Chengtao Li

List of Publications by Year
in descending order

118 papers	1,444 citations	361413 20 h-index	414414 32 g-index
120 all docs	120 docs citations	120 times ranked	1140 citing authors

#	Article	IF	Citations
1	Association between indel polymorphism in the promoter region of lncRNA GAS5 and the risk of hepatocellular carcinoma. Carcinogenesis, 2015, 36, 1136-1143.	2.8	107
2	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
3	Massively parallel sequencing of 32 forensic markers using the Precision ID GlobalFiler™ NGS STR Panel and the Ion PGM™ System. Forensic Science International: Genetics, 2017, 31, 126-134.	3.1	53
4	Developmental Validation of the Huaxia Platinum System and application in 3 main ethnic groups of China. Scientific Reports, 2016, 6, 31075.	3.3	46
5	Developmental validation of a custom panel including 273 SNPs for forensic application using Ion Torrent PGM. Forensic Science International: Genetics, 2017, 27, 50-57.	3.1	44
6	Development of a new 26plex Y-STRs typing system for forensic application. Forensic Science International: Genetics, 2014, 13, 112-120.	3.1	40
7	Differences of DNA methylation profiles between monozygotic twins' blood samples. Molecular Biology Reports, 2013, 40, 5275-5280.	2.3	38
8	Characterization of microRNA expression profiles in blood and saliva using the Ion Personal Genome Machine ® System (Ion PGM™ System). Forensic Science International: Genetics, 2016, 20, 140-146.	3.1	35
9	Pilot study for forensic evaluations of the Precision ID GlobalFiler™ NGS STR Panel v2 with the Ion S5™ system. Forensic Science International: Genetics, 2019, 43, 102147.	3.1	35
10	Genetic polymorphisms of 12 X-STR for forensic purposes in Shanghai Han population from China. Molecular Biology Reports, 2012, 39, 5705-5707.	2.3	31
11	Development and validation of a new STR 25-plex typing system. Forensic Science International: Genetics, 2015, 17, 61-69.	3.1	30
12	Analysis of genetic admixture in Uyghur using the 26 Y-STR loci system. Scientific Reports, 2016, 6, 19998.	3.3	30
13	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
14	Parallel Analysis of 124 Universal SNPs for Human Identification by Targeted Semiconductor Sequencing. Scientific Reports, 2015, 5, 18683.	3.3	28
15	Genetic polymorphism of 29 highly informative InDel markers for forensic use in the Chinese Han population. Forensic Science International: Genetics, 2011, 5, e27-e30.	3.1	27
16	Population genetics study using 26 Y-chromosomal STR loci in the Hui ethnic group in China. Forensic Science International: Genetics, 2017, 28, e26-e27.	3.1	26
17	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
18	Analysis of 14 highly informative SNP markers on X chromosome by TaqMan® SNP genotyping assay. Forensic Science International: Genetics, 2010, 4, e145-e148.	3.1	25

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19	Maternity exclusion with a very high autosomal STRs kinship index. International Journal of Legal Medicine, 2012, 126, 645-648.	2.2	23
20	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
21	Differentiating between monozygotic twins through next-generation mitochondrial genome sequencing. Analytical Biochemistry, 2015, 490, 1-6.	2.4	22
22	An insertion/deletion polymorphism within 3′UTR of RYR2 modulates sudden unexplained death risk in Chinese populations. Forensic Science International, 2017, 270, 165-172.	2.2	22
23	Genetic polymorphism of 17 STR loci for forensic use in Chinese population from Shanghai in East China. Forensic Science International: Genetics, 2009, 3, e117-e118.	3.1	20
24	Separation/extraction, detection, and interpretation of DNA mixtures in forensic science (review). International Journal of Legal Medicine, 2018, 132, 1247-1261.	2.2	20
25	Identical but not the same: The value of DNA methylation profiling in forensic discrimination within monozygotic twins. Forensic Science International: Genetics Supplement Series, 2011, 3, e337-e338.	0.3	19
26	Development of the 16 X‐STR loci typing system and genetic analysis in a Shanghai Han population from China. Electrophoresis, 2013, 34, 3008-3015.	2.4	19
27	Developmental validation of an X-Insertion/Deletion polymorphism panel and application in HAN population of China. Scientific Reports, 2015, 5, 18336.	3.3	19
28	Genome-wide screening for highly discriminative SNPs for personal identification and their assessment in world populations. Forensic Science International: Genetics, 2017, 28, 118-127.	3.1	19
29	A New Multiplex Assay of 17 Autosomal STRs and Amelogenin for Forensic Application. PLoS ONE, 2013, 8, e57471.	2.5	18
30	Bibliometric Analysis of Medical Malpractice Literature in Legal Medicine from 1975 to 2018: Web of Science Review. Journal of Clinical Forensic and Legal Medicine, 2019, 66, 167-183.	1.0	17
31	Apoptosis Induced by Ginkgo biloba (EGb761) in Melanoma Cells Is Mcl-1-Dependent. PLoS ONE, 2015, 10, e0124812.	2.5	17
32	Investigation of 12 X-STR loci in Mongolian and Eastern Han populations of China with comparison to other populations. Scientific Reports, 2018, 8, 4287.	3.3	16
33	Intra-Monozygotic Twin Pair Discordance and Longitudinal Variation of Whole-Genome Scale DNA Methylation in Adults. PLoS ONE, 2015, 10, e0135022.	2.5	15
34	Application of HLA‐DRB1 genotyping by oligonucleotide micro-array technology in forensic medicine. Forensic Science International, 2006, 162, 66-73.	2.2	14
35	Development of 11 X-STR loci typing system and genetic analysis in Tibetan and Northern Han populations from China. International Journal of Legal Medicine, 2011, 125, 753-756.	2.2	13
36	Population genetic study of 34 X-Chromosome markers in 5 main ethnic groups of China. Scientific Reports, 2015, 5, 17711.	3.3	13

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37	A common indel polymorphism of the Desmoglein-2 (DSG2) is associated with sudden cardiac death in Chinese populations. Forensic Science International, 2019, 301, 382-387.	2.2	13
38	Genetic polymorphisms in 12 autosomal <scp>STR</scp>s in a <scp>S</scp>hanghai <scp>H</scp>an population from China. Electrophoresis, 2013, 34, 613-617.	2.4	12
39	Development and validation of a multiplex insertion/deletion marker panel, SifaInDel 45plex system. Forensic Science International: Genetics, 2019, 41, 128-136.	3.1	12
40	Development and validation of a novel 29-plex Y-STR typing system for forensic application. Forensic Science International: Genetics, 2020, 44, 102169.	3.1	12
41	An Indel Polymorphism within pre-miR3131 Confers Risk for Hepatocellular Carcinoma. Carcinogenesis, 2017, 38, bgw206.	2.8	10
42	Development and validation of a novel SiFaSTR TM 23â€plex system. Electrophoresis, 2019, 40, 2644-2654.	2.4	10
43	Parallel sequencing of 87 STR and 294 SNP markers using the prototype of the SifaMPS panel on the MiSeq FGxâ„¢ system. Forensic Science International: Genetics, 2021, 52, 102490.	3.1	10
44	Selection of 29 highly informative InDel markers for human identification and paternity analysis in Chinese Han population by the SNPlex genotyping system. Molecular Biology Reports, 2012, 39, 3143-3152.	2.3	9
45	Association between an indel polymorphism in the 3â€²UTR of COL1A2 and the risk of sudden cardiac death in Chinese populations. Legal Medicine, 2017, 28, 22-26.	1.3	9
46	Analytical validation of an RI sample cartridge with the RapidHITÂ® ID system. International Journal of Legal Medicine, 2021, 135, 1257-1265.	2.2	9
47	Massively parallel sequencing of 231 autosomal SNPs with a custom panel: a SNP typing assay developed for human identification with Ion Torrent PGM. Forensic Sciences Research, 2017, 2, 26-33.	1.6	8
48	Characterization of the extra copy of TPOX locus with tri-allelic pattern. BMC Genetics, 2019, 20, 18.	2.7	8
49	Genetic association study of a novel indel polymorphism in HSPA1B with the risk of sudden cardiac death in the Chinese populations. Forensic Science International, 2021, 318, 110637.	2.2	8
50	Differentiating between monozygotic twins in forensics through next generation mtGenome sequencing. Forensic Science International: Genetics Supplement Series, 2015, 5, e58-e59.	0.3	7
51	Population genetics of 30 insertion/deletion polymorphisms in Han Chinese population from Zhejiang Province. Forensic Science International: Genetics, 2017, 28, e33-e35.	3.1	7
52	Forensic investigation of 23 autosomal STRs and application in Han and Mongolia ethnic groups. Forensic Sciences Research, 2018, 3, 138-144.	1.6	7
53	Genetic characterization of 27 Y-STR loci analyzed in the Nantong Han population residing along the Yangtze Basin. Forensic Science International: Genetics, 2019, 39, e10-e13.	3.1	7
54	A newly devised multiplex assay of novel polymorphic non-CODIS STRs as a valuable tool for forensic application. Forensic Science International: Genetics, 2020, 48, 102341.	3.1	7

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55	Pairwise kinship analysis of 17 pedigrees using massively parallel sequencing. Forensic Science International: Genetics, 2021, 57, 102647.	3.1	7
56	Sequence investigation of 34 forensic autosomal STRs with massively parallel sequencing. Scientific Reports, 2018, 8, 6810.	3.3	6
57	Genetic characterization of 21 autosomal STR loci of Goldeneyeâ"¢ DNA ID 22NC Kit in Chinese She group. Legal Medicine, 2019, 39, 45-48.	1.3	6
58	Forensic characteristics of 36 Y-STR loci in a Changzhou Han population and genetic distance analysis among several Chinese populations. Forensic Science International: Genetics, 2019, 40, e268-e270.	3.1	6
59	Mass spectrometry-based SNP genotyping as a potential tool for ancestry inference and human identification in Chinese Han and Uygur populations. Science and Justice - Journal of the Forensic Science Society, 2019, 59, 228-233.	2.1	6
60	Detecting genetic hypermutability of gastrointestinal tumor by using a forensic STR kit. Frontiers of Medicine, 2020, 14, 101-111.	3.4	6
61	Genetic investigation and phylogenetic analysis of three Chinese ethnic groups using 16 X chromosome STR loci. Annals of Human Biology, 2020, 47, 59-64.	1.0	6
62	Development and validation of a forensic sixâ€dye multiplex assay with 29 STR loci. Electrophoresis, 2021, 42, 1419-1430.	2.4	6
63	Application of insertion/deletion polymorphisms in human gastrointestinal tumour tissues for identification purpose. Forensic Science International: Genetics Supplement Series, 2011, 3, e297-e298.	0.3	5
64	Validation of the Investigator 24plex QS Kit: a 6-dye multiplex PCR assay for forensic application in the Chinese Han population. Forensic Sciences Research, 2022, 7, 172-180.	1.6	5
65	Genetic polymorphisms of 27 Y-STR loci in the Dezhou Han population from Shandong province, Eastern China. Forensic Science International: Genetics, 2019, 39, e26-e28.	3.1	5
66	Genetic polymorphism of both 29 Y-STRs and 213 Y-SNPs in Han populations from Shandong Province, China. Legal Medicine, 2020, 47, 101738.	1.3	5
67	STRsearch: a new pipeline for targeted profiling of short tandem repeats in massively parallel sequencing data. Hereditas, 2020, 157, 8.	1.4	5
68	Calculation of the Paternity Index for STR with tri-allelic patterns in paternity testing. Forensic Science International, 2021, 324, 110832.	2.2	5
69	Development of forensic standards in China: a review. Forensic Sciences Research, 2022, 7, 1-10.	1.6	5
70	Allelic alterations of STRs in archival paraffin embedded tissue as DNA source for paternity testing. Forensic Science International: Genetics Supplement Series, 2009, 2, 12-13.	0.3	4
71	Parallel sequencing of 60 X-chromosome genetic markers including STRs, SNPs and InDels. Forensic Science International: Genetics Supplement Series, 2017, 6, e317-e319.	0.3	4
72	Genetic polymorphisms in 16 X-STR loci analyzed in the She population from Zhejiang Province, China. Legal Medicine, 2019, 39, 25-28.	1.3	4

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73	Development and validation of a custom panel including 183 Yâ€SNPs for Chinese Yâ€chromosomal haplogroups dissection using a MALDIâ€TOF MS system. Electrophoresis, 2020, 41, 2047-2054.	2.4	4
74	Investigation of an Alternative Marker for Hypermutability Evaluation in Different Tumors. Genes, 2021, 12, 197.	2.4	4
75	Evaluation of reliability of STR typing in human colon carcinomas tissues used for identification purpose. Forensic Science International: Genetics Supplement Series, 2009, 2, 8-9.	0.3	3
76	Comparison study in determination of full sibling with Identifiler multiplex system between ITO method and identity by state scoring method. Forensic Science International: Genetics Supplement Series, 2011, 3, e335-e336.	0.3	3
77	Genetic analysis of the 11 X-STR loci in Uigur population from China. Forensic Science International: Genetics, 2012, 6, e139-e140.	3.1	3
78	Forensic genetics. Forensic Sciences Research, 2018, 3, 103-104.	1.6	3
79	Genetic polymorphisms of 21 STR loci of Golden*e*yeâ„¢ DNA ID 22NC kit in five ethnic groups of China. Forensic Sciences Research, 2019, 4, 348-350.	1.6	3
80	Genetic analysis of type 2 tri-allelic pattern at TPOX locus in the Chinese Han population. Molecular Genetics and Genomics, 2020, 295, 933-939.	2.1	3
81	A Functional Indel Polymorphism Within MIR155HG Is Associated With Sudden Cardiac Death Risk in a Chinese Population. Frontiers in Cardiovascular Medicine, 2021, 8, 671168.	2.4	3
82	Species identification through pyrosequencing 12S rRNA gene. Forensic Science International: Genetics Supplement Series, 2015, 5, e561-e563.	0.3	2
83	A study of the genetic diversity in the Heze Han population using a novel genotyping system based on 24 Y-chromosomal STR loci. Forensic Science International: Genetics Supplement Series, 2017, 6, e86-e88.	0.3	2
84	Genetic characterization of four dog breeds with Illumina CanineHD BeadChip. Forensic Sciences Research, 2019, 4, 354-357.	1.6	2
85	Mutation rates in father-son pairs of the 27 Y-STR loci in the Dezhou Han population from Shandong province, eastern China. Journal of Clinical Forensic and Legal Medicine, 2019, 67, 61-63.	1.0	2
86	Evaluating the amplification efficiency of the MALBACÂ® single-cell DNA Kit for trace DNA. Forensic Science International: Genetics Supplement Series, 2019, 7, 351-352.	0.3	2
87	Validation studies of the ParaDNA*Â®* Intelligence System with artificial evidence items. Forensic Sciences Research, 2021, 6, 84-91.	1.6	2
88	Multi-Locus Identification of *Psilocybe Cubensis* by High-Resolution Melting (HRM). Forensic Sciences Research, 2022, 7, 490-497.	1.6	2
89	Evaluating the effects of whole genome amplification strategies for amplifying trace DNA using capillary electrophoresis and massive parallel sequencing. Forensic Science International: Genetics, 2021, 56, 102599.	3.1	2
90	Modulation of STIM1 by a risk insertion/deletion polymorphism underlying genetics susceptibility to sudden cardiac death originated from coronary artery disease. Forensic Science International, 2021, 328, 111010.	2.2	2

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91	Forensic parameters of 41 Y-STR loci in Shandong Han individuals and comparison with 42 other populations. Forensic Sciences Research, 0, , 1-3.	1.6	2
92	Opportunity of Next-Generation Sequencing-Based Short Tandem Repeat System for Tumor Source Identification. Frontiers in Oncology, 2022, 12, 800028.	2.8	2
93	Genetic analysis of the 11 X-STR loci in Uigur and Northern Han populations from China. Forensic Science International: Genetics Supplement Series, 2011, 3, e423-e424.	0.3	1
94	Linkage disequilibrium analysis of 67 SNP loci on X chromosome. Forensic Science International: Genetics Supplement Series, 2011, 3, e431-e432.	0.3	1
95	UTI preventing DNA degradation of storing urinary samples for genotyping. Forensic Science International: Genetics Supplement Series, 2011, 3, e3-e4.	0.3	1
96	A new strategy for body source identification of tumor sample. Forensic Science International: Genetics Supplement Series, 2013, 4, e346-e347.	0.3	1
97	Investigation of parent-of-origin SNPs in 5 imprinted genes for forensic purpose. Forensic Science International: Genetics Supplement Series, 2013, 4, e304-e305.	0.3	1
98	Evaluation of HID-Ion Ampliseqâ„¢ panel in HAN population. Forensic Science International: Genetics Supplement Series, 2015, 5, e584-e586.	0.3	1
99	Genetic diversity of 21 forensic autosomal STRs and DYS391 in the Han population from Shanghai, Eastern China. Forensic Science International: Genetics, 2018, 37, e23-e25.	3.1	1
100	Analysis of full- and half-siblings using a combined system of STR, InDel and SNP markers. Forensic Science International: Genetics Supplement Series, 2019, 7, 349-350.	0.3	1
101	Developmental validation of the novel six-dye GoldeneyeTM DNAÂID System 35InDel kit for forensic application. Forensic Sciences Research, 0, , 1-12.	1.6	1
102	Genetic polymorphism of 125 Y-SNPs in Han population from Shandong province, China. Forensic Science International: Genetics Supplement Series, 2019, 7, 851-852.	0.3	1
103	Development and Validation of a Novel and Fast Detection Method for Cannabis sativa: A 19-Plex Short Tandem Repeat Typing System. Frontiers in Plant Science, 2022, 13, 837945.	3.6	1
104	Improving the system power of complex kinship analysis by combining multiple systems. Forensic Science International: Genetics, 2022, 60, 102741.	3.1	1
105	ABO genotyping by duplex amplification and oligonucleotide arrays assay. Forensic Science International: Genetics Supplement Series, 2009, 2, 131-133.	0.3	0
106	Development of 30 InDel markers typing system and genetic analysis in five different Chinese populations. Forensic Science International: Genetics Supplement Series, 2013, 4, e188-e189.	0.3	0
107	Logical Framework of Forensic Identification: Ability to Resist Fabricated DNA. Molecular Biotechnology, 2015, 57, 1030-1037.	2.4	0
108	Phylogenetic analysis of She population from Fujian Province in China based on 26 Y-STR Loci*. Forensic Science International: Genetics Supplement Series, 2015, 5, e520-e523.	0.3	0

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109	Genome-wide copy number variation analysis in monozygotic twins. Forensic Science International: Genetics Supplement Series, 2017, 6, e218-e220.	0.3	0
110	Response to commentary by Whittle, commentary on: More on the genomic identification of forensic STRs. Forensic Science International: Genetics, 2019, 40, e240-e242.	3.1	0
111	Forensic characteristics and phylogenetic structure of Eastern Chinese Han populations residing along the Yangtze Basin revealed by 19 autosomal STR loci. Molecular Biology Reports, 2019, 46, 2541-2546.	2.3	0
112	Parallel sequencing of 48 Y-chromosome STR and SNP markers. Forensic Science International: Genetics Supplement Series, 2019, 7, 347-348.	0.3	0
113	Genetic investigation of Chinese she ethnic based on autosomal STRs and X-STRs. Forensic Science International: Genetics Supplement Series, 2019, 7, 38-40.	0.3	0
114	Regulatory variation within 3â€™UTR of STAT5A correlates with sudden cardiac death in Chinese populations. Forensic Sciences Research, 0, , 1-10.	1.6	0
115	Genetic polymorphism of 190 Y-SNPs in Han population from Jiangsu province, China. Forensic Science International: Genetics Supplement Series, 2019, 7, 552-554.	0.3	0
116	Establishing an integrated pipeline for automatic and efficient detection of trace DNA encountered in forensic applications. Science and Justice - Journal of the Forensic Science Society, 2022, 62, 50-59.	2.1	0
117	Investigation on the genetic-inconsistent paternity cases using the MiSeq FGx system. Forensic Sciences Research, 0, , 1-6.	1.6	0
118	Novel Indel Variation of NPC1 Gene Associates With Risk of Sudden Cardiac Death. Frontiers in Genetics, 2022, 13, 869859.	2.3	0