Zheng Wang

List of Publications by Year
in descending order

117 papers	2,310 citations
218677 26 h-index	330143 37 g-index
128 all docs	128 docs citations
128 times ranked	1038 citing authors

#	ARTICLE	IF	CITATIONS
1	Screening and confirmation of microRNA markers for forensic body fluid identification. Forensic Science International: Genetics, 2013, 7, 116-123.	3.1	107
2	Forensic ancestry analysis in two Chinese minority populations using massively parallel sequencing of 165 ancestryâ€‘informative SNPs. Electrophoresis, 2018, 39, 2732-2742.	2.4	68
3	Forensic characteristics and genetic analysis of both 27 Y-STRs and 143 Y-SNPs in Eastern Han Chinese population. Forensic Science International: Genetics, 2019, 42, e13-e20.	3.1	64
4	A model for data analysis of microRNA expression in forensic body fluid identification. Forensic Science International: Genetics, 2012, 6, 419-423.	3.1	63
5	Population genetics of 30 insertionâ€"deletion polymorphisms in two Chinese populations using Qiagen InvestigatorÂ® DIPplex kit. Forensic Science International: Genetics, 2014, 11, e12-e14.	3.1	61
6	Forensic features and phylogenetic analyses of Sichuan Han population via 23 autosomal STR loci included in the Huaxia Platinum System. International Journal of Legal Medicine, 2018, 132, 1079-1082.	2.2	60
7	Highâ€‘Strength and Injectable Supramolecular Hydrogel Selfâ€‘Assembled by Monomeric Nucleoside for Toothâ€‘Extraction Wound Healing. Advanced Materials, 2022, 34, e2108300.	21.0	58
8	Genetic substructure and forensic characteristics of Chinese Hui populations using 157 Y-SNPs and 27 Y-STRs. Forensic Science International: Genetics, 2019, 41, 11-18.	3.1	55
9	Massively parallel sequencing of 32 forensic markers using the Precision ID GlobalFilerâ„¢ NGS STR Panel and the Ion PGMâ„¢ System. Forensic Science International: Genetics, 2017, 31, 126-134.	3.1	53
10	Forensic characteristics and phylogenetic analysis of both Y-STR and Y-SNP in the Li and Han ethnic groups from Hainan Island of China. Forensic Science International: Genetics, 2019, 39, e14-e20.	3.1	53
11	Inferring the population history of Tai-Kadai-speaking people and southernmost Han Chinese on Hainan Island by genome-wide array genotyping. European Journal of Human Genetics, 2020, 28, 1111-1123.	2.8	49
12	Developmental Validation of the Huaxia Platinum System and application in 3 main ethnic groups of China. Scientific Reports, 2016, 6, 31075.	3.3	46
13	Massively parallel sequencing of 165 ancestry informative SNPs in two Chinese Tibetan-Burmese minority ethnicities. Forensic Science International: Genetics, 2018, 34, 141-147.	3.1	44
14	Genetic diversity of 21 autosomal STR loci in the Han population from Sichuan province, Southwest China. Forensic Science International: Genetics, 2017, 31, e33-e35.	3.1	41
15	Development of a new 26plex Y-STRs typing system for forensic application. Forensic Science International: Genetics, 2014, 13, 112-120.	3.1	40
16	New insights into the fine-scale history of westernâ€"eastern admixture of the northwestern Chinese population in the Hexi Corridor via genome-wide genetic legacy. Molecular Genetics and Genomics, 2021, 296, 631-651.	2.1	38
17	Transcriptome sequencing of circular RNA reveals a novel circular RNA-has_circ_0114427 in the regulation of inflammation in acute kidney injury. Clinical Science, 2020, 134, 139-154.	4.3	37
18	Forensic characteristics and phylogenetic analysis of two Han populations from the southern coastal regions of China using 27 Y-STR loci. Forensic Science International: Genetics, 2017, 31, e17-e23.	3.1	36

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19	Genetic variations and forensic characteristics of Han Chinese population residing in the Pearl River Delta revealed by 23 autosomal STRs. Molecular Biology Reports, 2018, 45, 1125-1133.	2.3	36
20	Identification of Saliva Using Micro<scp>RNA</scp> Biomarkers for Forensic Purpose. Journal of Forensic Sciences, 2015, 60, 702-706.	1.6	35
21	Characterization of microRNA expression profiles in blood and saliva using the Ion Personal Genome Machine Â® System (Ion PGMâ„¢ System). Forensic Science International: Genetics, 2016, 20, 140-146.	3.1	35
22	Genetic characteristics and phylogenetic analysis of three Chinese ethnic groups using the Huaxia Platinum System. Scientific Reports, 2018, 8, 2429.	3.3	35
23	A strategy for co-analysis of microRNAs and DNA. Forensic Science International: Genetics, 2014, 12, 24-29.	3.1	32
24	Forensic features, genetic diversity and structure analysis of three Chinese populations using 47 autosomal InDels. Forensic Science International: Genetics, 2020, 45, 102227.	3.1	32
25	Genetic diversity and phylogenetic characteristics of Chinese Tibetan and Yi minority ethnic groups revealed by non-CODIS STR markers. Scientific Reports, 2018, 8, 5895.	3.3	31
26	Fineâ€scale genetic structure of Tujia and central Han Chinese revealing massive genetic admixture under language borrowing. Journal of Systematics and Evolution, 2021, 59, 1-20.	3.1	31
27	Development and validation of a new STR 25-plex typing system. Forensic Science International: Genetics, 2015, 17, 61-69.	3.1	30
28	Analysis of genetic admixture in Uyghur using the 26 Y-STR loci system. Scientific Reports, 2016, 6, 19998.	3.3	30
29	The potential use of Piwi-interacting RNA biomarkers in forensic body fluid identification: A proof-of-principle study. Forensic Science International: Genetics, 2019, 39, 129-135.	3.1	30
30	Next Generation Sequencing Plus (NGS+) with Y-chromosomal Markers for Forensic Pedigree Searches. Scientific Reports, 2017, 7, 11324.	3.3	29
31	Parallel Analysis of 124 Universal SNPs for Human Identification by Targeted Semiconductor Sequencing. Scientific Reports, 2015, 5, 18683.	3.3	28
32	Tai-Kadai-speaking Gelao population: Forensic features, genetic diversity and population structure. Forensic Science International: Genetics, 2019, 40, e231-e239.	3.1	27
33	Peopling History of the Tibetan Plateau and Multiple Waves of Admixture of Tibetans Inferred From Both Ancient and Modern Genome-Wide Data. Frontiers in Genetics, 2021, 12, 725243.	2.3	27
34	Genetic variation and forensic characterization of highland Tibetan ethnicity reveled by autosomal STR markers. International Journal of Legal Medicine, 2018, 132, 1097-1102.	2.2	26
35	Massively parallel sequencing of 124 SNPs included in the precision ID identity panel in three East Asian minority ethnicities. Forensic Science International: Genetics, 2018, 35, 141-148.	3.1	26
36	Fineâ€scale northâ€toâ€south genetic admixture profile in Shaanxi Han Chinese revealed by genomeâ€wide demographic history reconstruction. Journal of Systematics and Evolution, 2022, 60, 955-972.	3.1	26

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37	Evaluation of nutritional status and prognostic impact assessed by the prognostic nutritional index in children with chronic kidney disease. Medicine (United States), 2019, 98, e16713.	1.0	23
38	Developmental validation of a custom panel including 165 Y-SNPs for Chinese Y-chromosomal haplogroups dissection using the ion S5 XL system. Forensic Science International: Genetics, 2019, 38, 70-76.	3.1	23
39	Differentiating between monozygotic twins through next-generation mitochondrial genome sequencing. Analytical Biochemistry, 2015, 490, 1-6.	2.4	22
40	Phylogenetic analysis and forensic characteristics of 12 populations using 23 Y-STR loci. Forensic Science International: Genetics, 2015, 19, 130-133.	3.1	20
41	Massively parallel sequencing of mitogenome sequences reveals the forensic features and maternal diversity of tai-kadai-speaking hlai islanders. Forensic Science International: Genetics, 2020, 47, 102303.	3.1	20
42	Massively parallel sequencing of 165 ancestry-informative SNPs and forensic biogeographical ancestry inference in three southern Chinese Sinitic/Tai-Kadai populations. Forensic Science International: Genetics, 2021, 52, 102475.	3.1	20
43	Developmental validation of an X-Insertion/Deletion polymorphism panel and application in HAN population of China. Scientific Reports, 2015, 5, 18336.	3.3	19
44	Genetic structure and forensic characteristics of Tibeto-Burman-speaking Ãœ-Tsang and Kham Tibetan Highlanders revealed by 27 Y-chromosomal STRs. Scientific Reports, 2019, 9, 7739.	3.3	19
45	Genetic polymorphism and phylogenetic differentiation of the Huaxia Platinum System in three Chinese minority ethnicities. Scientific Reports, 2019, 9, 3371.	3.3	19
46	Genetic insights into the paternal admixture history of Chinese Mongolians via high-resolution customized Y-SNP SNaPshot panels. Forensic Science International: Genetics, 2021, 54, 102565.	3.1	19
47	Whole mitochondrial genome analysis of highland Tibetan ethnicity using massively parallel sequencing. Forensic Science International: Genetics, 2020, 44, 102197.	3.1	18
48	Profiling the differences of gut microbial structure between schizophrenia patients with and without violent behaviors based on 16S rRNA gene sequencing. International Journal of Legal Medicine, 2021, 135, 131-141.	2.2	18
49	Population Genetic Diversity and Phylogenetic Characteristics for High-Altitude Adaptive Kham Tibetan Revealed by DNATyperTM 19 Amplification System. Frontiers in Genetics, 2018, 9, 630.	2.3	17
50	Expression profile analysis of piwi-interacting RNA in forensically relevant biological fluids. Forensic Science International: Genetics, 2019, 42, 171-180.	3.1	17
51	Massively parallel sequencing of 10 autosomal STRs in Chinese using the ion torrent personal genome machine (PGM). Forensic Science International: Genetics, 2016, 25, 34-38.	3.1	15
52	New insight into the pathogenesis of minimal change nephrotic syndrome: Role of the persistence of respiratory tract virus in immune disorders. Autoimmunity Reviews, 2016, 15, 632-637.	5.8	15
53	Genetic Diversity and Phylogenetic Differentiation of Southwestern Chinese Han: a comprehensive and comparative analysis on 21 non-CODIS STRs. Scientific Reports, 2017, 7, 13730.	3.3	15
54	Genetic structure and forensic parameters of 30 InDels for human identification purposes in 10 Tibetan populations of China. Forensic Science International: Genetics, 2019, 40, e219-e227.	3.1	15

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55	Methylation‐Based Age Prediction Using Pyrosequencing Platform from Seminal Stains in Han Chinese Males. Journal of Forensic Sciences, 2020, 65, 610-619.	1.6	15
56	Synonymous point mutation of gtfB gene caused by therapeutic X-rays exposure reduced the biofilm formation and cariogenic abilities of Streptococcus mutans. Cell and Bioscience, 2021, 11, 91.	4.8	15
57	Fine-Scale Genetic Structure and Natural Selection Signatures of Southwestern Hans Inferred From Patterns of Genome-Wide Allele, Haplotype, and Haplogroup Lineages. Frontiers in Genetics, 2021, 12, 727821.	2.3	15
58	A collaborative exercise on DNA methylation-based age prediction and body fluid typing. Forensic Science International: Genetics, 2022, 57, 102656.	3.1	15
59	Melamine‐tainted milk product‐associated urinary stones in children. Pediatrics International, 2011, 53, 489-496.	0.5	14
60	Respiratory Syncytial Virus Aggravates Renal Injury through Cytokines and Direct Renal Injury. Frontiers in Cellular and Infection Microbiology, 2016, 6, 112.	3.9	14
61	Chinese population genetic substructure using 23 Y-chromosomal STRs. Forensic Science International: Genetics Supplement Series, 2017, 6, e110-e111.	0.3	14
62	Colonic J-pouch versus side-to-end anastomosis for rectal cancer: a systematic review and meta-analysis of randomized controlled trials. BMC Surgery, 2021, 21, 331.	1.3	14
63	Does Bonferroni correction "rescue" the deviation from Hardy-Weinberg equilibrium?. Forensic Science International: Genetics, 2020, 46, 102254.	3.1	13
64	Characterization of sequence variation at 30 autosomal STRs in Chinese Han and Tibetan populations. Electrophoresis, 2020, 41, 194-201.	2.4	13
65	Combined Low-/High-Density Modern and Ancient Genome-Wide Data Document Genomic Admixture History of High-Altitude East Asians. Frontiers in Genetics, 2021, 12, 582357.	2.3	13
66	Genomic history and forensic characteristics of Sherpa highlanders on the Tibetan Plateau inferred from high-resolution InDel panel and genome-wide SNPs. Forensic Science International: Genetics, 2022, 56, 102633.	3.1	13
67	Intermittent fasting enhances hippocampal NPY expression to promote neurogenesis after traumatic brain injury. Nutrition, 2022, 97, 111621.	2.4	12
68	Screening and selection of 21 novel microhaplotype markers for ancestry inference in ten Chinese subpopulations. Forensic Science International: Genetics, 2022, 58, 102687.	3.1	12
69	Cysteine Dioxygenase Type 1 Inhibits Osteogenesis by Regulating Wnt Signaling in Primary Mouse Bone Marrow Stromal Cells. Scientific Reports, 2016, 6, 19296.	3.3	11
70	Forensic characteristics and phylogenetic analysis of Hubei Han population in central China using 17 Y-STR loci. Forensic Science International: Genetics, 2017, 29, e4-e8.	3.1	10
71	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. Electrophoresis, 2021, 42, 774-785.	2.4	10
72	RANKL inhibition halts lesion progression and promotes bone remineralization in mice with fibrous dysplasia. Bone, 2022, 156, 116301.	2.9	10

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73	Revisiting the genetic background and phylogenetic structure of five Sino-Tibetan-speaking populations: insights from autosomal InDels. Molecular Genetics and Genomics, 2020, 295, 969-979.	2.1	9
74	Northern gene flow into southeastern East Asians inferred from genome–wide array genotyping. Journal of Systematics and Evolution, 2023, 61, 179-197.	3.1	9
75	Reconstructing the genetic admixture history of Tai–Kadai and Sinitic people: Insights from genome–wide SNP data from South China. Journal of Systematics and Evolution, 2023, 61, 157-178.	3.1	9
76	Exploring of microRNA markers for semen stains using massively parallel sequencing. Forensic Science International: Genetics Supplement Series, 2017, 6, e107-e109.	0.3	8
77	Genetic diversity and phylogenetic analysis of Chinese Han and Li ethnic populations from Hainan Island by 30 autosomal insertion/deletion polymorphisms. Forensic Sciences Research, 2022, 7, 189-195.	1.6	8
78	Bioinformatic analysis reveals novel hub genes and pathways associated with hypertensive nephropathy. Nephrology, 2019, 24, 1103-1114.	1.6	8
79	Molecular genetic survey and forensic characterization of Chinese Mongolians via the 47 autosomal insertion/deletion marker. Genomics, 2021, 113, 2199-2210.	2.9	8
80	Differentiating between monozygotic twins in forensics through next generation mtGenome sequencing. Forensic Science International: Genetics Supplement Series, 2015, 5, e58-e59.	0.3	7
81	Genetic variation and population structure analysis of Chinese Wuzhong Hui population using 30 Indels. Annals of Human Biology, 2020, 47, 300-303.	1.0	7
82	Population genetics, diversity, forensic characteristics of four Chinese populations inferred from X-chromosomal short tandem repeats. Legal Medicine, 2020, 43, 101677.	1.3	7
83	Optogenetics for Understanding and Treating Brain Injury: Advances in the Field and Future Prospects. International Journal of Molecular Sciences, 2022, 23, 1800.	4.1	7
84	Interaction among genes influencing ethanol metabolism and sex is association with alcohol use disorders in a Tibet population. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 561-569.	1.7	6
85	A case study of SNPSTR efficiency in paternity testing with locus incompatibility. Forensic Science International: Genetics, 2014, 9, 72-75.	3.1	6
86	Bioinformatic Analysis Reveals Novel Immune-Associated Hub Genes in Human Membranous Nephropathy. Genetic Testing and Molecular Biomarkers, 2019, 23, 23-31.	0.7	6
87	Bioinformatic analysis reveals that the OAS family may play an important role in lupus nephritis. Journal of the National Medical Association, 2020, 112, 567-577.	0.8	6
88	Forensic nanopore sequencing of microhaplotype markers using QitanTech's QNome. Forensic Science International: Genetics, 2022, 57, 102657.	3.1	6
89	To Explore the Characteristics of Fatality in Children Poisoned by Paraquat – with Analysis of 146 Cases. International Journal of Artificial Organs, 2016, 39, 51-55.	1.4	5
90	Integrated bioinformatics analysis reveals novel hub genes closely associated with pathological mechanisms of immunoglobulin A nephropathy. Experimental and Therapeutic Medicine, 2019, 18, 1235-1245.	1.8	5

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91	Applying machine learning algorithms to a real forensic case to predict Y-SNP haplogroup based on Y-STR haplotype. Forensic Science International: Genetics Supplement Series, 2019, 7, 637-638.	0.3	5
92	Application of weighted gene co‐expression network analysis to identify novel key genes in diabetic nephropathy. Journal of Diabetes Investigation, 2022, 13, 112-124.	2.4	5
93	Validating the consistency of cSNPs analysis results between DNA and RNA using SNaPshot method. Forensic Science International: Genetics Supplement Series, 2019, 7, 76-78.	0.3	5
94	MiR16 as a microRNA marker applied in species identification. Forensic Science International: Genetics Supplement Series, 2011, 3, e313-e314.	0.3	4
95	Next-generation sequencing of 74 Y-SNPs to construct a concise consensus phylogeny tree for Chinese population. Forensic Science International: Genetics Supplement Series, 2017, 6, e96-e98.	0.3	4
96	High expression of special AT‐rich sequence binding protein‐1 predicts esophageal squamous cell carcinoma relapse and poor prognosis. Oncology Letters, 2017, 14, 7455-7460.	1.8	4
97	Low molecular weight heparin may benefit nephrotic remission in steroid-sensitive nephrotic syndrome via inhibiting elastase. Molecular Medicine Reports, 2017, 16, 8613-8618.	2.4	4
98	Allele frequencies of 15 autosomal STRs in Chinese Nakhi and Yi populations. International Journal of Legal Medicine, 2019, 133, 105-108.	2.2	4
99	Expression profile analysis and stability evaluation of 18 small RNAs in the Chinese Han population. Electrophoresis, 2020, 41, 2021-2028.	2.4	4
100	Orthodontic maximum anchorages in malocclusion treatment: A systematic review and network meta‐analysis. Journal of Evidence-Based Medicine, 2021, 14, 295-302.	1.8	4
101	High‐Strength and Injectable Supramolecular Hydrogel Self‐Assembled by Monomeric Nucleoside for Tooth‐Extraction Wound Healing (Adv. Mater. 13/2022). Advanced Materials, 2022, 34, .	21.0	3
102	Application of a New Established System for Toxic Doses in Children With 4-Hydroxycoumarin Rodenticide Intoxication. Frontiers in Pediatrics, 2018, 6, 141.	1.9	2
103	Evaluation of Split Renal Function for Children with Kidney Diseases by Renal and Vascular Color Ultrasonography. Ultrasound in Medicine and Biology, 2018, 44, 2602-2608.	1.5	2
104	Sequence characterization of microvariant alleles at DYS627 and DYS458. Forensic Science International: Genetics Supplement Series, 2019, 7, 109-111.	0.3	2
105	Population Genetics and Forensic Efficiency of 30 InDel Markers in Four Chinese Ethnic Groups Residing in Sichuan. Forensic Sciences Research, 2022, 7, 498-502.	1.6	2
106	Intrinsic Contributions of 2′‐Hydroxyl to the Hydration of Nucleosides at the Monomeric Level. Chemistry - A European Journal, 2020, 26, 17046-17055.	3.3	2
107	Exploring of rare differences in mtGenomes between MZ twins using massively parallel sequencing. Forensic Science International: Genetics Supplement Series, 2019, 7, 70-72.	0.3	2
108	The FnBPA from methicillin-resistant *Staphylococcus aureus* promoted development of oral squamous cell carcinoma. Journal of Oral Microbiology, 2022, 14, .	2.7	2

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109	Evaluation of HID-Ion Ampliseqâ„¢ panel in HAN population. Forensic Science International: Genetics Supplement Series, 2015, 5, e584-e586.	0.3	1
110	Genetic polymorphism of 30 autosomal InDel loci in Chinese Hainan Li population. Forensic Science International: Genetics Supplement Series, 2019, 7, 107-108.	0.3	1
111	Risk Factors Associated With Abnormal Urinalysis in Children. Frontiers in Pediatrics, 2021, 9, 649068.	1.9	1
112	Forensic characteristics of Tibeto-Burman-speaking Tibetans revealed by 50 InDels. Forensic Science International: Genetics Supplement Series, 2019, 7, 758-759.	0.3	1
113	Logical Framework of Forensic Identification: Ability to Resist Fabricated DNA. Molecular Biotechnology, 2015, 57, 1030-1037.	2.4	0
114	Genome-wide copy number variation analysis in monozygotic twins. Forensic Science International: Genetics Supplement Series, 2017, 6, e218-e220.	0.3	0
115	Revisiting the matrilineal lineages and hypoxic adaptation of highland Tibetans. Forensic Science International: Genetics Supplement Series, 2019, 7, 73-75.	0.3	0
116	Mutation rates of six Y-chromosomal STR loci estimated from 210 pedigrees in Chinese Han population. Forensic Science International: Genetics Supplement Series, 2019, 7, 480-481.	0.3	0
117	Forensic features and genetic structure at insertion/deletion polymorphisms of Chinese Han with other 31 Chinese ethnic groups. Forensic Science International: Genetics Supplement Series, 2019, 7, 655-657.	0.3	0