index

96
ext. papers

10,954
ext. citations

12
avg, IF

6.31
L-index

#	Paper	IF	Citations
90	Molecular evolution of FOXP2, a gene involved in speech and language. <i>Nature</i> , 2002 , 418, 869-72	50.4	1128
89	Linkage disequilibrium in humans: models and data. <i>American Journal of Human Genetics</i> , 2001 , 69, 1-14	11	920
88	The signature of positive selection at randomly chosen loci. <i>Genetics</i> , 2002 , 160, 1179-89	4	374
87	Classic selective sweeps were rare in recent human evolution. <i>Science</i> , 2011 , 331, 920-4	33.3	345
86	How reliable are empirical genomic scans for selective sweeps?. <i>Genome Research</i> , 2006 , 16, 702-12	9.7	296
85	High-resolution mapping of crossovers reveals extensive variation in fine-scale recombination patterns among humans. <i>Science</i> , 2008 , 319, 1395-8	33.3	287
84	Pervasive natural selection in the Drosophila genome?. <i>PLoS Genetics</i> , 2009 , 5, e1000495	6	269
83	A neutral explanation for the correlation of diversity with recombination rates in humans. <i>American Journal of Human Genetics</i> , 2003 , 72, 1527-35	11	231
82	Adjusting the focus on human variation. <i>Trends in Genetics</i> , 2000 , 16, 296-302	8.5	231
81	Fine-scale recombination patterns differ between chimpanzees and humans. <i>Nature Genetics</i> , 2005 , 37, 429-34	36.3	226
80	A fine-scale chimpanzee genetic map from population sequencing. <i>Science</i> , 2012 , 336, 193-8	33.3	218
79	An evolutionary view of human recombination. <i>Nature Reviews Genetics</i> , 2007 , 8, 23-34	30.1	206
78	Determinants of mutation rate variation in the human germline. <i>Annual Review of Genomics and Human Genetics</i> , 2014 , 15, 47-70	9.7	204
77	Multiple instances of ancient balancing selection shared between humans and chimpanzees. <i>Science</i> , 2013 , 339, 1578-82	33.3	204
76	A new approach to estimate parameters of speciation models with application to apes. <i>Genome Research</i> , 2007 , 17, 1505-19	9.7	201
75	Stable recombination hotspots in birds. <i>Science</i> , 2015 , 350, 928-32	33.3	187
74	Natural selection interacts with recombination to shape the evolution of hybrid genomes. <i>Science</i> , 2018 , 360, 656-660	33.3	176

73	Natural selection on genes that underlie human disease susceptibility. <i>Current Biology</i> , 2008 , 18, 883-9	6.3	166
72	Testing models of selection and demography in <i>Drosophila simulans</i> . <i>Genetics</i> , 2002 , 162, 203-16	4	144
71	Variation in the molecular clock of primates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 10607-12	11.5	134
70	Variation in Rural African Gut Microbiota Is Strongly Correlated with Colonization by <i>Entamoeba</i> and Subsistence. <i>PLoS Genetics</i> , 2015 , 11, e1005658	6	134
69	A genome-wide departure from the standard neutral model in natural populations of <i>Drosophila</i> . <i>Genetics</i> , 2000 , 156, 257-68	4	133
68	Evidence for population growth in humans is confounded by fine-scale population structure. <i>Trends in Genetics</i> , 2002 , 18, 559-63	8.5	123
67	Genetic structure of chimpanzee populations. <i>PLoS Genetics</i> , 2007 , 3, e66	6	119
66	Variable prediction accuracy of polygenic scores within an ancestry group. <i>ELife</i> , 2020 , 9,	8.9	112
65	The timing of selection at the human <i>FOXP2</i> gene. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1257-9	8.3	109
64	Evidence for a complex demographic history of chimpanzees. <i>Molecular Biology and Evolution</i> , 2004 , 21, 799-808	8.3	104
63	When did the human population size start increasing?. <i>Genetics</i> , 2000 , 155, 1865-74	4	102
62	The ABO blood group is a trans-species polymorphism in primates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 18493-8	11.5	98
61	Absence of the TAP2 human recombination hotspot in chimpanzees. <i>PLoS Biology</i> , 2004 , 2, e155	9.7	98
60	Regions of lower crossing over harbor more rare variants in African populations of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2001 , 158, 657-65	4	86
59	Variation in human recombination rates and its genetic determinants. <i>PLoS ONE</i> , 2011 , 6, e20321	3.7	84
58	Evidence for positive selection and population structure at the human MAO-A gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 862-7	11.5	82
57	Estimating the time since the fixation of a beneficial allele. <i>Genetics</i> , 2003 , 164, 1667-76	4	79
56	Broad-scale recombination patterns underlying proper disjunction in humans. <i>PLoS Genetics</i> , 2009 , 5, e1000658	6	77

55	Interpreting the Dependence of Mutation Rates on Age and Time. <i>PLoS Biology</i> , 2016 , 14, e1002355	9.7	77
54	Overlooked roles of DNA damage and maternal age in generating human germline mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 9491-9500	11.5	75
53	A genetic method for dating ancient genomes provides a direct estimate of human generation interval in the last 45,000 years. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 5652-7	11.5	75
52	A population genetics-phylogenetics approach to inferring natural selection in coding sequences. <i>PLoS Genetics</i> , 2011 , 7, e1002395	6	72
51	Why is there so little intragenic linkage disequilibrium in humans?. <i>Genetical Research</i> , 2001 , 77, 143-51	1.1	71
50	Repeated losses of PRDM9-directed recombination despite the conservation of PRDM9 across vertebrates. <i>ELife</i> , 2017 , 6,	8.9	70
49	Population genetics of the coral : Toward genomic prediction of bleaching. <i>Science</i> , 2020 , 369,	33.3	69
48	Deconstructing the sources of genotype-phenotype associations in humans. <i>Science</i> , 2019 , 365, 1396-1400	39.3	68
47	Directional positive selection on an allele of arbitrary dominance. <i>Genetics</i> , 2006 , 172, 713-8	4	60
46	Shifts in the intensity of purifying selection: an analysis of genome-wide polymorphism data from two closely related yeast species. <i>Genome Research</i> , 2010 , 20, 1558-73	9.7	57
45	The case of the fickle fingers: how the PRDM9 zinc finger protein specifies meiotic recombination hotspots in humans. <i>PLoS Biology</i> , 2011 , 9, e1001211	9.7	57
44	Large, three-generation human families reveal post-zygotic mosaicism and variability in germline mutation accumulation. <i>ELife</i> , 2019 , 8,	8.9	50
43	Identifying genetic variants that affect viability in large cohorts. <i>PLoS Biology</i> , 2017 , 15, e2002458	9.7	49
42	Human Germline Mutation and the Erratic Evolutionary Clock. <i>PLoS Biology</i> , 2016 , 14, e2000744	9.7	48
41	Measuring intolerance to mutation in human genetics. <i>Nature Genetics</i> , 2019 , 51, 772-776	36.3	47
40	An estimate of the average number of recessive lethal mutations carried by humans. <i>Genetics</i> , 2015 , 199, 1243-54	4	45
39	No effect of recombination on the efficacy of natural selection in primates. <i>Genome Research</i> , 2008 , 18, 544-54	9.7	44
38	Recombination and the frequency spectrum in <i>Drosophila melanogaster</i> and <i>Drosophila simulans</i> . <i>Molecular Biology and Evolution</i> , 2001 , 18, 291-8	8.3	44

37	Different selective pressures shape the evolution of Toll-like receptors in human and African great ape populations. <i>Human Molecular Genetics</i> , 2013 , 22, 4829-40	5.6	38
36	Insights into recombination from patterns of linkage disequilibrium in humans. <i>Genetics</i> , 2004 , 167, 387-97	9.7	38
35	Evaluating the evidence for transmission distortion in human pedigrees. <i>Genetics</i> , 2012 , 191, 215-32	4	34
34	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions. <i>PLoS Biology</i> , 2020 , 18, e3000838	9.7	23
33	Signatures of replication timing, recombination, and sex in the spectrum of rare variants on the human X chromosome and autosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 17916-17924	11.5	22
32	The population genetics of human disease: The case of recessive, lethal mutations. <i>PLoS Genetics</i> , 2017 , 13, e1006915	6	21
31	Ancestry runs deeper than blood: the evolutionary history of ABO points to cryptic variation of functional importance. <i>BioEssays</i> , 2013 , 35, 862-7	4.1	20
30	The rise and fall of the chemoattractant receptor GPR33. <i>Journal of Biological Chemistry</i> , 2005 , 280, 31068-75	9.4	19
29	Variable prediction accuracy of polygenic scores within an ancestry group		18
28	Evolutionary history inferred from the de novo assembly of a nonmodel organism, the blue-eyed black lemur. <i>Molecular Ecology</i> , 2015 , 24, 4392-405	5.7	16
27	Contrasting Determinants of Mutation Rates in Germline and Soma. <i>Genetics</i> , 2017 , 207, 255-267	4	14
26	An evaluation of a hierarchical branching process as a model for species diversification. <i>Paleobiology</i> , 1998 , 24, 498-511	2.6	11
25	The evolution of group differences in changing environments. <i>PLoS Biology</i> , 2021 , 19, e3001072	9.7	10
24	Combining sperm typing and linkage disequilibrium analyses reveals differences in selective pressures or recombination rates across human populations. <i>Genetics</i> , 2007 , 175, 795-804	4	9
23	The convergent evolution of blue iris pigmentation in primates took distinct molecular paths. <i>American Journal of Physical Anthropology</i> , 2013 , 151, 398-407	2.5	8
22	Genetics. Motivating hotspots. <i>Science</i> , 2005 , 310, 247-8	33.3	7
21	Population genetics of the coral <i>Acropora millepora</i> : Towards a genomic predictor of bleaching		7
20	Author response: Variable prediction accuracy of polygenic scores within an ancestry group 2019 ,		6

19	Natural selection interacts with the local recombination rate to shape the evolution of hybrid genomes	6
18	Large, three-generation CEPH families reveal post-zygotic mosaicism and variability in germline mutation accumulation	5
17	Genome-sequencing anniversary. The golden age of human population genetics. <i>Science</i> , 2011 , 331, 547-553	4
16	Mutation saturation for fitness effects at human CpG sites. <i>ELife</i> , 2021 , 10, 8.9	4
15	Overlooked roles of DNA damage and maternal age in generating human germline mutations	4
14	Impact of essential workers in the context of social distancing for epidemic control. <i>PLoS ONE</i> , 2021 , 16, e0255680	3.7
13	Measuring Intolerance to Mutation in Human Genetics	3
12	Signatures of replication timing, recombination and sex in the spectrum of rare variants on the human X chromosome and autosomes	3
11	losses in vertebrates are coupled to those of paralogs and .. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5
10	Lottery, luck, or legacy?. <i>Evolution; International Journal of Organic Evolution</i> , 2022 ,	3.8
9	A paternal bias in germline mutation is widespread across amniotes and can arise independently of cell divisions	1
8	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions	1
7	Impact of essential workers in the context of social distancing for epidemic control	1
6	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions 2020 , 18, e3000838	
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