

Jeffrey D Wall

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

3,934
citations

293460

24
h-index

325983

40
g-index

49
all docs

49
docs citations

49
times ranked

7841
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Resolution Estimates of Crossover and Noncrossover Recombination from a Captive Baboon Colony. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	9
2	Genomic signatures of high-altitude adaptation and chromosomal polymorphism in geladas. <i>Nature Ecology and Evolution</i> , 2022, 6, 630-643.	3.4	13
3	Response to Bakker et al.. <i>Current Biology</i> , 2022, 32, R358-R359.	1.8	1
4	Evolution of genes involved in the unusual genitals of the bear macaque, <i>Macaca arctoides</i> . <i>Ecology and Evolution</i> , 2022, 12, .	0.8	2
5	Genetic profiles of 103,106 individuals in the Taiwan Biobank provide insights into the health and history of Han Chinese. <i>Npj Genomic Medicine</i> , 2021, 6, 10.	1.7	100
6	Genomic Variation and Recent Population Histories of Spotted (<i>Strix occidentalis</i>) and Barred (<i>Strix varia</i>) Owls. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	1
7	Genome-wide diversity in the California condor tracks its prehistoric abundance and decline. <i>Current Biology</i> , 2021, 31, 2939-2946.e5.	1.8	35
8	Accurate assembly of the olive baboon (<i>Papio anubis</i>) genome using long-read and Hi-C data. <i>GigaScience</i> , 2020, 9, .	3.3	18
9	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions. <i>PLoS Biology</i> , 2020, 18, e3000838.	2.6	64
10	Evaluating the quality of the 1000 genomes project data. <i>BMC Genomics</i> , 2019, 20, 620.	1.2	36
11	Analysis of 100 high-coverage genomes from a pedigreed captive baboon colony. <i>Genome Research</i> , 2019, 29, 848-856.	2.4	27
12	Identification of African-Specific Admixture between Modern and Archaic Humans. <i>American Journal of Human Genetics</i> , 2019, 105, 1254-1261.	2.6	16
13	Disentangling Immediate Adaptive Introgression from Selection on Standing Introgressed Variation in Humans. <i>Molecular Biology and Evolution</i> , 2018, 35, 623-630.	3.5	46
14	Whole-Genome Analysis of Introgression Between the Spotted Owl and Barred Owl (<i>Strix</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Genes, <i>Genomes, Genetics</i> , 2018, 8, 3945-3952.	0.8	9
15	Inferring Human Demographic Histories of Non-African Populations from Patterns of Allele Sharing. <i>American Journal of Human Genetics</i> , 2017, 100, 766-772.	2.6	23
16	Response to Hohenlohe et al. .. <i>Science Advances</i> , 2017, 3, e1701233.	4.7	6
17	A hybrid approach for de novo human genome sequence assembly and phasing. <i>Nature Methods</i> , 2016, 13, 587-590.	9.0	225
18	Archaic admixture in human history. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 93-97.	1.5	26

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19	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	13.7	439
20	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242.	13.7	360
21	Whole-genome sequence analysis shows that two endemic species of North American wolf are admixtures of the coyote and gray wolf. <i>Science Advances</i> , 2016, 2, e1501714.	4.7	150
22	Efficient Genome-Wide Sequencing and Low-Coverage Pedigree Analysis from Noninvasively Collected Samples. <i>Genetics</i> , 2016, 203, 699-714.	1.2	76
23	Detecting Recombination Hotspots from Patterns of Linkage Disequilibrium. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2265-2271.	0.8	23
24	Genomewide ancestry and divergence patterns from low-coverage sequencing data reveal a complex history of admixture in wild baboons. <i>Molecular Ecology</i> , 2016, 25, 3469-3483.	2.0	73
25	Whole-genome sequence analyses of Western Central African Pygmy hunter-gatherers reveal a complex demographic history and identify candidate genes under positive natural selection. <i>Genome Research</i> , 2016, 26, 279-290.	2.4	54
26	Model-based analyses of whole-genome data reveal a complex evolutionary history involving archaic introgression in Central African Pygmies. <i>Genome Research</i> , 2016, 26, 291-300.	2.4	87
27	The Time Scale of Recombination Rate Evolution in Great Apes. <i>Molecular Biology and Evolution</i> , 2016, 33, 928-945.	3.5	92
28	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6413-6418.	3.3	75
29	Inference of Gorilla Demographic and Selective History from Whole-Genome Sequence Data. <i>Molecular Biology and Evolution</i> , 2015, 32, 600-612.	3.5	55
30	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	6.0	449
31	Estimating genotype error rates from high-coverage next-generation sequence data. <i>Genome Research</i> , 2014, 24, 1734-1739.	2.4	121
32	Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , 2014, 346, 1113-1118.	6.0	287
33	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	13.7	320
34	Higher Levels of Neanderthal Ancestry in East Asians than in Europeans. <i>Genetics</i> , 2013, 194, 199-209.	1.2	219
35	Incomplete Lineage Sorting Is Common in Extant Gibbon Genera. <i>PLoS ONE</i> , 2013, 8, e53682.	1.1	19
36	Paleopopulation Genetics. <i>Annual Review of Genetics</i> , 2012, 46, 635-649.	3.2	17

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37	Genetic Variation in Native Americans, Inferred from Latino SNP and Resequencing Data. <i>Molecular Biology and Evolution</i> , 2011, 28, 2231-2237.	3.5	25
38	Detecting Ancient Admixture and Estimating Demographic Parameters in Multiple Human Populations. <i>Molecular Biology and Evolution</i> , 2009, 26, 1823-1827.	3.5	113
39	A novel DNA sequence database for analyzing human demographic history. <i>Genome Research</i> , 2008, 18, 1354-1361.	2.4	74
40	Inconsistencies in Neanderthal Genomic DNA Sequences. <i>PLoS Genetics</i> , 2007, 3, e175.	1.5	140