

Kelley Harris

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7325214/publications.pdf>

Version: 2024-02-01

26
papers

2,478
citations

567281

15
h-index

580821

25
g-index

40
all docs

40
docs citations

40
times ranked

4285
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutational Signatures of Replication Timing and Epigenetic Modification Persist through the Global Divergence of Mutation Spectra across the Great Ape Phylogeny. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	21
2	The Mutationathon highlights the importance of reaching standardization in estimates of pedigree-based germline mutation rates. <i>ELife</i> , 2022, 11, .	6.0	38
3	Resilience integrates concepts in aging research. <i>IScience</i> , 2022, 25, 104199.	4.1	9
4	The apportionment of citations: a scientometric analysis of Lewontin 1972. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200409.	4.0	5
5	A natural mutator allele shapes mutation spectrum variation in mice. <i>Nature</i> , 2022, 605, 497-502.	27.8	38
6	Nonparametric coalescent inference of mutation spectrum history and demography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	34
7	A modified fluctuation assay reveals a natural mutator phenotype that drives mutation spectrum variation within <i>Saccharomyces cerevisiae</i> . <i>ELife</i> , 2021, 10, .	6.0	28
8	Quantifying and contextualizing the impact of bioRxiv preprints through automated social media audience segmentation. <i>PLoS Biology</i> , 2020, 18, e3000860.	5.6	35
9	Selection against archaic hominin genetic variation in regulatory regions. <i>Nature Ecology and Evolution</i> , 2020, 4, 1558-1566.	7.8	40
10	Inferring evolutionary dynamics of mutation rates through the lens of mutation spectrum variation. <i>Current Opinion in Genetics and Development</i> , 2020, 62, 50-57.	3.3	24
11	From a database of genomes to a forest of evolutionary trees. <i>Nature Genetics</i> , 2019, 51, 1306-1307.	21.4	17
12	Genetic rescue and the maintenance of native ancestry. <i>Conservation Genetics</i> , 2019, 20, 59-64.	1.5	37
13	Genomic Evidence of Widespread Admixture from Polar Bears into Brown Bears during the Last Ice Age. <i>Molecular Biology and Evolution</i> , 2018, 35, 1120-1129.	8.9	91
14	The randomness that shapes our DNA. <i>ELife</i> , 2018, 7, .	6.0	7
15	Reading the genome like a history book. <i>Science</i> , 2017, 358, 1265-1265.	12.6	0
16	Rapid evolution of the human mutation spectrum. <i>ELife</i> , 2017, 6, .	6.0	144
17	Q&A: Where did the Neanderthals go?. <i>BMC Biology</i> , 2017, 15, 73.	3.8	3
18	The Genetic Cost of Neanderthal Introgression. <i>Genetics</i> , 2016, 203, 881-891.	2.9	342

#	ARTICLE	IF	CITATIONS
19	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	12.6	449
20	Evidence for recent, population-specific evolution of the human mutation rate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3439-3444.	7.1	170
21	The Projection of a Test Genome onto a Reference Population and Applications to Humans and Archaic Hominins. <i>Genetics</i> , 2014, 198, 1655-1670.	2.9	10
22	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. <i>Cell</i> , 2014, 157, 785-794.	28.9	363
23	Error-prone polymerase activity causes multinucleotide mutations in humans. <i>Genome Research</i> , 2014, 24, 1445-1454.	5.5	92
24	Decoding Coalescent Hidden Markov Models in Linear Time. <i>Lecture Notes in Computer Science</i> , 2014, 8394, 100-114.	1.3	9
25	Inferring Demographic History from a Spectrum of Shared Haplotype Lengths. <i>PLoS Genetics</i> , 2013, 9, e1003521.	3.5	228
26	Estimating Variable Effective Population Sizes from Multiple Genomes: A Sequentially Markov Conditional Sampling Distribution Approach. <i>Genetics</i> , 2013, 194, 647-662.	2.9	187