

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	<i>PRDM9</i> losses in vertebrates are coupled to those of paralogs <i>ZCWPW1</i> and <i>ZCWPW2</i> . Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	24
2	Lottery, luck, or legacy. A review of “The Genetic Lottery: Why DNA matters for social equality”. Evolution; International Journal of Organic Evolution, 2022, 76, 846-853.	2.3	23
3	Impact of essential workers in the context of social distancing for epidemic control. PLoS ONE, 2021, 16, e0255680.	2.5	13
4	The evolution of group differences in changing environments. PLoS Biology, 2021, 19, e3001072.	5.6	37
5	Mutation saturation for fitness effects at human CpG sites. ELife, 2021, 10, .	6.0	23
6	Population genetics of the coral <i>Acropora millepora</i> : Toward genomic prediction of bleaching. Science, 2020, 369, .	12.6	167
7	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions. PLoS Biology, 2020, 18, e3000838.	5.6	64
8	Variable prediction accuracy of polygenic scores within an ancestry group. ELife, 2020, 9, .	6.0	268
9	Deconstructing the sources of genotype-phenotype associations in humans. Science, 2019, 365, 1396-1400.	12.6	170
10	Overlooked roles of DNA damage and maternal age in generating human germline mutations. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9491-9500.	7.1	155
11	Measuring intolerance to mutation in human genetics. Nature Genetics, 2019, 51, 772-776.	21.4	100
12	Signatures of replication timing, recombination, and sex in the spectrum of rare variants on the human X chromosome and autosomes. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17916-17924.	7.1	40
13	Large, three-generation human families reveal post-zygotic mosaicism and variability in germline mutation accumulation. ELife, 2019, 8, .	6.0	116
14	Natural selection interacts with recombination to shape the evolution of hybrid genomes. Science, 2018, 360, 656-660.	12.6	314
15	Contrasting Determinants of Mutation Rates in Germline and Soma. Genetics, 2017, 207, 255-267.	2.9	24
16	Identifying genetic variants that affect viability in large cohorts. PLoS Biology, 2017, 15, e2002458.	5.6	71
17	The population genetics of human disease: The case of recessive, lethal mutations. PLoS Genetics, 2017, 13, e1006915.	3.5	42
18	Repeated losses of PRDM9-directed recombination despite the conservation of PRDM9 across vertebrates. ELife, 2017, 6, .	6.0	115

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19	Human Germline Mutation and the Erratic Evolutionary Clock. PLoS Biology, 2016, 14, e2000744.	5.6	70
20	A genetic method for dating ancient genomes provides a direct estimate of human generation interval in the last 45,000 years. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5652-5657.	7.1	141
21	Variation in the molecular clock of primates. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10607-10612.	7.1	189
22	Interpreting the Dependence of Mutation Rates on Age and Time. PLoS Biology, 2016, 14, e1002355.	5.6	113
23	Evolutionary history inferred from the de novo assembly of a nonmodel organism, the blue-eyed black lemur. Molecular Ecology, 2015, 24, 4392-4405.	3.9	25
24	An Estimate of the Average Number of Recessive Lethal Mutations Carried by Humans. Genetics, 2015, 199, 1243-1254.	2.9	69
25	Stable recombination hotspots in birds. Science, 2015, 350, 928-932.	12.6	280
26	Variation in Rural African Gut Microbiota Is Strongly Correlated with Colonization by Entamoeba and Subsistence. PLoS Genetics, 2015, 11, e1005658.	3.5	171
27	Determinants of Mutation Rate Variation in the Human Germline. Annual Review of Genomics and Human Genetics, 2014, 15, 47-70.	6.2	295
28	Multiple Instances of Ancient Balancing Selection Shared Between Humans and Chimpanzees. Science, 2013, 339, 1578-1582.	12.6	253
29	The convergent evolution of blue iris pigmentation in primates took distinct molecular paths. American Journal of Physical Anthropology, 2013, 151, 398-407.	2.1	14
30	Ancestry runs deeper than blood: The evolutionary history of <i>ABO</i> points to cryptic variation of functional importance. BioEssays, 2013, 35, 862-867.	2.5	26
31	Different selective pressures shape the evolution of Toll-like receptors in human and African great ape populations. Human Molecular Genetics, 2013, 22, 4829-4840.	2.9	49
32	Evaluating the Evidence for Transmission Distortion in Human Pedigrees. Genetics, 2012, 191, 215-232.	2.9	43
33	The ABO blood group is a trans-species polymorphism in primates. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18493-18498.	7.1	127
34	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. Science, 2012, 336, 193-198.	12.6	273
35	Classic Selective Sweeps Were Rare in Recent Human Evolution. Science, 2011, 331, 920-924.	12.6	432
36	The Golden Age of Human Population Genetics. Science, 2011, 331, 547-547.	12.6	4

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37	A Population Genetics-Phylogenetics Approach to Inferring Natural Selection in Coding Sequences. PLoS Genetics, 2011, 7, e1002395.	3.5	78
38	The Case of the Fickle Fingers: How the PRDM9 Zinc Finger Protein Specifies Meiotic Recombination Hotspots in Humans. PLoS Biology, 2011, 9, e1001211.	5.6	62
39	Variation in Human Recombination Rates and Its Genetic Determinants. PLoS ONE, 2011, 6, e20321.	2.5	101
40	Shifts in the intensity of purifying selection: An analysis of genome-wide polymorphism data from two closely related yeast species. Genome Research, 2010, 20, 1558-1573.	5.5	74
41	Pervasive Natural Selection in the Drosophila Genome?. PLoS Genetics, 2009, 5, e1000495.	3.5	329
42	Broad-Scale Recombination Patterns Underlying Proper Disjunction in Humans. PLoS Genetics, 2009, 5, e1000658.	3.5	107
43	Natural Selection on Genes that Underlie Human Disease Susceptibility. Current Biology, 2008, 18, 883-889.	3.9	207
44	High-Resolution Mapping of Crossovers Reveals Extensive Variation in Fine-Scale Recombination Patterns Among Humans. Science, 2008, 319, 1395-1398.	12.6	340
45	The Timing of Selection at the Human FOXP2 Gene. Molecular Biology and Evolution, 2008, 25, 1257-1259.	8.9	132
46	No effect of recombination on the efficacy of natural selection in primates. Genome Research, 2008, 18, 544-554.	5.5	51
47	Genetic Structure of Chimpanzee Populations. PLoS Genetics, 2007, 3, e66.	3.5	139
48	A new approach to estimate parameters of speciation models with application to apes. Genome Research, 2007, 17, 1505-1519.	5.5	223
49	Combining Sperm Typing and Linkage Disequilibrium Analyses Reveals Differences in Selective Pressures or Recombination Rates Across Human Populations. Genetics, 2007, 175, 795-804.	2.9	10
50	An evolutionary view of human recombination. Nature Reviews Genetics, 2007, 8, 23-34.	16.3	259
51	Directional Positive Selection on an Allele of Arbitrary Dominance. Genetics, 2006, 172, 713-718.	2.9	73
52	How reliable are empirical genomic scans for selective sweeps?. Genome Research, 2006, 16, 702-712.	5.5	352
53	Fine-scale recombination patterns differ between chimpanzees and humans. Nature Genetics, 2005, 37, 429-434.	21.4	263
54	The Rise and Fall of the Chemoattractant Receptor GPR33. Journal of Biological Chemistry, 2005, 280, 31068-31075.	3.4	25

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55	GENETICS: Motivating Hotspots. <i>Science</i> , 2005, 310, 247-248.	12.6	8
56	Evidence for a Complex Demographic History of Chimpanzees. <i>Molecular Biology and Evolution</i> , 2004, 21, 799-808.	8.9	114
57	Insights Into Recombination From Patterns of Linkage Disequilibrium in Humans. <i>Genetics</i> , 2004, 167, 387-397.	2.9	43
58	Absence of the TAP2 Human Recombination Hotspot in Chimpanzees. <i>PLoS Biology</i> , 2004, 2, e155.	5.6	112
59	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
60	Estimating the Time Since the Fixation of a Beneficial Allele. <i>Genetics</i> , 2003, 164, 1667-1676.	2.9	92
61	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
62	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
63	Molecular evolution of FOXP2, a gene involved in speech and language. <i>Nature</i> , 2002, 418, 869-872.	27.8	1,481
64	The Signature of Positive Selection at Randomly Chosen Loci. <i>Genetics</i> , 2002, 160, 1179-1189.	2.9	464
65	Testing Models of Selection and Demography in <i>Drosophila simulans</i> . <i>Genetics</i> , 2002, 162, 203-216.	2.9	181
66	Linkage Disequilibrium in Humans: Models and Data. <i>American Journal of Human Genetics</i> , 2001, 69, 1-14.	6.2	1,166
67	Why is there so little intragenic linkage disequilibrium in humans ?. <i>Genetical Research</i> , 2001, 77, 143-151.	0.9	81
68	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
69	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
70	Adjusting the focus on human variation. <i>Trends in Genetics</i> , 2000, 16, 296-302.	6.7	275
71	When Did the Human Population Size Start Increasing?. <i>Genetics</i> , 2000, 155, 1865-1874.	2.9	133
72	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

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73	An evaluation of a hierarchical branching process as a model for species diversification. <i>Paleobiology</i> , 1998, 24, 498-511.	2.0	12