

Jianye Ge

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

1,323
citations

331670

21
h-index

361022

35
g-index

50
all docs

50
docs citations

50
times ranked

1004
citing authors

#	ARTICLE	IF	CITATIONS
1	skater: an R package for SNP-based kinship analysis, testing, and evaluation. <i>F1000Research</i> , 2022, 11, 18.	1.6	5
2	Genetic study with 21 autosomal STRs in five Peruvian macro regions for human identification purposes. <i>Legal Medicine</i> , 2022, 57, 102073.	1.3	3
3	Forensic investigation approaches of searching relatives in DNA databases. <i>Journal of Forensic Sciences</i> , 2021, 66, 430-443.	1.6	32
4	Linkage and linkage disequilibrium among the markers in the forensic MPS panels. <i>Journal of Forensic Sciences</i> , 2021, 66, 1637-1646.	1.6	2
5	Genetic study with autosomal STR markers in people of the Peruvian jungle for human identification purposes. <i>Journal of the Canadian Society of Forensic Science</i> , 2021, 54, 117-138.	0.9	5
6	Developmental validation of VeriFiler [®] , [®] Plus PCR Amplification Kit: A 6-dye multiplex assay designed for casework samples. <i>Forensic Science International: Genetics</i> , 2021, 53, 102494.	3.1	16
7	Enhanced mixture interpretation with macrohaplotypes based on long-read DNA sequencing. <i>International Journal of Legal Medicine</i> , 2021, 135, 2189-2198.	2.2	5
8	Precision DNA Mixture Interpretation with Single-Cell Profiling. <i>Genes</i> , 2021, 12, 1649.	2.4	8
9	How many familial relationship testing results could be wrong?. <i>PLoS Genetics</i> , 2020, 16, e1008929.	3.5	15
10	Ancestry inference and admixture component estimations of Chinese Kazak group based on 165 AIM-SNPs via NGS platform. <i>Journal of Human Genetics</i> , 2020, 65, 461-468.	2.3	12
11	Developmental validation of the Huaxia [®] , [®] Platinum PCR amplification kit: A 6-dye multiplex direct amplification assay designed for Chinese reference samples. <i>Forensic Science International: Genetics</i> , 2019, 42, 190-197.	3.1	6
12	SNP typing using the HID-Ion AmpliSeq [®] , [®] Identity Panel in a southern Chinese population. <i>International Journal of Legal Medicine</i> , 2018, 132, 997-1006.	2.2	22
13	Developmental validation of the Yfiler [®] Plus PCR Amplification Kit: An enhanced Y-STR multiplex for casework and database applications. <i>Forensic Science International: Genetics</i> , 2016, 24, 164-175.	3.1	100
14	A convenient guideline to determine if two Y-STR profiles are from the same lineage. <i>Electrophoresis</i> , 2016, 37, 1659-1668.	2.4	14
15	Joseon Funerary Texts Tested Using Ancient DNA Analysis of a Korean Mummy. <i>Anatomical Record</i> , 2015, 298, 1191-1207.	1.4	16
16	Blind study evaluation illustrates utility of the Ion PGM [®] , [®] system for use in human identity DNA typing. <i>Croatian Medical Journal</i> , 2015, 56, 218-229.	0.7	37
17	Future directions of forensic DNA databases. <i>Croatian Medical Journal</i> , 2014, 55, 163-166.	0.7	47
18	Age estimation via quantification of signal-joint T cell receptor excision circles in Koreans. <i>Legal Medicine</i> , 2014, 16, 135-138.	1.3	21

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19	Characterization of 114 insertion/deletion (INDEL) polymorphisms, and selection for a global INDEL panel for human identification. <i>Legal Medicine</i> , 2014, 16, 26-32.	1.3	37
20	Modeling one complete versus triplicate analyses in low template DNA typing. <i>International Journal of Legal Medicine</i> , 2014, 128, 259-267.	2.2	5
21	Population genetics analysis of 38 STR loci in the She population from Fujian Province of China. <i>Legal Medicine</i> , 2014, 16, 314-318.	1.3	29
22	Developmental validation of the EX20+4 system. <i>Forensic Science International: Genetics</i> , 2014, 11, 207-213.	3.1	5
23	Mutation rates at 16 Y-chromosome STRs in the South China Han population. <i>International Journal of Legal Medicine</i> , 2013, 127, 369-372.	2.2	9
24	Population genetic analyses of the STR loci of the AmpFISTR NGM SElectâ„¢ kit for Han population in Fujian Province, China. <i>International Journal of Legal Medicine</i> , 2013, 127, 345-346.	2.2	7
25	Prototype PowerPlexÂ® Y23 System: A concordance study. <i>Forensic Science International: Genetics</i> , 2013, 7, 204-208.	3.1	34
26	Single nucleotide polymorphism typing with massively parallel sequencing for human identification. <i>International Journal of Legal Medicine</i> , 2013, 127, 1079-1086.	2.2	112
27	Variants observed for STR locus SE33: A concordance study. <i>Forensic Science International: Genetics</i> , 2012, 6, 494-497.	3.1	19
28	INNULs: A Novel Design Amplification Strategy for Retrotransposable Elements for Studying Population Variation. <i>Human Heredity</i> , 2012, 74, 27-35.	0.8	14
29	Kinship Index Variations among Populations and Thresholds for Familial Searching. <i>PLoS ONE</i> , 2012, 7, e37474.	2.5	15
30	Population data of 21 non-CODIS STR loci in Han population of northern China. <i>International Journal of Legal Medicine</i> , 2012, 126, 659-664.	2.2	35
31	A validation study of the Qiagen Investigator DIPplexÂ® kit; an INDEL-based assay for human identification. <i>International Journal of Legal Medicine</i> , 2012, 126, 533-540.	2.2	92
32	Maternity exclusion with a very high autosomal STRs kinship index. <i>International Journal of Legal Medicine</i> , 2012, 126, 645-648.	2.2	23
33	Developing criteria and data to determine best options for expanding the core CODIS loci. <i>Investigative Genetics</i> , 2012, 3, 1.	3.3	58
34	Choosing Relatives for DNA Identification of Missing Persons. <i>Journal of Forensic Sciences</i> , 2011, 56, S23-8.	1.6	56
35	Comparisons of Familial DNA Database Searching Strategies. <i>Journal of Forensic Sciences</i> , 2011, 56, 1448-1456.	1.6	52
36	Pedigree likelihood ratio for lineage markers. <i>International Journal of Legal Medicine</i> , 2011, 125, 519-525.	2.2	7

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37	Population genetic analyses of the NGM STR loci. <i>International Journal of Legal Medicine</i> , 2011, 125, 101-109.	2.2	58
38	Y-STR loci diversity in native Alaskan populations. <i>International Journal of Legal Medicine</i> , 2011, 125, 559-563.	2.2	8
39	Use of prior odds for missing persons identifications. <i>Investigative Genetics</i> , 2011, 2, 15.	3.3	33
40	Comments on "Interpreting Y chromosome STR haplotype mixture". <i>Legal Medicine</i> , 2011, 13, 52.	1.3	4
41	Haplotype block: a new type of forensic DNA markers. <i>International Journal of Legal Medicine</i> , 2010, 124, 353-361.	2.2	39
42	Interpreting Y chromosome STR haplotype mixture. <i>Legal Medicine</i> , 2010, 12, 137-143.	1.3	22
43	US forensic Y-chromosome short tandem repeats database. <i>Legal Medicine</i> , 2010, 12, 289-295.	1.3	29
44	DNA identification by pedigree likelihood ratio accommodating population substructure and mutations. <i>Investigative Genetics</i> , 2010, 1, 8.	3.3	32
45	Texas Population Substructure and Its Impact on Estimating the Rarity of Y STR Haplotypes from DNA Evidence*. <i>Journal of Forensic Sciences</i> , 2009, 54, 1016-1021.	1.6	35
46	The effects of Asian population substructure on Y STR forensic analyses. <i>Legal Medicine</i> , 2009, 11, 64-69.	1.3	22
47	Mutation rates at Y chromosome short tandem repeats in Texas populations. <i>Forensic Science International: Genetics</i> , 2009, 3, 179-184.	3.1	65