

Jiang-Wei Yan

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

1,268
citations

361413

20
h-index

414414

32
g-index

68
all docs

68
docs citations

68
times ranked

919
citing authors

#	ARTICLE	IF	CITATIONS
1	DLRAPom: a hybrid pipeline of Optimized XGBoost-guided integrative multiomics analysis for identifying targetable disease-related lncRNA-miRNA-mRNA regulatory axes. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	9
2	Role of dopamine D3 receptors in methamphetamine-induced behavioural sensitization and the characterization of dopamine receptors (D1R-D5R) gene expression in the brain. <i>Folia Neuropathologica</i> , 2022, 60, 105-113.	1.2	0
3	A new set of 20 Multi-Deletion markers for forensic application. <i>Electrophoresis</i> , 2022, 43, 1193-1202.	2.4	2
4	Typing of semen-containing mixtures using ARMS-based semen-specific CpG-InDel/STR markers. <i>International Journal of Legal Medicine</i> , 2022, 136, 1163-1176.	2.2	2
5	Estimating the time since deposition (TsD) in saliva stains using temporal changes in microbial markers. <i>Forensic Science International: Genetics</i> , 2022, 60, 102747.	3.1	6
6	Artificial intelligence applications for oncological positron emission tomography imaging. <i>European Journal of Radiology</i> , 2021, 134, 109448.	2.6	13
7	Development and validation of a multiplex 19 X-chromosomal short tandem repeats typing system for forensic purposes. <i>Scientific Reports</i> , 2021, 11, 609.	3.3	7
8	Predicting human age by detecting DNA methylation status in hair. <i>Electrophoresis</i> , 2021, 42, 1255-1261.	2.4	18
9	Development of a multiplex methylation-sensitive restriction enzyme-based SNP typing system for deconvolution of semen-containing mixtures. <i>International Journal of Legal Medicine</i> , 2021, 135, 1281-1294.	2.2	5
10	Forensic nanopore sequencing of STRs and SNPs using Verogen's ForenSeq DNA Signature Prep Kit and MinION. <i>International Journal of Legal Medicine</i> , 2021, 135, 1685-1693.	2.2	20
11	Predicting the postmortem interval of burial cadavers based on microbial community succession. <i>Forensic Science International: Genetics</i> , 2021, 52, 102488.	3.1	22
12	Identification of coding region SNPs from specific and sensitive mRNA biomarkers for the deconvolution of the semen donor in a body fluid mixture. <i>Forensic Science International: Genetics</i> , 2021, 52, 102483.	3.1	10
13	Actual mutational research of 19 autosomal STRs based on restricted mutation model and big data. <i>Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji</i> , 2021, 43, 949-961.	0.2	1
14	Genetic polymorphisms and mutation rates of 16 X-STRs in a Han Chinese population of Beijing and application examples in second-degree kinship cases. <i>International Journal of Legal Medicine</i> , 2020, 134, 163-168.	2.2	3
15	Levo-tetrahydropalmatine attenuates methamphetamine reward behavior and the accompanying activation of ERK phosphorylation in mice. <i>Neuroscience Letters</i> , 2020, 714, 134416.	2.1	14
16	Multiple methods used for type detection of uniparental disomy in paternity testing. <i>International Journal of Legal Medicine</i> , 2020, 134, 885-893.	2.2	6
17	Comparison of CE- and MPS-based analyses of forensic markers in a single cell after whole genome amplification. <i>Forensic Science International: Genetics</i> , 2020, 45, 102211.	3.1	12
18	A method of identifying the blood contributor in mixture stains through detecting blood-specific mRNA polymorphism. <i>Electrophoresis</i> , 2020, 41, 1364-1373.	2.4	9

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19	DNA typing from skeletal remains: a comparison between capillary electrophoresis and massively parallel sequencing platforms. <i>International Journal of Legal Medicine</i> , 2020, 134, 2029-2035.	2.2	0
20	Age estimation using bloodstain miRNAs based on massive parallel sequencing and machine learning: A pilot study. <i>Forensic Science International: Genetics</i> , 2020, 47, 102300.	3.1	14
21	The construction and application of a new 17-plex Y-STR system using universal fluorescent PCR. <i>International Journal of Legal Medicine</i> , 2020, 134, 2015-2027.	2.2	12
22	Non-pathological complete paternal uniparental isodisomy of chromosome 2 revealed in a maternity testing case. <i>International Journal of Legal Medicine</i> , 2019, 133, 993-997.	2.2	8
23	Multiple genetic analyses to investigate the polymorphisms of Chinese Mongolian population with an efficient short tandem repeat panel. <i>Croatian Medical Journal</i> , 2019, 60, 191-200.	0.7	5
24	MicroRNA profile analysis for discrimination of monozygotic twins using massively parallel sequencing and real-time PCR. <i>Forensic Science International: Genetics</i> , 2019, 38, 23-31.	3.1	15
25	Massively parallel sequencing of microRNA in bloodstains and evaluation of environmental influences on miRNA candidates using realtime polymerase chain reaction. <i>Forensic Science International: Genetics</i> , 2019, 38, 32-38.	3.1	20
26	A case of mother-daughter relationship with five inconsistencies with hereditary pattern out of 56 autosomal short tandem repeat markers. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 358-359.	0.3	0
27	A 472-SNP panel for pairwise kinship testing of second-degree relatives. <i>Forensic Science International: Genetics</i> , 2018, 34, 178-185.	3.1	37
28	Tri-allelic patterns of STRs and partially homologous non-sister chromatid crossover observed in a parentage test. <i>Legal Medicine</i> , 2018, 30, 34-37.	1.3	3
29	Inferring Chinese surnames with Y-STR profiles. <i>Forensic Science International: Genetics</i> , 2018, 33, 66-71.	3.1	12
30	Inconsistent genotyping call at DYS389 locus and implications for interpretation. <i>International Journal of Legal Medicine</i> , 2018, 132, 1043-1048.	2.2	3
31	Development of a massively parallel sequencing assay for investigating sequence polymorphisms of 15 short tandem repeats in a Chinese Northern Han population. <i>Electrophoresis</i> , 2018, 39, 2725-2731.	2.4	11
32	Haplotypic polymorphisms and mutation rate estimates of 22 Y-chromosome STRs in the Northern Chinese Han father-son pairs. <i>Scientific Reports</i> , 2018, 8, 7135.	3.3	9
33	Forensic effectiveness and population differentiations study of AGCU 21 + 1 fluorescence multiplex in Chinese Henan Han population. <i>Forensic Science International: Genetics</i> , 2017, 28, e18-e21.	3.1	5
34	Genetic polymorphism in three ethnic groups in the Chongqing region of China. <i>Forensic Science International: Genetics</i> , 2017, 30, e6-e7.	3.1	0
35	Genetic variability and forensic efficiency of 39 microsatellite loci in the Li ethnic group from Hainan Island in the South China Sea. <i>Annals of Human Biology</i> , 2017, 44, 467-474.	1.0	6
36	Development of a rapid 21-plex autosomal STR typing system for forensic applications. <i>Electrophoresis</i> , 2016, 37, 2789-2799.	2.4	5

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37	Allele and haplotype diversity of new multiplex of 19 ChrX-STR loci in Han population from Guanzhong region (China). <i>Electrophoresis</i> , 2016, 37, 1669-1675.	2.4	23
38	Genetic polymorphism analyses of a novel panel of 19 X-STR loci in the Chinese Uyгур ethnic minority. <i>Journal of Zhejiang University: Science B</i> , 2016, 17, 367-374.	2.8	13
39	A 30-InDel Assay for Genetic Variation and Population Structure Analysis of Chinese Tujia Group. <i>Scientific Reports</i> , 2016, 6, 36842.	3.3	32
40	A novel strategy for forensic age prediction by DNA methylation and support vector regression model. <i>Scientific Reports</i> , 2015, 5, 17788.	3.3	118
41	Genetic Variability and Phylogenetic Analysis of Han Population from Guanzhong Region of China based on 21 non-CODIS STR Loci. <i>Scientific Reports</i> , 2015, 5, 8872.	3.3	26
42	Developmental validation of the AGCU 21+1 STR kit: A novel multiplex assay for forensic application. <i>Electrophoresis</i> , 2015, 36, 271-276.	2.4	48
43	Genetic diversities of 20 novel autosomal STRs in Chinese Xibe ethnic group and its genetic relationships with neighboring populations. <i>Gene</i> , 2015, 557, 222-228.	2.2	20
44	Genetic distribution of 39 STR loci in 1027 unrelated Han individuals from Northern China. <i>Forensic Science International: Genetics</i> , 2015, 19, 205-206.	3.1	28
45	Concurrent copy number variations on chromosome 8 and 22 combined with mutation at FGA locus revealed in a parentage testing case. <i>Forensic Science International: Genetics</i> , 2015, 19, 81-85.	3.1	3
46	24 Y-chromosomal STR haplotypic polymorphisms for Chinese Uyгур ethnic group and its phylogenetic analysis with other Chinese groups. <i>Electrophoresis</i> , 2015, 36, 626-632.	2.4	9
47	Analysis of 19 STR loci reveals genetic characteristic of eastern Chinese Han population. <i>Forensic Science International: Genetics</i> , 2015, 14, 108-109.	3.1	38
48	Future directions of forensic DNA databases. <i>Croatian Medical Journal</i> , 2014, 55, 163-166.	0.7	47
49	Structural polymorphism analysis of Chinese Mongolian ethnic group revealed by a new STR panel: Genetic relationship to other groups. <i>Electrophoresis</i> , 2014, 35, 2008-2013.	2.4	15
50	Diversity study of 12 X-chromosomal STR loci in Hui ethnic from China. <i>Electrophoresis</i> , 2014, 35, 2001-2007.	2.4	15
51	Genetic profile characterization and population study of 21 autosomal STR in Chinese Kazak ethnic minority group. <i>Electrophoresis</i> , 2014, 35, 503-510.	2.4	31
52	Application of Next-generation Sequencing Technology in Forensic Science. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 190-197.	6.9	146
53	Polymorphic distribution and forensic effectiveness study of eight miniSTR in Chinese Uyghur ethnic group. <i>Molecular Biology Reports</i> , 2014, 41, 2371-2375.	2.3	5
54	Genetic analysis of 17 Y-chromosomal STR loci of Chinese Tujia ethnic group residing in Youyang Region of Southern China. <i>Legal Medicine</i> , 2014, 16, 173-175.	1.3	14

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55	Allelic frequency distributions of 21 non-combined DNA index system STR loci in a Russian ethnic minority group from Inner Mongolia, China. <i>Journal of Zhejiang University: Science B</i> , 2013, 14, 533-540.	2.8	23
56	Transcriptome dynamics during human erythroid differentiation and development. <i>Genomics</i> , 2013, 102, 431-441.	2.9	22
57	Allelic polymorphic investigation of 21 autosomal short tandem repeat loci in a Chinese Bai ethnic group. <i>Legal Medicine</i> , 2013, 15, 109-113.	1.3	27
58	Allelic diversity distributions of 21 new autosomal short tandem repeat loci in Chinese Ningxia Han population. <i>Forensic Science International: Genetics</i> , 2013, 7, e78-e79.	3.1	19
59	Polymorphic analysis of 21 new STR loci in Chinese Uigur group. <i>Forensic Science International: Genetics</i> , 2013, 7, e97-e98.	3.1	11
60	Population genetics and forensic efficiency of twenty-one novel microsatellite loci of Chinese Yi ethnic group. <i>Electrophoresis</i> , 2013, 34, 3345-3351.	2.4	18
61	Genetic data provided by 21 autosomal STR loci from Chinese Tujia ethnic group. <i>Molecular Biology Reports</i> , 2012, 39, 10265-10271.	2.3	28
62	Genetic variation of new 21 autosomal short tandem repeat loci in a Chinese Salar ethnic group. <i>Molecular Biology Reports</i> , 2012, 39, 1465-1470.	2.3	29
63	Genetic diversities of 21 non-CODIS autosomal STRs of a Chinese Tibetan ethnic minority group in Lhasa. <i>International Journal of Legal Medicine</i> , 2011, 125, 581-585.	2.2	39
64	Genetic polymorphisms for 17 Y-chromosomal STRs haplotypes in Chinese Hui population. <i>Legal Medicine</i> , 2008, 10, 163-169.	1.3	29
65	Population genetic polymorphisms for 17 Y-chromosomal STRs haplotypes of Chinese Salar ethnic minority group. <i>Legal Medicine</i> , 2007, 9, 203-209.	1.3	24
66	Genetic analysis of 15 STR loci on Chinese Tibetan in Qinghai Province. <i>Forensic Science International</i> , 2007, 169, e3-e6.	2.2	44