

Molly Przeworski

List of Publications by Year in descending order

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Version: 2024-02-01

73
papers

12,274
citations

41344

49
h-index

76900

74
g-index

96
all docs

96
docs citations

96
times ranked

13223
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular evolution of FOXP2, a gene involved in speech and language. <i>Nature</i> , 2002, 418, 869-872.	27.8	1,481
2	Linkage Disequilibrium in Humans: Models and Data. <i>American Journal of Human Genetics</i> , 2001, 69, 1-14.	6.2	1,166
3	The Signature of Positive Selection at Randomly Chosen Loci. <i>Genetics</i> , 2002, 160, 1179-1189.	2.9	464
4	Classic Selective Sweeps Were Rare in Recent Human Evolution. <i>Science</i> , 2011, 331, 920-924.	12.6	432
5	How reliable are empirical genomic scans for selective sweeps?. <i>Genome Research</i> , 2006, 16, 702-712.	5.5	352
6	High-Resolution Mapping of Crossovers Reveals Extensive Variation in Fine-Scale Recombination Patterns Among Humans. <i>Science</i> , 2008, 319, 1395-1398.	12.6	340
7	Pervasive Natural Selection in the Drosophila Genome?. <i>PLoS Genetics</i> , 2009, 5, e1000495.	3.5	329
8	Natural selection interacts with recombination to shape the evolution of hybrid genomes. <i>Science</i> , 2018, 360, 656-660.	12.6	314
9	Determinants of Mutation Rate Variation in the Human Germline. <i>Annual Review of Genomics and Human Genetics</i> , 2014, 15, 47-70.	6.2	295
10	Stable recombination hotspots in birds. <i>Science</i> , 2015, 350, 928-932.	12.6	280
11	Adjusting the focus on human variation. <i>Trends in Genetics</i> , 2000, 16, 296-302.	6.7	275
12	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. <i>Science</i> , 2012, 336, 193-198.	12.6	273
13	Variable prediction accuracy of polygenic scores within an ancestry group. <i>ELife</i> , 2020, 9, .	6.0	268
14	Fine-scale recombination patterns differ between chimpanzees and humans. <i>Nature Genetics</i> , 2005, 37, 429-434.	21.4	263
15	A Neutral Explanation for the Correlation of Diversity with Recombination Rates in Humans. <i>American Journal of Human Genetics</i> , 2003, 72, 1527-1535.	6.2	261
16	An evolutionary view of human recombination. <i>Nature Reviews Genetics</i> , 2007, 8, 23-34.	16.3	259
17	Multiple Instances of Ancient Balancing Selection Shared Between Humans and Chimpanzees. <i>Science</i> , 2013, 339, 1578-1582.	12.6	253
18	A new approach to estimate parameters of speciation models with application to apes. <i>Genome Research</i> , 2007, 17, 1505-1519.	5.5	223

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19	Natural Selection on Genes that Underlie Human Disease Susceptibility. <i>Current Biology</i> , 2008, 18, 883-889.	3.9	207
20	Variation in the molecular clock of primates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10607-10612.	7.1	189
21	Testing Models of Selection and Demography in <i>Drosophila simulans</i> . <i>Genetics</i> , 2002, 162, 203-216.	2.9	181
22	Variation in Rural African Gut Microbiota Is Strongly Correlated with Colonization by <i>Entamoeba</i> and Subsistence. <i>PLoS Genetics</i> , 2015, 11, e1005658.	3.5	171
23	Deconstructing the sources of genotype-phenotype associations in humans. <i>Science</i> , 2019, 365, 1396-1400.	12.6	170
24	Population genetics of the coral <i>Acropora millepora</i> : Toward genomic prediction of bleaching. <i>Science</i> , 2020, 369, .	12.6	167
25	A Genome-Wide Departure From the Standard Neutral Model in Natural Populations of <i>Drosophila</i> . <i>Genetics</i> , 2000, 156, 257-268.	2.9	163
26	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.	7.1	155
27	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, 5652-5657.	7.1	141
28	Genetic Structure of Chimpanzee Populations. <i>PLoS Genetics</i> , 2007, 3, e66.	3.5	139
29	When Did the Human Population Size Start Increasing?. <i>Genetics</i> , 2000, 155, 1865-1874.	2.9	133
30	Evidence for population growth in humans is confounded by fine-scale population structure. <i>Trends in Genetics</i> , 2002, 18, 559-563.	6.7	132
31	The Timing of Selection at the Human <i>FOXP2</i> Gene. <i>Molecular Biology and Evolution</i> , 2008, 25, 1257-1259.	8.9	132
32	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, 18493-18498.	7.1	127
33	Large, three-generation human families reveal post-zygotic mosaicism and variability in germline mutation accumulation. <i>ELife</i> , 2019, 8, .	6.0	116
34	Repeated losses of PRDM9-directed recombination despite the conservation of PRDM9 across vertebrates. <i>ELife</i> , 2017, 6, .	6.0	115
35	Evidence for a Complex Demographic History of Chimpanzees. <i>Molecular Biology and Evolution</i> , 2004, 21, 799-808.	8.9	114
36	Interpreting the Dependence of Mutation Rates on Age and Time. <i>PLoS Biology</i> , 2016, 14, e1002355.	5.6	113

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37	Absence of the TAP2 Human Recombination Hotspot in Chimpanzees. <i>PLoS Biology</i> , 2004, 2, e155.	5.6	112
38	Regions of Lower Crossing Over Harbor More Rare Variants in African Populations of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2001, 158, 657-665.	2.9	111
39	Broad-Scale Recombination Patterns Underlying Proper Disjunction in Humans. <i>PLoS Genetics</i> , 2009, 5, e1000658.	3.5	107
40	Variation in Human Recombination Rates and Its Genetic Determinants. <i>PLoS ONE</i> , 2011, 6, e20321.	2.5	101
41	Measuring intolerance to mutation in human genetics. <i>Nature Genetics</i> , 2019, 51, 772-776.	21.4	100
42	Estimating the Time Since the Fixation of a Beneficial Allele. <i>Genetics</i> , 2003, 164, 1667-1676.	2.9	92
43	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, 862-867.	7.1	90
44	Why is there so little intragenic linkage disequilibrium in humans ?. <i>Genetical Research</i> , 2001, 77, 143-151.	0.9	81
45	A Population Genetics-Phylogenetics Approach to Inferring Natural Selection in Coding Sequences. <i>PLoS Genetics</i> , 2011, 7, e1002395.	3.5	78
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, 1558-1573.	5.5	74
47	Directional Positive Selection on an Allele of Arbitrary Dominance. <i>Genetics</i> , 2006, 172, 713-718.	2.9	73
48	Identifying genetic variants that affect viability in large cohorts. <i>PLoS Biology</i> , 2017, 15, e2002458.	5.6	71
49	Human Germline Mutation and the Erratic Evolutionary Clock. <i>PLoS Biology</i> , 2016, 14, e2000744.	5.6	70
50	An Estimate of the Average Number of Recessive Lethal Mutations Carried by Humans. <i>Genetics</i> , 2015, 199, 1243-1254.	2.9	69
51	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions. <i>PLoS Biology</i> , 2020, 18, e3000838.	5.6	64
52	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.	5.6	62
53	Recombination and the Frequency Spectrum in <i>Drosophila melanogaster</i> and <i>Drosophila simulans</i> . <i>Molecular Biology and Evolution</i> , 2001, 18, 291-298.	8.9	55
54	No effect of recombination on the efficacy of natural selection in primates. <i>Genome Research</i> , 2008, 18, 544-554.	5.5	51

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55	Different selective pressures shape the evolution of Toll-like receptors in human and African great ape populations. <i>Human Molecular Genetics</i> , 2013, 22, 4829-4840.	2.9	49
56	Insights Into Recombination From Patterns of Linkage Disequilibrium in Humans. <i>Genetics</i> , 2004, 167, 387-397.	2.9	43
57	Evaluating the Evidence for Transmission Distortion in Human Pedigrees. <i>Genetics</i> , 2012, 191, 215-232.	2.9	43
58	The population genetics of human disease: The case of recessive, lethal mutations. <i>PLoS Genetics</i> , 2017, 13, e1006915.	3.5	42
59	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.	7.1	40
60	The evolution of group differences in changing environments. <i>PLoS Biology</i> , 2021, 19, e3001072.	5.6	37
61	Ancestry runs deeper than blood: The evolutionary history of <i>ABO</i> points to cryptic variation of functional importance. <i>BioEssays</i> , 2013, 35, 862-867.	2.5	26
62	The Rise and Fall of the Chemoattractant Receptor GPR33. <i>Journal of Biological Chemistry</i> , 2005, 280, 31068-31075.	3.4	25
63	Evolutionary history inferred from the de novo assembly of a nonmodel organism, the blue-eyed black lemur. <i>Molecular Ecology</i> , 2015, 24, 4392-4405.	3.9	25
64	Contrasting Determinants of Mutation Rates in Germline and Soma. <i>Genetics</i> , 2017, 207, 255-267.	2.9	24
65	<i>PRDM9</i> losses in vertebrates are coupled to those of paralogs <i>ZCWPW1</i> and <i>ZCWPW2</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	24
66	Mutation saturation for fitness effects at human CpG sites. <i>ELife</i> , 2021, 10, .	6.0	23
67	Lottery, luck, or legacy. A review of "The Genetic Lottery: Why DNA matters for social equality" Evolution; <i>International Journal of Organic Evolution</i> , 2022, 76, 846-853.	2.3	23
68	The convergent evolution of blue iris pigmentation in primates took distinct molecular paths. <i>American Journal of Physical Anthropology</i> , 2013, 151, 398-407.	2.1	14
69	Impact of essential workers in the context of social distancing for epidemic control. <i>PLoS ONE</i> , 2021, 16, e0255680.	2.5	13
70	An evaluation of a hierarchical branching process as a model for species diversification. <i>Paleobiology</i> , 1998, 24, 498-511.	2.0	12
71	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.	2.9	10
72	GENETICS: Motivating Hotspots. <i>Science</i> , 2005, 310, 247-248.	12.6	8

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73	The Golden Age of Human Population Genetics. Science, 2011, 331, 547-547.	12.6	4