

Ying Zhou

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6275116/publications.pdf>

Version: 2024-02-01

24
papers

2,409
citations

687363

13
h-index

580821

25
g-index

28
all docs

28
docs citations

28
times ranked

3437
citing authors

#	ARTICLE	IF	CITATIONS
1	A One-Penny Imputed Genome from Next-Generation Reference Panels. <i>American Journal of Human Genetics</i> , 2018, 103, 338-348.	6.2	1,168
2	Analysis of Human Sequence Data Reveals Two Pulses of Archaic Denisovan Admixture. <i>Cell</i> , 2018, 173, 53-61.e9.	28.9	271
3	Fast two-stage phasing of large-scale sequence data. <i>American Journal of Human Genetics</i> , 2021, 108, 1880-1890.	6.2	250
4	Ancestral Origins and Genetic History of Tibetan Highlanders. <i>American Journal of Human Genetics</i> , 2016, 99, 580-594.	6.2	208
5	A Fast and Simple Method for Detecting Identity-by-Descent Segments in Large-Scale Data. <i>American Journal of Human Genetics</i> , 2020, 106, 426-437.	6.2	89
6	Differentiated demographic histories and local adaptations between Sherpas and Tibetans. <i>Genome Biology</i> , 2017, 18, 115.	8.8	67
7	Genetic History of Xinjiang's Uyghurs Suggests Bronze Age Multiple-Way Contacts in Eurasia. <i>Molecular Biology and Evolution</i> , 2017, 34, 2572-2582.	8.9	63
8	Distribution of ancestral chromosomal segments in admixed genomes and its implications for inferring population history and admixture mapping. <i>European Journal of Human Genetics</i> , 2014, 22, 930-937.	2.8	30
9	Core component EccB1 of the <i>Mycobacterium tuberculosis</i> type VII secretion system is a periplasmic ATPase. <i>FASEB Journal</i> , 2015, 29, 4804-4814.	0.5	26
10	Quantitating and Dating Recent Gene Flow between European and East Asian Populations. <i>Scientific Reports</i> , 2015, 5, 9500.	3.3	25
11	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. <i>American Journal of Human Genetics</i> , 2022, 109, 1175-1181.	6.2	25
12	Population-Specific Recombination Maps from Segments of Identity by Descent. <i>American Journal of Human Genetics</i> , 2020, 107, 137-148.	6.2	24
13	Length Distribution of Ancestral Tracks under a General Admixture Model and Its Applications in Population History Inference. <i>Scientific Reports</i> , 2016, 6, 20048.	3.3	23
14	Modeling Continuous Admixture Using Admixture-Induced Linkage Disequilibrium. <i>Scientific Reports</i> , 2017, 7, 43054.	3.3	17
15	A new method for modeling coalescent processes with recombination. <i>BMC Bioinformatics</i> , 2014, 15, 273.	2.6	16
16	Discovery and characterization of Ku acetylation in <i>Mycobacterium smegmatis</i> . <i>FEMS Microbiology Letters</i> , 2015, 362, .	1.8	16
17	The β clamp in the <i>Mycobacterium tuberculosis</i> DNA polymerase III replicase promotes polymerization and reduces exonuclease activity. <i>Scientific Reports</i> , 2016, 6, 18418.	3.3	15
18	IBDkin: fast estimation of kinship coefficients from identity by descent segments. <i>Bioinformatics</i> , 2020, 36, 4519-4520.	4.1	15

#	ARTICLE	IF	CITATIONS
19	Structure and function of <i>Mycobacterium smegmatis</i> 7-keto-8-aminopelargonic acid (KAPA) synthase. <i>International Journal of Biochemistry and Cell Biology</i> , 2015, 58, 71-80.	2.8	14
20	Models, methods and tools for ancestry inference and admixture analysis. <i>Quantitative Biology</i> , 2017, 5, 236-250.	0.5	13
21	POPdemog: visualizing population demographic history from simulation scripts. <i>Bioinformatics</i> , 2018, 34, 2854-2855.	4.1	9
22	Protocol for detecting introgressed archaic variants with SPrime. <i>STAR Protocols</i> , 2021, 2, 100550.	1.2	6
23	AdmixSim: A Forward-Time Simulator for Various Complex Scenarios of Population Admixture. <i>Frontiers in Genetics</i> , 2020, 11, 601439.	2.3	4
24	The putative polyketide cyclase MSMEG_0129 from <i>Mycobacterium smegmatis</i> : purification, crystallization and X-ray crystallographic analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 437-442.	0.8	2