Guang-Lin He

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105 972 17 24 g-index

121 1,728 3.7 4.55 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
105	Genomic insights into the formation of human populations in East Asia. <i>Nature</i> , 2021 , 591, 413-419	50.4	62
104	Forensic ancestry analysis in two Chinese minority populations using massively parallel sequencing of 165 ancestry-informative SNPs. <i>Electrophoresis</i> , 2018 , 39, 2732-2742	3.6	34
103	Forensic characteristics and phylogenetic analysis of two Han populations from the southern coastal regions of China using 27 Y-STR loci. <i>Forensic Science International: Genetics</i> , 2017 , 31, e17-e23	4.3	33
102	Forensic features and phylogenetic analyses of Sichuan Han population via 23 autosomal STR loci included in the Huaxia Platinum System. <i>International Journal of Legal Medicine</i> , 2018 , 132, 1079-1082	3.1	33
101	Genetic polymorphism investigation of the Chinese Yi minority using PowerPlex Y23 STR amplification system. <i>International Journal of Legal Medicine</i> , 2017 , 131, 663-666	3.1	31
100	Forensic characteristics and phylogenetic analyses of the Chinese Yi population via 19 X-chromosomal STR loci. <i>International Journal of Legal Medicine</i> , 2017 , 131, 1243-1246	3.1	29
99	Massively parallel sequencing of 165 ancestry informative SNPs in two Chinese Tibetan-Burmese minority ethnicities. <i>Forensic Science International: Genetics</i> , 2018 , 34, 141-147	4.3	24
98	X-chromosomal STR-based genetic structure of Sichuan Tibetan minority ethnicity group and its relationships to various groups. <i>International Journal of Legal Medicine</i> , 2018 , 132, 409-413	3.1	24
97	Genetic diversity of 21 autosomal STR loci in the Han population from Sichuan province, Southwest China. <i>Forensic Science International: Genetics</i> , 2017 , 31, e33-e35	4.3	24
96	Inferring the population history of Tai-Kadai-speaking people and southernmost Han Chinese on Hainan Island by genome-wide array genotyping. <i>European Journal of Human Genetics</i> , 2020 , 28, 1111-1	123	23
95	Genetic polymorphisms for 19 X-STR loci of Sichuan Han ethnicity and its comparison with Chinese populations. <i>Legal Medicine</i> , 2017 , 29, 6-12	1.9	22
94	Genetic characteristics and phylogenetic analysis of three Chinese ethnic groups using the Huaxia Platinum System. <i>Scientific Reports</i> , 2018 , 8, 2429	4.9	20
93	Genetic diversity and haplotype analysis of Guizhou Miao identified with 19 X-chromosomal short tandem repeats. <i>International Journal of Legal Medicine</i> , 2019 , 133, 99-101	3.1	19
92	Genetic diversities and phylogenetic analyses of three Chinese main ethnic groups in southwest China: A Y-Chromosomal STR study. <i>Scientific Reports</i> , 2018 , 8, 15339	4.9	19
91	Population Genetic Analysis of Modern and Ancient DNA Variations Yields New Insights Into the Formation, Genetic Structure, and Phylogenetic Relationship of Northern Han Chinese. <i>Frontiers in Genetics</i> , 2019 , 10, 1045	4.5	18
90	Genetic structure and polymorphisms of Gelao ethnicity residing in southwest china revealed by X-chromosomal genetic markers. <i>Scientific Reports</i> , 2018 , 8, 14585	4.9	18
89	Forensic characterization and genetic polymorphisms of 19 X-chromosomal STRs in 1344 Han Chinese individuals and comprehensive population relationship analyses among 20 Chinese groups. <i>PLoS ONE</i> , 2018 , 13, e0204286	3.7	17

88	The potential use of Piwi-interacting RNA biomarkers in forensic body fluid identification: A proof-of-principle study. <i>Forensic Science International: Genetics</i> , 2019 , 39, 129-135	4.3	16	
87	Population genetics, diversity and forensic characteristics of Tai-Kadai-speaking Bouyei revealed by insertion/deletions markers. <i>Molecular Genetics and Genomics</i> , 2019 , 294, 1343-1357	3.1	15	
86	Tai-Kadai-speaking Gelao population: Forensic features, genetic diversity and population structure. <i>Forensic Science International: Genetics</i> , 2019 , 40, e231-e239	4.3	15	
85	Genetic diversity and phylogenetic characteristics of Chinese Tibetan and Yi minority ethnic groups revealed by non-CODIS STR markers. <i>Scientific Reports</i> , 2018 , 8, 5895	4.9	15	
84	Genetic Diversity and Phylogenetic Differentiation of Southwestern Chinese Han: a comprehensive and comparative analysis on 21 non-CODIS STRs. <i>Scientific Reports</i> , 2017 , 7, 13730	4.9	14	
83	A comprehensive exploration of the genetic legacy and forensic features of Afghanistan and Pakistan Mongolian-descent Hazara. <i>Forensic Science International: Genetics</i> , 2019 , 42, e1-e12	4.3	14	
82	Genetic variations and forensic characteristics of Han Chinese population residing in the Pearl River Delta revealed by 23 autosomal STRs. <i>Molecular Biology Reports</i> , 2018 , 45, 1125-1133	2.8	14	
81	The Genomic Formation of Human Populations in East Asia		14	
80	Forensic features, genetic diversity and structure analysis of three Chinese populations using 47 autosomal InDels. <i>Forensic Science International: Genetics</i> , 2020 , 45, 102227	4.3	14	
79	Population data of 19 autosomal STR loci in the Li population from Hainan Province in southernmost China. <i>International Journal of Legal Medicine</i> , 2019 , 133, 429-431	3.1	14	
78	Genetic diversity and phylogenetic study of the Chinese Gelao ethnic minority via 23 Y-STR loci. <i>International Journal of Legal Medicine</i> , 2018 , 132, 1093-1096	3.1	14	
77	Massively parallel sequencing of 124 SNPs included in the precision ID identity panel in three East Asian minority ethnicities. <i>Forensic Science International: Genetics</i> , 2018 , 35, 141-148	4.3	13	
76	Genetic structure and forensic characteristics of Tibeto-Burman-speaking ETsang and Kham Tibetan Highlanders revealed by 27 Y-chromosomal STRs. <i>Scientific Reports</i> , 2019 , 9, 7739	4.9	12	
75	Genetic diversity, structure and forensic characteristics of Hmong-Mien-speaking Miao revealed by autosomal insertion/deletion markers. <i>Molecular Genetics and Genomics</i> , 2019 , 294, 1487-1498	3.1	12	
74	New insights into the fine-scale history of western-eastern admixture of the northwestern Chinese population in the Hexi Corridor via genome-wide genetic legacy. <i>Molecular Genetics and Genomics</i> , 2021 , 296, 631-651	3.1	12	
73	Population Genetic Diversity and Phylogenetic Characteristics for High-Altitude Adaptive Kham Tibetan Revealed by DNATyper 19 Amplification System. <i>Frontiers in Genetics</i> , 2018 , 9, 630	4.5	12	
72	Genetic structure and forensic characterisation of 19 X-chromosomal STR loci in Guizhou Sui population. <i>Annals of Human Biology</i> , 2019 , 46, 246-253	1.7	11	
71	Population genetic analyses of 20 autosomal STR loci in Chinese Han population from Tianjin in Northern China. <i>Forensic Science International: Genetics</i> , 2017 , 27, 184-185	4.3	10	

70	Genetic variation and forensic characterization of highland Tibetan ethnicity reveled by autosomal STR markers. <i>International Journal of Legal Medicine</i> , 2018 , 132, 1097-1102	3.1	10
69	Whole mitochondrial genome analysis of highland Tibetan ethnicity using massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2020 , 44, 102197	4.3	10
68	Developmental validation of a custom panel including 165 Y-SNPs for Chinese Y-chromosomal haplogroups dissection using the ion S5 XL system. <i>Forensic Science International: Genetics</i> , 2019 , 38, 70-76	4.3	10
67	Forensic characteristics and phylogenetic analysis of Hubei Han population in central China using 17 Y-STR loci. <i>Forensic Science International: Genetics</i> , 2017 , 29, e4-e8	4.3	9
66	Expression profile analysis of piwi-interacting RNA in forensically relevant biological fluids. <i>Forensic Science International: Genetics</i> , 2019 , 42, 171-180	4.3	9
65	Fine-scale genetic structure of Tujia and central Han Chinese revealing massive genetic admixture under language borrowing. <i>Journal of Systematics and Evolution</i> , 2021 , 59, 1-20	2.9	9
64	Fine-scale north-to-south genetic admixture profile in Shaanxi Han Chinese revealed by genome-wide demographic history reconstruction. <i>Journal of Systematics and Evolution</i> , 2021 ,	2.9	9
63	Genetic polymorphism and phylogenetic differentiation of the Huaxia Platinum System in three Chinese minority ethnicities. <i>Scientific Reports</i> , 2019 , 9, 3371	4.9	8
62	Massively parallel sequencing of mitogenome sequences reveals the forensic features and maternal diversity of tai-kadai-speaking hlai islanders. <i>Forensic Science International: Genetics</i> , 2020 , 47, 102303	4.3	8
61	Phylogenetic analysis among 27 Chinese populations and genetic polymorphisms of 20 autosomal STR loci in a Chinese Uyghur ethnic minority group. <i>Australian Journal of Forensic Sciences</i> , 2018 , 50, 493	- 5 62	8
60	Forensic Features and Population Genetic Structure of Dong, Yi, Han, and Chuanqing Human Populations in Southwest China Inferred From Insertion/Deletion Markers. <i>Frontiers in Genetics</i> , 2020 , 11, 360	4.5	7
59	Population genetic analysis of Shaanxi male Han Chinese population reveals genetic differentiation and homogenization of East Asians. <i>Molecular Genetics & Enomic Medicine</i> , 2020 , 8, e1209	2.3	7
58	Genetic diversity and phylogenetic structure of four Tibeto-Burman-speaking populations in Tibetan-Yi corridor revealed by insertion/deletion polymorphisms. <i>Molecular Genetics & amp; Genomic Medicine</i> , 2020 , 8, e1140	2.3	7
57	Genetic portrait and phylogenetic analysis of an Aksu Uyghur population based on the 19 X-STR system. <i>International Journal of Legal Medicine</i> , 2019 , 133, 91-93	3.1	7
56	Molecular genetic survey and forensic characterization of Chinese Mongolians via the 47 autosomal insertion/deletion marker. <i>Genomics</i> , 2021 , 113, 2199-2210	4.3	7
55	Genetic diversity and phylogenetic analysis of Chinese Han and Li ethnic populations from Hainan Island by 30 autosomal insertion/deletion polymorphisms. <i>Forensic Sciences Research</i> , 2019 , 1-7	3.6	7
54	Forensic genetic polymorphisms and population structure of the Guizhou Bouyei people based on 19 X-STR loci. <i>Annals of Human Biology</i> , 2019 , 46, 574-580	1.7	7
53	Revisiting the genetic background and phylogenetic structure of five Sino-Tibetan-speaking populations: insights from autosomal InDels. <i>Molecular Genetics and Genomics</i> , 2020 , 295, 969-979	3.1	6

52	Peopling of Tibet Plateau and multiple waves of admixture of Tibetans inferred from both modern and ancient genome-wide data		6	
51	Massively parallel sequencing of 165 ancestry-informative SNPs and forensic biogeographical ancestry inference in three southern Chinese Sinitic/Tai-Kadai populations. <i>Forensic Science International: Genetics</i> , 2021 , 52, 102475	4.3	6	
50	Significant East Asian Affinity of the Sichuan Hui Genomic Structure Suggests the Predominance of the Cultural Diffusion Model in the Genetic Formation Process. <i>Frontiers in Genetics</i> , 2021 , 12, 626710	4.5	6	
49	Genomic Insights Into the Admixture History of Mongolic- and Tungusic-Speaking Populations From Southwestern East Asia. <i>Frontiers in Genetics</i> , 2021 , 12, 685285	4.5	6	
48	Forensic characteristics and phylogenetic analysis of 23 Y-STR loci in the Miao population from Guizhou province, southwest China. <i>Annals of Human Biology</i> , 2019 , 46, 84-87	1.7	6	
47	Genome-wide analysis of unrecognised ethnic group Chuanqing people revealing a close affinity with Southern Han Chinese. <i>Annals of Human Biology</i> , 2020 , 47, 465-471	1.7	5	
46	Haplotype diversity and phylogenetic characteristics for Guanzhong Han population from Northwest China via 38 Y-STRs using Yfiler Platinum Amplification System. <i>Molecular Genetics & Mamp; Genomic Medicine</i> , 2020 , 8, e1187	2.3	5	
45	Chinese population genetic substructure using 23 Y-chromosomal STRs. <i>Forensic Science International: Genetics Supplement Series</i> , 2017 , 6, e110-e111	0.5	5	
44	Genomic Insights into the Demographic History of Southern Chinese		5	
43	Combined Low-/High-Density Modern and Ancient Genome-Wide Data Document Genomic Admixture History of High-Altitude East Asians. <i>Frontiers in Genetics</i> , 2021 , 12, 582357	4.5	5	
42	Fine-Scale Genetic Structure and Natural Selection Signatures of Southwestern Hans Inferred From Patterns of Genome-Wide Allele, Haplotype, and Haplogroup Lineages. <i>Frontiers in Genetics</i> , 2021 , 12, 727821	4.5	5	
41	Genetic insights into the paternal admixture history of Chinese Mongolians via high-resolution customized Y-SNP SNaPshot panels. <i>Forensic Science International: Genetics</i> , 2021 , 54, 102565	4.3	5	
40	Forensic performance of 30 InDels included in the Investigator DIPplex system in Miao population and comprehensive genetic relationship in China. <i>International Journal of Legal Medicine</i> , 2019 , 133, 13	8 <i>9</i> :139	2 ⁴	
39	Population genetics, diversity, forensic characteristics of four Chinese populations inferred from X-chromosomal short tandem repeats. <i>Legal Medicine</i> , 2020 , 43, 101677	1.9	4	
38	Genetic admixture history and forensic characteristics of Turkic-speaking Kyrgyz population via 23 autosomal STRs. <i>Annals of Human Biology</i> , 2019 , 46, 498-501	1.7	4	
37	Genetic substructure and admixture of Mongolians and Kazakhs inferred from genome-wide array genotyping. <i>Annals of Human Biology</i> , 2020 , 47, 620-628	1.7	4	
36	Forensic features and genetic structure of the Hotan Uyghur inferred from 27 forensic markers. <i>Annals of Human Biology</i> , 2019 , 46, 589-600	1.7	4	
35	Peopling History of the Tibetan Plateau and Multiple Waves of Admixture of Tibetans Inferred From Both Ancient and Modern Genome-Wide Data. <i>Frontiers in Genetics</i> , 2021 , 12, 725243	4.5	4	

34	Forensic features and genetic structure of 23 autosomal STRs in Artux Turkic-speaking population residing in southwestern Xinjiang Uyghur Autonomous Region. <i>International Journal of Legal Medicine</i> , 2019 , 133, 1393-1395	3.1	3
33	Genetic variation and population structure analysis of Chinese Wuzhong Hui population using 30 Indels. <i>Annals of Human Biology</i> , 2020 , 47, 300-303	1.7	3
32	Allele frequencies of 15 autosomal STRs in Chinese Nakhi and Yi populations. <i>International Journal of Legal Medicine</i> , 2019 , 133, 105-108	3.1	3
31	Male-Dominated Migration and Massive Assimilation of Indigenous East Asians in the Formation of Muslim Hui People in Southwest China. <i>Frontiers in Genetics</i> , 2020 , 11, 618614	4.5	3
30	Genetic polymorphism of 21 non-CODIS STR loci in Chengdu Han population and its interpopulation analysis between 25 populations in China. <i>Legal Medicine</i> , 2018 , 31, 14-16	1.9	3
29	Genomic insights into the differentiated population admixture structure and demographic history of North East Asians		3
28	Population background exploration and genetic distribution analysis of Pakistan Hazara via 23 autosomal STRs. <i>Annals of Human Biology</i> , 2019 , 46, 514-518	1.7	2
27	Genetic diversity and forensic characteristics of 15 autosomal short tandem repeats in Tibet highland and Guangdong lowland Han Chinese populations. <i>Annals of Human Biology</i> , 2019 , 46, 181-186	1.7	2
26	Phylogenetic relationship and genetic history of Central Asian Kazakhs inferred from Y-chromosome and autosomal variations. <i>Molecular Genetics and Genomics</i> , 2020 , 295, 221-231	3.1	2
25	Genomic Insight Into the Population Structure and Admixture History of Tai-Kadai-Speaking Sui People in Southwest China. <i>Frontiers in Genetics</i> , 2021 , 12, 735084	4.5	2
24	Genomic Insight Into the Population Admixture History of Tungusic-Speaking Manchu People in Northeast China. <i>Frontiers in Genetics</i> , 2021 , 12, 754492	4.5	2
23	Exploitation of a novel slowly mutating Y-STRs set and evaluation of slowly mutating Y-STRs plus Y-SNPs typing strategy in forensic genetics and evolutionary research. <i>Electrophoresis</i> , 2021 , 42, 774-78	5 ^{3.6}	2
22	Screening and selection of 21 novel microhaplotype markers for ancestry inference in ten Chinese subpopulations <i>Forensic Science International: Genetics</i> , 2022 , 58, 102687	4.3	2
21	Comprehensive genetic structure analysis of Han population from Dalian City revealed by 20 Y-STRs. <i>Molecular Genetics & Enomic Medicine</i> , 2020 , 8, e1149	2.3	1
20	Updated population genetic data of 15 autosomal STR loci in a Shandong Han population from East China and genetic relationships among 26 Chinese populations. <i>Annals of Human Biology</i> , 2020 , 47, 472-	477	1
19	Genomic Insights Into the Population History and Biological Adaptation of Southwestern Chinese Hmong-Mien People <i>Frontiers in Genetics</i> , 2021 , 12, 815160	4.5	1
18	Screening and selection of 21 novel microhaplotype markers for ancestry inference in ten Chinese Subp	opula	tiøns
17	Forensic characteristics of Tibeto-Burman-speaking Tibetans revealed by 50 InDels. <i>Forensic Science International: Genetics Supplement Series</i> , 2019 , 7, 758-759	0.5	1

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16	Population genetics and forensic efficiency of 30 InDel markers in four Chinese ethnic groups residing in Sichuan. <i>Forensic Sciences Research</i> , 2020 , 1-5	3.6	1
15	Genetic characterisation for YanXan Han population in Northern Shaanxi Province, China, via 38Y-STRs using YfilerIPlatinum. <i>Annals of Human Biology</i> , 2021 , 48, 327-334	1.7	1
14	Genomic history and forensic characteristics of Sherpa highlanders on the Tibetan Plateau inferred from high-resolution genome-wide InDels and SNPs		1
13	Systematic analysis of safety profile for darunavir and its boosted agents using data mining in the FDA Adverse Event Reporting System database. <i>Scientific Reports</i> , 2021 , 11, 12438	4.9	1
12	New insights from the combined discrimination of modern/ancient genome-wide shared alleles and haplotypes: Differentiated demographic history reconstruction of Tai-Kadai and Sinitic people in South China		1
11	Paternal Y chromosomal genotyping reveals multiple large-scale admixtures in the formation of Lolo-Burmese-speaking populations in southwest China. <i>Annals of Human Biology</i> , 2019 , 46, 581-588	1.7	1
10	Genomic insight into the population history of Central Han Chinese. <i>Annals of Human Biology</i> , 2021 , 48, 49-55	1.7	1
9	Reconstructing the genetic admixture history of Tai-Kadai and Sinitic people: Insights from genome-wide SNP data from South China. <i>Journal of Systematics and Evolution</i> ,	2.9	1
8	The genomic history of southwestern Chinese populations demonstrated massive population migration and admixture among proto-Hmong-Mien speakers and incoming migrants <i>Molecular Genetics and Genomics</i> , 2022 , 297, 241	3.1	О
7	Genomic history and forensic characteristics of Sherpa highlanders on the Tibetan Plateau inferred from high-resolution InDel panel and genome-wide SNPs. <i>Forensic Science International: Genetics</i> , 2022 , 56, 102633	4.3	Ο
6	Expression profile analysis and stability evaluation of 18 small RNAs in the Chinese Han population. <i>Electrophoresis</i> , 2020 , 41, 2021-2028	3.6	Ο
5	Fine-Scale Population Admixture Landscape of Tai-Kadai-Speaking Maonan in Southwest China Inferred From Genome-Wide SNP Data <i>Frontiers in Genetics</i> , 2022 , 13, 815285	4.5	O
4	Genomic Insights Into the Genetic Structure and Natural Selection of Mongolians <i>Frontiers in Genetics</i> , 2021 , 12, 735786	4.5	О
3	Forensic features and genetic structure at insertion/deletion polymorphisms of Chinese Han with other 31 Chinese ethnic groups. <i>Forensic Science International: Genetics Supplement Series</i> , 2019 , 7, 655	-637	
2	Genetic structure and forensic characteristics of the Korean population revealed by GoldenEye 20A. <i>Annals of Human Biology</i> , 2020 , 47, 560-563	1.7	
1	Revisiting the matrilineal lineages and hypoxic adaptation of highland Tibetans. <i>Forensic Science International: Genetics Supplement Series</i> , 2019 , 7, 73-75	0.5	