

Haiyi Lou

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10430988/publications.pdf>

Version: 2024-02-01

24
papers

1,421
citations

516215

16
h-index

610482

24
g-index

27
all docs

27
docs citations

27
times ranked

2311
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Dissection of Population Substructure of Han Chinese and Its Implication in Association Studies. <i>American Journal of Human Genetics</i> , 2009, 85, 762-774.	2.6	338
2	A Genome-Wide Search for Signals of High-Altitude Adaptation in Tibetans. <i>Molecular Biology and Evolution</i> , 2011, 28, 1003-1011.	3.5	311
3	Ancestral Origins and Genetic History of Tibetan Highlanders. <i>American Journal of Human Genetics</i> , 2016, 99, 580-594.	2.6	208
4	A 3.4-kb Copy-Number Deletion near EPAS1 Is Significantly Enriched in High-Altitude Tibetans but Absent from the Denisovan Sequence. <i>American Journal of Human Genetics</i> , 2015, 97, 54-66.	2.6	69
5	Differentiated demographic histories and local adaptations between Sherpas and Tibetans. <i>Genome Biology</i> , 2017, 18, 115.	3.8	67
6	Genetic History of Xinjiang's Uyghurs Suggests Bronze Age Multiple-Way Contacts in Eurasia. <i>Molecular Biology and Evolution</i> , 2017, 34, 2572-2582.	3.5	63
7	A Map of Copy Number Variations in Chinese Populations. <i>PLoS ONE</i> , 2011, 6, e27341.	1.1	44
8	A panel of ancestry informative markers to estimate and correct potential effects of population stratification in Han Chinese. <i>European Journal of Human Genetics</i> , 2014, 22, 248-253.	1.4	39
9	Genome-wide variants of Eurasian facial shape differentiation and a prospective model of DNA based face prediction. <i>Journal of Genetics and Genomics</i> , 2018, 45, 419-432.	1.7	38
10	Prioritizing natural-selection signals from the deep-sequencing genomic data suggests multi-variant adaptation in Tibetan highlanders. <i>National Science Review</i> , 2019, 6, 1201-1222.	4.6	30
11	<i>De novo</i> assembly of a Tibetan genome and identification of novel structural variants associated with high-altitude adaptation. <i>National Science Review</i> , 2020, 7, 391-402.	4.6	28
12	Genome-wide scans reveal variants at EDAR predominantly affecting hair straightness in Han Chinese and Uyghur populations. <i>Human Genetics</i> , 2016, 135, 1279-1286.	1.8	27
13	Quantitating and Dating Recent Gene Flow between European and East Asian Populations. <i>Scientific Reports</i> , 2015, 5, 9500.	1.6	25
14	A metagenomic approach to dissect the genetic composition of enterotypes in Han Chinese and two Muslim groups. <i>Systematic and Applied Microbiology</i> , 2018, 41, 1-12.	1.2	24
15	Genetic architectures of ADME genes in five Eurasian admixed populations and implications for drug safety and efficacy. <i>Journal of Medical Genetics</i> , 2014, 51, 614-622.	1.5	22
16	Copy number variations and genetic admixtures in three Xinjiang ethnic minority groups. <i>European Journal of Human Genetics</i> , 2015, 23, 536-542.	1.4	22
17	Refining models of archaic admixture in Eurasia with ArchaicSeeker 2.0. <i>Nature Communications</i> , 2021, 12, 6232.	5.8	19
18	Genome-wide comparison of allele-specific gene expression between African and European populations. <i>Human Molecular Genetics</i> , 2018, 27, 1067-1077.	1.4	15

#	ARTICLE	IF	CITATIONS
19	Haplotype-resolved de novo assembly of a Tujia genome suggests the necessity for high-quality population-specific genome references. <i>Cell Systems</i> , 2022, 13, 321-333.e6.	2.9	10
20	Assessing genome-wide copy number variation in the Han Chinese population. <i>Journal of Medical Genetics</i> , 2017, 54, 685-692.	1.5	7
21	A missense point mutation in COL10A1 identified with whole-genome deep sequencing in a 7-generation Pakistan dwarf family. <i>Heredity</i> , 2018, 120, 83-89.	1.2	6
22	Analysis of five deep-sequenced trio-genomes of the Peninsular Malaysia Orang Asli and North Borneo populations. <i>BMC Genomics</i> , 2019, 20, 842.	1.2	3
23	Improved NGS variant calling tool for the PRSS1-PRSS2 locus. <i>Gut</i> , 2023, 72, 210-212.	6.1	3
24	CNVbase: Batch identification of novel and rare copy number variations based on multi-ethnic population data. <i>Journal of Genetics and Genomics</i> , 2017, 44, 367-370.	1.7	1