Hongling Zhang

List of Publications by Year
in descending order

20 papers	286 citations	1039406 9 h-index	996533 15 g-index
21 all docs	21 docs citations	21 times ranked	93 citing authors

#	Article	IF	Citations
1	Fine-Scale Population Admixture Landscape of Tai–Kadai-Speaking Maonan in Southwest China Inferred From Genome-Wide SNP Data. Frontiers in Genetics, 2022, 13, 815285.	1.1	10
2	Developmental Validation of a Rapidly Mutating Y-STR Panel Labeled by Six Fluoresceins for Forensic Research. Frontiers in Genetics, 2022, 13, 777440.	1.1	0
3	Genomic Insights Into the Admixture History of Mongolic- and Tungusic-Speaking Populations From Southwestern East Asia. Frontiers in Genetics, 2021, 12, 685285.	1.1	23
4	The mitochondrial DNA control region sequences from the Chinese sui population of southwestern China. Annals of Human Biology, 2021, 48, 635-640.	0.4	4
5	X-chromosomal STRs for genetic composition analysis of Guizhou Dong group and its phylogenetic relationships with other reference populations. Annals of Human Biology, 2021, , 1-9.	0.4	2
6	Forensic Features and Population Genetic Structure of Dong, Yi, Han, and Chuanqing Human Populations in Southwest China Inferred From Insertion/Deletion Markers. Frontiers in Genetics, 2020, 11, 360.	1.1	17
7	Genome-wide analysis of unrecognised ethnic group Chuanqing people revealing a close affinity with Southern Han Chinese. Annals of Human Biology, 2020, 47, 465-471.	0.4	9
8	Genetic structure and forensic characterisation of 36 Y-chromosomal STR loci in Hmong-Mien-speaking Miao population. Annals of Human Biology, 2020, 47, 541-548.	0.4	11
9	Male-Dominated Migration and Massive Assimilation of Indigenous East Asians in the Formation of Muslim Hui People in Southwest China. Frontiers in Genetics, 2020, 11, 618614.	1.1	11
10	Genetic diversity, structure and forensic characteristics of Hmong–Mien-speaking Miao revealed by autosomal insertion/deletion markers. Molecular Genetics and Genomics, 2019, 294, 1487-1498.	1.0	32
11	Population genetic analysis of 36 Y-chromosomal STRs yields comprehensive insights into the forensic features and phylogenetic relationship of Chinese Tai-Kadai-speaking Bouyei. PLoS ONE, 2019, 14, e0224601.	1.1	15
12	Population genetics, diversity and forensic characteristics of Tai–Kadai-speaking Bouyei revealed by insertion/deletions markers. Molecular Genetics and Genomics, 2019, 294, 1343-1357.	1.0	32
13	Genetic structure and forensic characterisation of 19 X-chromosomal STR loci in Guizhou Sui population. Annals of Human Biology, 2019, 46, 246-253.	0.4	16
14	The mitochondrial DNA control region sequences from the Chinese Miao population of southeastern China. Annals of Human Biology, 2019, 46, 606-609.	0.4	7
15	Forensic genetic polymorphisms and population structure of the Guizhou Bouyei people based on 19 X-STR loci. Annals of Human Biology, 2019, 46, 574-580.	0.4	12
16	Population genetic data of 22 autosomal STRs in Guizhou Bouyei population, Southwestern China. Forensic Science International: Genetics, 2018, 33, e11-e12.	1.6	3
17	Population genetic data of 22 autosomal STRs in the Guizhou Miao population, southwestern China. Forensic Science International: Genetics, 2018, 32, e7-e8.	1.6	6
18	Genetic profile of 23 Y chromosomal STR loci in Guizhou Shui population, southwest China. Forensic Science International: Genetics, 2017, 28, e16-e17.	1.6	17

#	Article	IF	Citations
19	Population genetic data and mutations of 22 autosomal STR loci in Guizhou Han population. Forensic Science International: Genetics, 2017, 29, e29-e30.	1.6	33
20	Genetic profile of 17 Y chromosome STRs in the Guizhou Han population of southwestern China. Forensic Science International: Genetics, 2016, 25, e6-e7.	1.6	21