

# Zheng Wang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8817678/publications.pdf>

Version: 2024-02-01

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	Northern gene flow into southeastern East Asians inferred from genome-wide array genotyping. <i>Journal of Systematics and Evolution</i> , 2023, 61, 179-197.	3.1	9
2	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> , 2023, 61, 157-178.	3.1	9
3	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.	1.6	8
4	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.	1.6	2
5	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> , 2022, 60, 955-972.	3.1	26
6	Application of weighted gene co-expression network analysis to identify novel key genes in diabetic nephropathy. <i>Journal of Diabetes Investigation</i> , 2022, 13, 112-124.	2.4	5
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.	3.1	13
8	A collaborative exercise on DNA methylation-based age prediction and body fluid typing. <i>Forensic Science International: Genetics</i> , 2022, 57, 102656.	3.1	15
9	RANKL inhibition halts lesion progression and promotes bone remineralization in mice with fibrous dysplasia. <i>Bone</i> , 2022, 156, 116301.	2.9	10
10	Forensic nanopore sequencing of microhaplotype markers using QitanTech's QNome. <i>Forensic Science International: Genetics</i> , 2022, 57, 102657.	3.1	6
11	High-strength and Injectable Supramolecular Hydrogel Self-Assembled by Monomeric Nucleoside for Tooth-Extraction Wound Healing. <i>Advanced Materials</i> , 2022, 34, e2108300.	21.0	58
12	Intermittent fasting enhances hippocampal NPY expression to promote neurogenesis after traumatic brain injury. <i>Nutrition</i> , 2022, 97, 111621.	2.4	12
13	Optogenetics for Understanding and Treating Brain Injury: Advances in the Field and Future Prospects. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1800.	4.1	7
14	High-strength and Injectable Supramolecular Hydrogel Self-Assembled by Monomeric Nucleoside for Tooth-Extraction Wound Healing (Adv. Mater. 13/2022). <i>Advanced Materials</i> , 2022, 34, .	21.0	3
15	Screening and selection of 21 novel microhaplotype markers for ancestry inference in ten Chinese subpopulations. <i>Forensic Science International: Genetics</i> , 2022, 58, 102687.	3.1	12
16	The FnBPA from methicillin-resistant <i>Staphylococcus aureus</i> promoted development of oral squamous cell carcinoma. <i>Journal of Oral Microbiology</i> , 2022, 14, .	2.7	2
17	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.	3.1	31
18	Profiling the differences of gut microbial structure between schizophrenia patients with and without violent behaviors based on 16S rRNA gene sequencing. <i>International Journal of Legal Medicine</i> , 2021, 135, 131-141.	2.2	18

#	ARTICLE	IF	CITATIONS
19	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.	2.3	13
20	Risk Factors Associated With Abnormal Urinalysis in Children. <i>Frontiers in Pediatrics</i> , 2021, 9, 649068.	1.9	1
21	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.	2.1	38
22	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.	3.1	20
23	Synonymous point mutation of <i>gtfB</i> gene caused by therapeutic X-rays exposure reduced the biofilm formation and cariogenic abilities of <i>Streptococcus mutans</i> . <i>Cell and Bioscience</i> , 2021, 11, 91.	4.8	15
24	Molecular genetic survey and forensic characterization of Chinese Mongolians via the 47 autosomal insertion/deletion marker. <i>Genomics</i> , 2021, 113, 2199-2210.	2.9	8
25	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.	2.3	15
26	Colonic J-pouch versus side-to-end anastomosis for rectal cancer: a systematic review and meta-analysis of randomized controlled trials. <i>BMC Surgery</i> , 2021, 21, 331.	1.3	14
27	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.	3.1	19
28	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.	2.3	27
29	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.	2.4	10
30	Orthodontic maximum anchorages in malocclusion treatment: A systematic review and network meta-analysis. <i>Journal of Evidence-Based Medicine</i> , 2021, 14, 295-302.	1.8	4
31	Methylation-Based Age Prediction Using Pyrosequencing Platform from Seminal Stains in Han Chinese Males. <i>Journal of Forensic Sciences</i> , 2020, 65, 610-619.	1.6	15
32	Whole mitochondrial genome analysis of highland Tibetan ethnicity using massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2020, 44, 102197.	3.1	18
33	Forensic features, genetic diversity and structure analysis of three Chinese populations using 47 autosomal InDels. <i>Forensic Science International: Genetics</i> , 2020, 45, 102227.	3.1	32
34	Expression profile analysis and stability evaluation of 18 small RNAs in the Chinese Han population. <i>Electrophoresis</i> , 2020, 41, 2021-2028.	2.4	4
35	Intrinsic Contributions of 2'-OH to the Hydration of Nucleosides at the Monomeric Level. <i>Chemistry - A European Journal</i> , 2020, 26, 17046-17055.	3.3	2
36	Genetic variation and population structure analysis of Chinese Wuzhong Hui population using 30 Indels. <i>Annals of Human Biology</i> , 2020, 47, 300-303.	1.0	7

#	ARTICLE	IF	CITATIONS
37	Bioinformatic analysis reveals that the OAS family may play an important role in lupus nephritis. <i>Journal of the National Medical Association</i> , 2020, 112, 567-577.	0.8	6
38	Does Bonferroni correction "rescue" the deviation from Hardy-Weinberg equilibrium?. <i>Forensic Science International: Genetics</i> , 2020, 46, 102254.	3.1	13
39	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.	2.8	49
40	Characterization of sequence variation at 30 autosomal STRs in Chinese Han and Tibetan populations. <i>Electrophoresis</i> , 2020, 41, 194-201.	2.4	13
41	Population genetics, diversity, forensic characteristics of four Chinese populations inferred from X-chromosomal short tandem repeats. <i>Legal Medicine</i> , 2020, 43, 101677.	1.3	7
42	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.	2.1	9
43	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.	3.1	20
44	Transcriptome sequencing of circular RNA reveals a novel circular RNA-has_circ_0114427 in the regulation of inflammation in acute kidney injury. <i>Clinical Science</i> , 2020, 134, 139-154.	4.3	37
45	Integrated bioinformatics analysis reveals novel hub genes closely associated with pathological mechanisms of immunoglobulin A nephropathy. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 1235-1245.	1.8	5
46	Expression profile analysis of piwi-interacting RNA in forensically relevant biological fluids. <i>Forensic Science International: Genetics</i> , 2019, 42, 171-180.	3.1	17
47	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.	3.1	64
48	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.	3.3	19
49	Tai-Kadai-speaking Gelao population: Forensic features, genetic diversity and population structure. <i>Forensic Science International: Genetics</i> , 2019, 40, e231-e239.	3.1	27
50	Genetic polymorphism and phylogenetic differentiation of the Huaxia Platinum System in three Chinese minority ethnicities. <i>Scientific Reports</i> , 2019, 9, 3371.	3.3	19
51	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.	3.1	55
52	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.	3.1	15
53	Applying machine learning algorithms to a real forensic case to predict Y-SNP haplogroup based on Y-STR haplotype. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 637-638.	0.3	5
54	Genetic polymorphism of 30 autosomal InDel loci in Chinese Hainan Li population. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 107-108.	0.3	1

#	ARTICLE	IF	CITATIONS
55	Sequence characterization of microvariant alleles at DYS627 and DYS458. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 109-111.	0.3	2
56	Revisiting the matrilineal lineages and hypoxic adaptation of highland Tibetans. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 73-75.	0.3	0
57	Evaluation of nutritional status and prognostic impact assessed by the prognostic nutritional index in children with chronic kidney disease. <i>Medicine (United States)</i> , 2019, 98, e16713.	1.0	23
58	Allele frequencies of 15 autosomal STRs in Chinese Nakhi and Yi populations. <i>International Journal of Legal Medicine</i> , 2019, 133, 105-108.	2.2	4
59	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.	3.1	30
60	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.	3.1	23
61	Bioinformatic Analysis Reveals Novel Immune-Associated Hub Genes in Human Membranous Nephropathy. <i>Genetic Testing and Molecular Biomarkers</i> , 2019, 23, 23-31.	0.7	6
62	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.	3.1	53
63	Bioinformatic analysis reveals novel hub genes and pathways associated with hypertensive nephropathy. <i>Nephrology</i> , 2019, 24, 1103-1114.	1.6	8
64	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.	0.3	5
65	Forensic characteristics of Tibeto-Burman-speaking Tibetans revealed by 50 InDels. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 758-759.	0.3	1
66	Mutation rates of six Y-chromosomal STR loci estimated from 210 pedigrees in Chinese Han population. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 480-481.	0.3	0
67	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.	0.3	2
68	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, 655-657.	0.3	0
69	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.	3.1	44
70	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.	3.3	31
71	Genetic characteristics and phylogenetic analysis of three Chinese ethnic groups using the Huaxia Platinum System. <i>Scientific Reports</i> , 2018, 8, 2429.	3.3	35
72	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.	2.2	26

#	ARTICLE	IF	CITATIONS
73	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.	2.2	60
74	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.	2.3	17
75	Application of a New Established System for Toxic Doses in Children With 4-Hydroxycoumarin Rodenticide Intoxication. <i>Frontiers in Pediatrics</i> , 2018, 6, 141.	1.9	2
76	Evaluation of Split Renal Function for Children with Kidney Diseases by Renal and Vascular Color Ultrasonography. <i>Ultrasound in Medicine and Biology</i> , 2018, 44, 2602-2608.	1.5	2
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.	3.1	26
78	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.	2.3	36
79	Forensic ancestry analysis in two Chinese minority populations using massively parallel sequencing of 165 ancestry-informative SNPs. <i>Electrophoresis</i> , 2018, 39, 2732-2742.	2.4	68
80	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.	3.1	10
81	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.	3.3	15
82	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.	3.1	36
83	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.	0.3	4
84	Genome-wide copy number variation analysis in monozygotic twins. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e218-e220.	0.3	0
85	Exploring of microRNA markers for semen stains using massively parallel sequencing. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e107-e109.	0.3	8
86	Massively parallel sequencing of 32 forensic markers using the Precision ID GlobalFiler™, NGS STR Panel and the Ion PGM™ System. <i>Forensic Science International: Genetics</i> , 2017, 31, 126-134.	3.1	53
87	Chinese population genetic substructure using 23 Y-chromosomal STRs. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e110-e111.	0.3	14
88	Next Generation Sequencing Plus (NGS+) with Y-chromosomal Markers for Forensic Pedigree Searches. <i>Scientific Reports</i> , 2017, 7, 11324.	3.3	29
89	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.	3.1	41
90	High expression of special AT-rich sequence binding protein 1 predicts esophageal squamous cell carcinoma relapse and poor prognosis. <i>Oncology Letters</i> , 2017, 14, 7455-7460.	1.8	4

#	ARTICLE	IF	CITATIONS
91	Low molecular weight heparin may benefit nephrotic remission in steroid-sensitive nephrotic syndrome via inhibiting elastase. <i>Molecular Medicine Reports</i> , 2017, 16, 8613-8618.	2.4	4
92	Respiratory Syncytial Virus Aggravates Renal Injury through Cytokines and Direct Renal Injury. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 112.	3.9	14
93	Massively parallel sequencing of 10 autosomal STRs in Chinese using the ion torrent personal genome machine (PGM). <i>Forensic Science International: Genetics</i> , 2016, 25, 34-38.	3.1	15
94	Developmental Validation of the Huaxia Platinum System and application in 3 main ethnic groups of China. <i>Scientific Reports</i> , 2016, 6, 31075.	3.3	46
95	Analysis of genetic admixture in Uyghur using the 26 Y-STR loci system. <i>Scientific Reports</i> , 2016, 6, 19998.	3.3	30
96	Cysteine Dioxygenase Type 1 Inhibits Osteogenesis by Regulating Wnt Signaling in Primary Mouse Bone Marrow Stromal Cells. <i>Scientific Reports</i> , 2016, 6, 19296.	3.3	11
97	To Explore the Characteristics of Fatality in Children Poisoned by Paraquat “ with Analysis of 146 Cases. <i>International Journal of Artificial Organs</i> , 2016, 39, 51-55.	1.4	5
98	Characterization of microRNA expression profiles in blood and saliva using the Ion Personal Genome Machine “ System (Ion PGM“ System). <i>Forensic Science International: Genetics</i> , 2016, 20, 140-146.	3.1	35
99	New insight into the pathogenesis of minimal change nephrotic syndrome: Role of the persistence of respiratory tract virus in immune disorders. <i>Autoimmunity Reviews</i> , 2016, 15, 632-637.	5.8	15
100	Parallel Analysis of 124 Universal SNPs for Human Identification by Targeted Semiconductor Sequencing. <i>Scientific Reports</i> , 2015, 5, 18683.	3.3	28
101	Developmental validation of an X-Insertion/Deletion polymorphism panel and application in HAN population of China. <i>Scientific Reports</i> , 2015, 5, 18336.	3.3	19
102	Evaluation of HID-Ion Ampliseq“ panel in HAN population. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e584-e586.	0.3	1
103	Identification of Saliva Using MicroRNA Biomarkers for Forensic Purpose. <i>Journal of Forensic Sciences</i> , 2015, 60, 702-706.	1.6	35
104	Phylogenetic analysis and forensic characteristics of 12 populations using 23 Y-STR loci. <i>Forensic Science International: Genetics</i> , 2015, 19, 130-133.	3.1	20
105	Development and validation of a new STR 25-plex typing system. <i>Forensic Science International: Genetics</i> , 2015, 17, 61-69.	3.1	30
106	Logical Framework of Forensic Identification: Ability to Resist Fabricated DNA. <i>Molecular Biotechnology</i> , 2015, 57, 1030-1037.	2.4	0
107	Differentiating between monozygotic twins in forensics through next generation mtGenome sequencing. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e58-e59.	0.3	7
108	Differentiating between monozygotic twins through next-generation mitochondrial genome sequencing. <i>Analytical Biochemistry</i> , 2015, 490, 1-6.	2.4	22

#	ARTICLE	IF	CITATIONS
109	Development of a new 26plex Y-STRs typing system for forensic application. Forensic Science International: Genetics, 2014, 13, 112-120.	3.1	40
110	Population genetics of 30 insertion-deletion polymorphisms in two Chinese populations using Qiagen Investigator® DIPplex kit. Forensic Science International: Genetics, 2014, 11, e12-e14.	3.1	61
111	A case study of SNPSTR efficiency in paternity testing with locus incompatibility. Forensic Science International: Genetics, 2014, 9, 72-75.	3.1	6
112	A strategy for co-analysis of microRNAs and DNA. Forensic Science International: Genetics, 2014, 12, 24-29.	3.1	32
113	Screening and confirmation of microRNA markers for forensic body fluid identification. Forensic Science International: Genetics, 2013, 7, 116-123.	3.1	107
114	A model for data analysis of microRNA expression in forensic body fluid identification. Forensic Science International: Genetics, 2012, 6, 419-423.	3.1	63
115	MiR16 as a microRNA marker applied in species identification. Forensic Science International: Genetics Supplement Series, 2011, 3, e313-e314.	0.3	4
116	Melamine-contaminated milk product-associated urinary stones in children. Pediatrics International, 2011, 53, 489-496.	0.5	14
117	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