

# Yiping Hou

## List of Publications by Year in descending order

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177  
papers

3,525  
citations

126708

33  
h-index

205818

48  
g-index

186  
all docs

186  
docs citations

186  
times ranked

2756  
citing authors

#	ARTICLE	IF	CITATIONS
1	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. <i>Forensic Science International: Genetics</i> , 2014, 12, 12-23.	1.6	214
2	A calibrated human Y-chromosomal phylogeny based on resequencing. <i>Genome Research</i> , 2013, 23, 388-395.	2.4	128
3	The G protein $\beta$ subunit $G\beta$ is a tumor suppressor in Sonic hedgehog <sup>3</sup> -driven medulloblastoma. <i>Nature Medicine</i> , 2014, 20, 1035-1042.	15.2	110
4	Screening and confirmation of microRNA markers for forensic body fluid identification. <i>Forensic Science International: Genetics</i> , 2013, 7, 116-123.	1.6	107
5	Developing a DNA methylation assay for human age prediction in blood and bloodstain. <i>Forensic Science International: Genetics</i> , 2015, 17, 129-136.	1.6	77
6	Allele sequences of six new Y-STR loci and haplotypes in the Chinese Han population. <i>Forensic Science International</i> , 2001, 118, 147-152.	1.3	75
7	Forensic ancestry analysis in two Chinese minority populations using massively parallel sequencing of 165 ancestry-informative SNPs. <i>Electrophoresis</i> , 2018, 39, 2732-2742.	1.3	68
8	Forensic characteristics and genetic analysis of both 27 Y-STRs and 143 Y-SNPs in Eastern Han Chinese population. <i>Forensic Science International: Genetics</i> , 2019, 42, e13-e20.	1.6	64
9	A model for data analysis of microRNA expression in forensic body fluid identification. <i>Forensic Science International: Genetics</i> , 2012, 6, 419-423.	1.6	63
10	Collaborative genetic mapping of 12 forensic short tandem repeat (STR) loci on the human X chromosome. <i>Forensic Science International: Genetics</i> , 2012, 6, 778-784.	1.6	60
11	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.	1.2	60
12	Genetic polymorphism investigation of the Chinese Yi minority using PowerPlex <sup>®</sup> Y23 STR amplification system. <i>International Journal of Legal Medicine</i> , 2017, 131, 663-666.	1.2	57
13	Genetic substructure and forensic characteristics of Chinese Hui populations using 157 Y-SNPs and 27 Y-STRs. <i>Forensic Science International: Genetics</i> , 2019, 41, 11-18.	1.6	55
14	Massively parallel sequencing of 32 forensic markers using the Precision ID GlobalFiler <sup>®</sup> , <sup>®</sup> NGS STR Panel and the Ion PGM <sup>®</sup> , <sup>®</sup> System. <i>Forensic Science International: Genetics</i> , 2017, 31, 126-134.	1.6	53
15	Forensic characteristics and phylogenetic analysis of both Y-STR and Y-SNP in the Li and Han ethnic groups from Hainan Island of China. <i>Forensic Science International: Genetics</i> , 2019, 39, e14-e20.	1.6	53
16	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, 1111-1123.	1.4	49
17	Developmental Validation of the Huaxia Platinum System and application in 3 main ethnic groups of China. <i>Scientific Reports</i> , 2016, 6, 31075.	1.6	46
18	Developmental validation of a custom panel including 273 SNPs for forensic application using Ion Torrent PGM. <i>Forensic Science International: Genetics</i> , 2017, 27, 50-57.	1.6	44

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19	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.	1.6	44
20	Asian online Y-STR Haplotype Reference Database. <i>Legal Medicine</i> , 2003, 5, S160-S163.	0.6	42
21	DNA commission of the International Society of Forensic Genetics (ISFG): Recommendations on the interpretation of Y-STR results in forensic analysis. <i>Forensic Science International: Genetics</i> , 2020, 48, 102308.	1.6	42
22	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.	1.6	41
23	The A5.1 allele of the major histocompatibility complex class I chain-related gene A is associated with psoriasis vulgaris in Chinese. <i>British Journal of Dermatology</i> , 2000, 143, 324-329.	1.4	40
24	Differences of DNA methylation profiles between monozygotic twins' blood samples. <i>Molecular Biology Reports</i> , 2013, 40, 5275-5280.	1.0	38
25	Characterization of tissue-specific biomarkers with the expression of circRNAs in forensically relevant body fluids. <i>International Journal of Legal Medicine</i> , 2019, 133, 1321-1331.	1.2	38
26	Population genetics for 23 Y-STR loci in Tibetan in China and confirmation of DYS448 null allele. <i>Forensic Science International: Genetics</i> , 2015, 16, e7-e10.	1.6	37
27	Multi-InDel Analysis for Ancestry Inference of Sub-Populations in China. <i>Scientific Reports</i> , 2016, 6, 39797.	1.6	37
28	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.	1.6	36
29	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.	1.0	36
30	Characteristics of eight X-STR loci for forensic purposes in the Chinese population. <i>International Journal of Legal Medicine</i> , 2011, 125, 127-131.	1.2	35
31	Identification of Saliva Using MicroRNA Biomarkers for Forensic Purpose. <i>Journal of Forensic Sciences</i> , 2015, 60, 702-706.	0.9	35
32	Characterization of microRNA expression profiles in blood and saliva using the Ion Personal Genome Machine <sup>®</sup> System (Ion PGM <sup>™</sup> , <sub>CG</sub> System). <i>Forensic Science International: Genetics</i> , 2016, 20, 140-146.	1.6	35
33	Genetic characteristics and phylogenetic analysis of three Chinese ethnic groups using the Huaxia Platinum System. <i>Scientific Reports</i> , 2018, 8, 2429.	1.6	35
34	Genetic polymorphism of 23 Y-STR loci in the Zhuang minority population in Guangxi of China. <i>International Journal of Legal Medicine</i> , 2015, 129, 737-738.	1.2	34
35	A strategy for co-analysis of microRNAs and DNA. <i>Forensic Science International: Genetics</i> , 2014, 12, 24-29.	1.6	32
36	Direct visualization of membrane architecture of myelinating cells in transgenic mice expressing membrane-anchored EGFP. <i>Genesis</i> , 2014, 52, 341-349.	0.8	31

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37	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.	1.6	31
38	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.	1.6	30
39	CYP1A1 and CYP1B1 genetic polymorphisms and uterine leiomyoma risk in Chinese women. <i>Journal of Assisted Reproduction and Genetics</i> , 2008, 25, 389-394.	1.2	29
40	A novel method for the analysis of 20 multi-locus STR polymorphisms and its forensic application. <i>Electrophoresis</i> , 2014, 35, 487-493.	1.3	29
41	Next Generation Sequencing Plus (NGS+) with Y-chromosomal Markers for Forensic Pedigree Searches. <i>Scientific Reports</i> , 2017, 7, 11324.	1.6	29
42	Parallel Analysis of 124 Universal SNPs for Human Identification by Targeted Semiconductor Sequencing. <i>Scientific Reports</i> , 2015, 5, 18683.	1.6	28
43	Tai-Kadai-speaking Gelao population: Forensic features, genetic diversity and population structure. <i>Forensic Science International: Genetics</i> , 2019, 40, e231-e239.	1.6	27
44	Association of Matrix Metalloproteinases-9 Gene Polymorphisms with Genetic Susceptibility to Esophageal Squamous Cell Carcinoma. <i>DNA and Cell Biology</i> , 2008, 27, 553-557.	0.9	26
45	Genetic variation and forensic characterization of highland Tibetan ethnicity revealed by autosomal STR markers. <i>International Journal of Legal Medicine</i> , 2018, 132, 1097-1102.	1.2	26
46	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.	1.6	26
47	Y chromosome interstitial deletion induced Y-STR allele dropout in AMELY-negative individuals. <i>International Journal of Legal Medicine</i> , 2012, 126, 713-724.	1.2	25
48	Developed and evaluated a multiplex mRNA profiling system for body fluid identification in Chinese Han population. <i>Journal of Clinical Forensic and Legal Medicine</i> , 2015, 35, 73-80.	0.5	25
49	Mutational analysis of 33 autosomal short tandem repeat (STR) loci in southwest Chinese Han population based on trio parentage testing. <i>Forensic Science International: Genetics</i> , 2016, 23, 86-90.	1.6	25
50	Novel P143L polymorphism of the LCAT gene is associated with dyslipidemia in Chinese patients who have coronary atherosclerotic heart disease. <i>Biochemical and Biophysical Research Communications</i> , 2004, 318, 4-10.	1.0	23
51	Maternity exclusion with a very high autosomal STRs kinship index. <i>International Journal of Legal Medicine</i> , 2012, 126, 645-648.	1.2	23
52	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.	1.6	23
53	Validation of the Microreader, 23sp ID system: A new STR 23-plex system for forensic application. <i>Forensic Science International: Genetics</i> , 2017, 27, 67-73.	1.6	22
54	Phylogenetic analysis and forensic characteristics of 12 populations using 23 Y-STR loci. <i>Forensic Science International: Genetics</i> , 2015, 19, 130-133.	1.6	20

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55	Separation/extraction, detection, and interpretation of DNA mixtures in forensic science (review). <i>International Journal of Legal Medicine</i> , 2018, 132, 1247-1261.	1.2	20
56	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.	1.6	20
57	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.	1.6	20
58	Population genetics of 23 Y-STR loci in the Mongolian minority population in Inner Mongolia of China. <i>International Journal of Legal Medicine</i> , 2016, 130, 1509-1511.	1.2	19
59	Genetic structure and polymorphisms of Gelao ethnicity residing in southwest china revealed by X-chromosomal genetic markers. <i>Scientific Reports</i> , 2018, 8, 14585.	1.6	19
60	Genetic structure and forensic characteristics of Tibeto-Burman-speaking Åœ-Tsang and Kham Tibetan Highlanders revealed by 27 Y-chromosomal STRs. <i>Scientific Reports</i> , 2019, 9, 7739.	1.6	19
61	Genetic polymorphism and phylogenetic differentiation of the Huaxia Platinum System in three Chinese minority ethnicities. <i>Scientific Reports</i> , 2019, 9, 3371.	1.6	19
62	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.	1.6	19
63	Whole mitochondrial genome analysis of highland Tibetan ethnicity using massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2020, 44, 102197.	1.6	18
64	The Application of Mitochondrial DNA Cytochrome Oxidase II Gene for the Identification of Forensically Important Blowflies in Western China. <i>American Journal of Forensic Medicine and Pathology</i> , 2007, 28, 308-313.	0.4	17
65	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, 493-502.	0.7	17
66	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.	1.2	17
67	Population Genetic Diversity and Phylogenetic Characteristics for High-Altitude Adaptive Kham Tibetan Revealed by DNATyperTM 19 Amplification System. <i>Frontiers in Genetics</i> , 2018, 9, 630.	1.1	17
68	Expression profile analysis of piwi-interacting RNA in forensically relevant biological fluids. <i>Forensic Science International: Genetics</i> , 2019, 42, 171-180.	1.6	17
69	Evaluation of 12 Multi-InDel markers for forensic ancestry prediction in Asian populations. <i>Forensic Science International: Genetics</i> , 2019, 43, 102155.	1.6	17
70	A novel allele in the promoter of the hepatic lipase is associated with increased concentration of HDL-C and decreased promoter activity. <i>Journal of Lipid Research</i> , 2002, 43, 1595-1601.	2.0	16
71	Characterization and haplotype analysis of 10 novel Y-STR loci in Chinese Han population. <i>Forensic Science International</i> , 2004, 145, 47-55.	1.3	15
72	Carriers of three polymorphisms of cholesteryl ester transfer protein gene are at increased risk to coronary heart disease in a Chinese population. <i>International Journal of Cardiology</i> , 2005, 103, 259-265.	0.8	15

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73	Haplotype of 12 Y-STR loci of the PowerPlex Y-system in Sichuan Han ethnic group in west China. <i>Forensic Science International</i> , 2008, 175, 244-249.	1.3	15
74	Exploring of triallelic SNPs using Pyrosequencing and the SNPshot methods for forensic application. <i>Electrophoresis</i> , 2012, 33, 841-848.	1.3	15
75	Development of a candidate method for forensic microbial genotyping using multiplex pyrosequencing combined with a universal biotinylated primer. <i>Forensic Science International</i> , 2015, 246, e1-e6.	1.3	15
76	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.	1.6	15
77	Genetic structure and forensic parameters of 30 InDels for human identification purposes in 10 Tibetan populations of China. <i>Forensic Science International: Genetics</i> , 2019, 40, e219-e227.	1.6	15
78	Methylation-Based Age Prediction Using Pyrosequencing Platform from Seminal Stains in Han Chinese Males. <i>Journal of Forensic Sciences</i> , 2020, 65, 610-619.	0.9	15
79	A collaborative exercise on DNA methylation-based age prediction and body fluid typing. <i>Forensic Science International: Genetics</i> , 2022, 57, 102656.	1.6	15
80	Population data of 21 non-CODIS STR loci in the Chinese Uygur ethnic minority. <i>Forensic Science International: Genetics</i> , 2014, 13, e1-e2.	1.6	14
81	Chinese population genetic substructure using 23 Y-chromosomal STRs. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e110-e111.	0.1	14
82	Analysis of 15 STR loci in Chinese population from Sichuan in West China. <i>Forensic Science International</i> , 2007, 171, 222-225.	1.3	13
83	BAY61-3606 potentiates the anti-tumor effects of TRAIL against colon cancer through up-regulating DR4 and down-regulating NF- $\kappa$ B. <i>Cancer Letters</i> , 2016, 383, 145-153.	3.2	13
84	Does Bonferroni correction "rescue" the deviation from Hardy-Weinberg equilibrium?. <i>Forensic Science International: Genetics</i> , 2020, 46, 102254.	1.6	13
85	Characterization of sequence variation at 30 autosomal STRs in Chinese Han and Tibetan populations. <i>Electrophoresis</i> , 2020, 41, 194-201.	1.3	13
86	Genetic structure and paternal admixture of the modern Chinese Zhuang population based on 37 Y-STRs and 233 Y-SNPs. <i>Forensic Science International: Genetics</i> , 2022, 58, 102681.	1.6	13
87	D20S161 data for three ethnic populations and forensic validation. <i>International Journal of Legal Medicine</i> , 1999, 112, 400-402.	1.2	12
88	Genetic polymorphisms of 22 autosomal STR loci in Chinese Han population. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e45-e47.	0.1	12
89	Developmental validation of the Yfiler Platinum PCR Amplification Kit for forensic genetic caseworks and databases. <i>Electrophoresis</i> , 2021, 42, 126-133.	1.3	12
90	Genetic reconstruction and phylogenetic analysis by 193 Y-SNPs and 27 Y-STRs in a Chinese Yi ethnic group. <i>Electrophoresis</i> , 2021, 42, 1480-1487.	1.3	12

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91	Screening and selection of 21 novel microhaplotype markers for ancestry inference in ten Chinese subpopulations. <i>Forensic Science International: Genetics</i> , 2022, 58, 102687.	1.6	12
92	Characterization of eight Y-STR loci and haplotypes in a Chinese Han population. <i>International Journal of Legal Medicine</i> , 2003, 117, 263-270.	1.2	11
93	Decreased expression of repulsive guidance molecule member A by DNA methylation in colorectal cancer is related to tumor progression. <i>Oncology Reports</i> , 2012, 27, 1653-9.	1.2	11
94	Microarray expression profile of circular RNAs in human body fluids. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e55-e56.	0.1	11
95	Exploring of new Y-chromosome SNP loci using Pyrosequencing and the SNaPshot methods. <i>International Journal of Legal Medicine</i> , 2012, 126, 825-833.	1.2	10
96	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.	1.6	10
97	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, 774-785.	1.3	10
98	Identification of body fluid using tissue-specific DNA methylation markers. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e151-e153.	0.1	9
99	Screening of Multi-InDel markers on X-chromosome for forensic purpose. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e42-e44.	0.1	9
100	Use of multi-InDels as novel markers to analyze 13 X-chromosome haplotype loci for forensic purposes. <i>Electrophoresis</i> , 2015, 36, 2931-2938.	1.3	9
101	Population study and mutation analysis for 28 short tandem repeat loci in southwest Chinese Han population. <i>Journal of Clinical Forensic and Legal Medicine</i> , 2016, 44, 10-13.	0.5	9
102	Northern gene flow into southeastern East Asians inferred from genome-wide array genotyping. <i>Journal of Systematics and Evolution</i> , 2023, 61, 179-197.	1.6	9
103	Multiplex Mutagenically Separated Polymerase Chain Reaction Assay for Rapid Detection of Human Mitochondrial DNA Variations in Coding Area. <i>Croatian Medical Journal</i> , 2008, 49, 32-38.	0.2	8
104	Developing a multiplex mtSNP assay for forensic application in Han Chinese based on mtDNA phylogeny and hot spot. <i>Electrophoresis</i> , 2015, 36, 633-639.	1.3	8
105	Massively parallel sequencing of 231 autosomal SNPs with a custom panel: a SNP typing assay developed for human identification with Ion Torrent PGM. <i>Forensic Sciences Research</i> , 2017, 2, 26-33.	0.9	8
106	Exploring of microRNA markers for semen stains using massively parallel sequencing. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e107-e109.	0.1	8
107	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> , 2022, 7, 189-195.	0.9	8
108	Molecular genetic survey and forensic characterization of Chinese Mongolians via the 47 autosomal insertion/deletion marker. <i>Genomics</i> , 2021, 113, 2199-2210.	1.3	8

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109	Age-associated DNA methylation determination of semen by pyrosequencing in Chinese Han population. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e99-e100.	0.1	7
110	Genetic variation and population structure analysis of Chinese Wuzhong Hui population using 30 Indels. <i>Annals of Human Biology</i> , 2020, 47, 300-303.	0.4	7
111	Population genetics, diversity, forensic characteristics of four Chinese populations inferred from X-chromosomal short tandem repeats. <i>Legal Medicine</i> , 2020, 43, 101677.	0.6	7
112	Paternal genetic structure of Kyrgyz ethnic group in China revealed by high-resolution Y-chromosome STRs and SNPs. <i>Electrophoresis</i> , 2021, 42, 1892-1899.	1.3	7
113	Single-nucleotide polymorphisms in the lipoprotein lipase gene associated with coronary heart disease in Chinese. <i>European Journal of Pharmacology</i> , 2002, 454, 9-18.	1.7	6
114	Diatom taxa identification based on single-cell isolation and rDNA sequencing. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e308-e309.	0.1	6
115	A case study of SNPSTR efficiency in paternity testing with locus incompatibility. <i>Forensic Science International: Genetics</i> , 2014, 9, 72-75.	1.6	6
116	Comprehensive mutation analysis of 53 Y-STR markers in father-son pairs. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e57-e58.	0.1	6
117	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.	0.6	6
118	Forensic nanopore sequencing of microhaplotype markers using QitanTech's QNome. <i>Forensic Science International: Genetics</i> , 2022, 57, 102657.	1.6	6
119	Further characterization and population data for the pentanucleotide STR polymorphism D10S2325. <i>Forensic Science International</i> , 2001, 123, 107-110.	1.3	5
120	6 Y-SNP Typing of China and Korean Samples Using Primer Extension and DHPLC. <i>Journal of Forensic Sciences</i> , 2007, 52, 235-236.	0.9	5
121	False homozygosities at CSF1PO loci revealed by discrepancies between two kits in Chinese population. <i>International Journal of Legal Medicine</i> , 2010, 124, 457-458.	1.2	5
122	Validating the consistency of cSNPs analysis results between DNA and RNA using SNaPshot method. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 76-78.	0.1	5
123	Typing Y Chromosome STR Haplotypes Using Redesigned Primers. <i>Journal of Forensic Sciences</i> , 2002, 47, 215-217.	0.9	5
124	How many markers are enough for motherless cases of parentage testing. <i>Forensic Science International: Genetics Supplement Series</i> , 2008, 1, 649-651.	0.1	4
125	MiR16 as a microRNA marker applied in species identification. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e313-e314.	0.1	4
126	Next-generation sequencing of 74 Y-SNPs to construct a concise consensus phylogeny tree for Chinese population. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e96-e98.	0.1	4



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127	Multiplex PCR for 19 X-chromosomal STRs in Chinese population. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e24-e26.	0.1	4
128	Allele frequencies of 15 autosomal STRs in Chinese Nakhi and Yi populations. <i>International Journal of Legal Medicine</i> , 2019, 133, 105-108.	1.2	4
129	Expression profile analysis and stability evaluation of 18 small RNAs in the Chinese Han population. <i>Electrophoresis</i> , 2020, 41, 2021-2028.	1.3	4
130	Typing Y chromosome STR haplotypes using redesigned primers. <i>Journal of Forensic Sciences</i> , 2002, 47, 215-7.	0.9	4
131	No association between schizophrenia and rs27388 of the MEGF10 gene in Chinese caseâ€“control sample. <i>Psychiatry Research</i> , 2011, 186, 467-468.	1.7	3
132	Substitution mutation induced migration anomaly of a D10S2325 allele on capillary electrophoresis. <i>International Journal of Legal Medicine</i> , 2013, 127, 363-368.	1.2	3
133	Genetic Variation of the Amplified VNTR Polymorphism COL2A1 in Chinese and German Populations. <i>Human Heredity</i> , 1994, 44, 114-119.	0.4	2
134	Population Genetics of Two STR Loci D2S1346 and D2S1353 in a Han Population of Chinese. <i>Journal of Forensic Sciences</i> , 2006, 51, 705-705.	0.9	2
135	A novel diagnostic strategy for trisomyâ€“21 using short tandem repeats. <i>Electrophoresis</i> , 2006, 27, 416-422.	1.3	2
136	Forensic DNA typing in China. <i>Legal Medicine</i> , 2009, 11, S103-S105.	0.6	2
137	Haplotypes of six miniY-STR loci in the Han population from Sichuan province and the Zhuang population in Guangxi Zhuang autonomous region. <i>Forensic Science International: Genetics</i> , 2009, 3, e49-e51.	1.6	2
138	Utility of multilocus variable number tandem repeat analysis as a microbial forensic tool for subtyping Chinese <i>Escherichia coli</i> O157:H7 strains. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e293-e294.	0.1	2
139	Screening of mtDNA SNPs in Chinese Han population using pyrosequencing. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e316-e317.	0.1	2
140	Validation of a multiplex system with 20 tri-allelic SNP loci for forensic identification purposes. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e324-e325.	0.1	2
141	Characteristics of the two microbial markers in vaginal secretions in Chinese Han population. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e312-e313.	0.1	2
142	Comparison of two online algorithm methods for forensic ancestry inference. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e559-e560.	0.1	2
143	Genetic diversity of 23 autosomal STR loci in a Tibetan population. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e101-e103.	0.1	2
144	Sequence characterization of microvariant alleles at DYS627 and DYS458. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 109-111.	0.1	2

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145	Population Genetics and Forensic Efficiency of 30 InDel Markers in Four Chinese Ethnic Groups Residing in Sichuan. <i>Forensic Sciences Research</i> , 2022, 7, 498-502.	0.9	2
146	Exploring of rare differences in mtGenomes between MZ twins using massively parallel sequencing. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 70-72.	0.1	2
147	D20S161 data for three ethnic populations and forensic validation. <i>International Journal of Legal Medicine</i> , 2002, 116, 253-253.	1.2	1
148	Y-SNP typing with the matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>International Congress Series</i> , 2006, 1288, 16-18.	0.2	1
149	Mitochondrial DNA typing with the matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Forensic Science International: Genetics Supplement Series</i> , 2008, 1, 279-281.	0.1	1
150	The polymorphisms of 9 SNP loci on mitochondrial DNA in the Chinese Han population. <i>Forensic Science International: Genetics Supplement Series</i> , 2009, 2, 347-348.	0.1	1
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