Hongyu Sun

List of Publications by Year
in descending order

50 papers	2,378 citations	430874 18 h-index	206112 48 g-index
53 all docs	53 docs citations	53 times ranked	2421 citing authors

#	Article	IF	Citations
1	Maternal Plasma DNA Sequencing Reveals the Genome-Wide Genetic and Mutational Profile of the Fetus. Science Translational Medicine, 2010, 2, 61ra91.	12.4	878
2	Non-invasive prenatal assessment of trisomy 21 by multiplexed maternal plasma DNA sequencing: large scale validity study. BMJ: British Medical Journal, 2011, 342, c7401-c7401.	2.3	641
3	Genetic polymorphisms and mutation rates of 27 Y-chromosomal STRs in a Han population from Guangdong Province, Southern China. Forensic Science International: Genetics, 2016, 21, 5-9.	3.1	76
4	Future directions of forensic DNA databases. Croatian Medical Journal, 2014, 55, 163-166.	0.7	47
5	Improved pairwise kinship analysis using massively parallel sequencing. Forensic Science International: Genetics, 2019, 38, 77-85.	3.1	46
6	Polymorphism analysis and evaluation of 19 STR loci in the Han population of Southern China. Annals of Human Biology, 2013, 40, 191-196.	1.0	42
7	Predicting Human Age with Bloodstains by sjTREC Quantification. PLoS ONE, 2012, 7, e42412.	2.5	42
8	Haplotype analysis of the polymorphic 40 Y-STR markers in Chinese populations. Forensic Science International: Genetics, 2015, 19, 255-262.	3.1	34
9	Null alleles of the X and Y chromosomal amelogenin gene in a Chinese population. International Journal of Legal Medicine, 2012, 126, 513-518.	2.2	33
10	Detection and quantification of the age-related sjTREC decline in human peripheral blood. International Journal of Legal Medicine, 2011, 125, 603-608.	2.2	29
11	Increased Expression and Altered Methylation of HERVWE1 in the Human Placentas of Smaller Fetuses from Monozygotic, Dichorionic, Discordant Twins. PLoS ONE, 2012, 7, e33503.	2.5	28
12	Genetic polymorphisms of twelve X-chromosomal STR loci in Chinese Han population from Guangdong Province. Forensic Science International: Genetics, 2011, 5, e114-e116.	3.1	26
13	Comparison of southern Chinese Han and Brazilian Caucasian mutation rates at autosomal short tandem repeat loci used in human forensic genetics. International Journal of Legal Medicine, 2014, 128, 1-9.	2.2	25
14	Epigenomeâ€wide <scp>DNA</scp> methylation assay reveals placental epigenetic markers for noninvasive fetal singleâ€nucleotide polymorphism genotyping in maternal plasma. Transfusion, 2014, 54, 2523-2533.	1.6	23
15	SNP typing using the HID-Ion AmpliSeqâ„¢ Identity Panel in a southern Chinese population. International Journal of Legal Medicine, 2018, 132, 997-1006.	2.2	22
16	Characterizing stutter variants in forensic STRs with massively parallel sequencing. Forensic Science International: Genetics, 2020, 45, 102225.	3.1	21
17	Identification of sequence polymorphisms at 58 STRs and 94 iiSNPs in a Tibetan population using massively parallel sequencing. Scientific Reports, 2020, 10, 12225.	3.3	20
18	Developmental validation of the MGIEasy Signature Identification Library Prep Kit, an all-in-one multiplex system for forensic applications. International Journal of Legal Medicine, 2021, 135, 739-753.	2.2	20

#	Article	IF	Citations
19	Detection of the deletion on Yp11.2 in a Chinese population. Forensic Science International: Genetics, 2014, 8, 73-79.	3.1	19
20	Complete paternal uniparental isodisomy for Chromosomeâ€ƒ2 revealed in a parentage testing case. Transfusion, 2013, 53, 1266-1269.	1.6	18
21	Development of a five ChX STRs loci typing system. International Journal of Legal Medicine, 2008, 122, 261-265.	2.2	17
22	Noninvasive fetal genotyping of paternally inherited alleles using targeted massively parallel sequencing in parentage testing cases. Transfusion, 2017, 57, 1505-1514.	1.6	16
23	Identification and sequencing of 59 highly polymorphic microhaplotypes for analysis of DNA mixtures. International Journal of Legal Medicine, 2021, 135, 1137-1149.	2.2	15
24	Investigation of the Application of miR10b and miR135b in the Identification of Semen Stains. PLoS ONE, 2015, 10, e0137067.	2.5	12
25	Pairwise kinship testing with microhaplotypes: Can advancements be made in kinship inference with these markers?. Forensic Science International, 2021, 325, 110875.	2.2	12
26	Genetic polymorphism and population structure of Torghut Mongols and comparison with a Mongolian population 3000 kilometers away. Forensic Science International: Genetics, 2019, 42, 235-243.	3.1	11
27	An SNP panel for the analysis of paternally inherited alleles in maternal plasma using ion Torrent PGM. International Journal of Legal Medicine, 2018, 132, 343-352.	2.2	10
28	A paternity case with mutations at three CODIS core STR loci. Forensic Science International: Genetics, 2012, 6, e61-e62.	3.1	9
29	Genome-wide screen for universal individual identification SNPs based on the HapMap and 1000 Genomes databases. Scientific Reports, 2018, 8, 5553.	3.3	9
30	Analysis of 17 Yâ€STR loci haplotype and Yâ€chromosome haplogroup distribution in five Chinese ethnic groups. Electrophoresis, 2015, 36, 2546-2552.	2.4	8
31	Detecting hypermethylated fetal <scp>RASSF</scp>1<scp>A</scp> sequences in maternal plasma: implications for noninvasive paternity testing in pregnancy. Transfusion, 2013, 53, 1856-1858.	1.6	7
32	Analysis of 24 Y-STR haplotype data in a Chinese Han population from Guangdong Province. International Journal of Legal Medicine, 2016, 130, 689-691.	2.2	7
33	The novel HLAâ€ÐQB1*03:01:01:12 allele, identified by nextâ€generation sequencing in a Chinese family. Hla, 2018, 91, 221-222.	0.6	7
34	Revisiting the potential power of human leukocyte antigen (HLA) genes on relationship testing by massively parallel sequencing-based HLA typing in an extended family. Journal of Human Genetics, 2019, 64, 29-38.	2.3	7
35	Noninvasive Prenatal Paternity Testing with a Combination of Well-Established SNP and STR Markers Using Massively Parallel Sequencing. Genes, 2021, 12, 454.	2.4	7
36	Polymorphism analysis of 15 STR loci in a large sample of the Han population in southern China. Forensic Science International: Genetics, 2009, 4, e27-e29.	3.1	6

#	Article	IF	Citations
37	Identification of the sequence variations of 15 autosomal STR loci in a Chinese population. Annals of Human Biology, 2014, 41, 524-530.	1.0	6
38	Nextâ€generation sequencingâ€based typing of a new allele HLAâ€DQB1*03:01:01:20 in a Chinese family. Hla, 2018, 91, 223-224.	0.6	6
39	Integrated massively parallel sequencing of 15 autosomal STRs and Amelogenin using a simplified library preparation approach. Electrophoresis, 2018, 39, 1466-1473.	2.4	5
40	HLAâ€A*02:01:01:28, a novel HLA allele identified by nextâ€generation sequencing in a Chinese family. Hla, 2018, 91, 195-196.	0.6	5
41	Genetic analysis of 39 Y-STR loci in a Han population from Henan province, central China. International Journal of Legal Medicine, 2019, 133, 95-97.	2.2	4
42	Genetic diversity of 17 autosomal STR loci in Meizhou Hakka population. International Journal of Legal Medicine, 2021, 135, 443-444.	2.2	4
43	Identification of the new HLAâ€DRB5*01:01:01:02 allele in a Chinese individual. Hla, 2019, 93, 56-57.	0.6	3
44	Characterization of genetic polymorphisms in Nigerians residing in Guangzhou using massively parallel sequencing. Forensic Science International: Genetics, 2020, 48, 102323.	3.1	3
45	Development and validation of a new 18 Xâ€STR typing assay for forensic applications. Electrophoresis, 2021, 42, 766-773.	2.4	3
46	Development of New mRNA Markers for the Identification of Menstrual Blood. Annals of Clinical and Laboratory Science, 2018, 48, 55-62.	0.2	3
47	The new allele HLAâ€DRB1*14:54:01:04 in a Chinese family identified using nextâ€generation sequencing. Hla, 2018, 92, 320-321.	0.6	2
48	Comparative evaluation of autosomal STRs and X-chromosome STRs as a complement of autosomal STRs in kinship testing in Southern Han Chinese. Annals of Human Biology, 2021, 48, 66-69.	1.0	2
49	Linkage and linkage disequilibrium among the markers in the forensic MPS panels. Journal of Forensic Sciences, 2021, 66, 1637-1646.	1.6	2
50	Identification of a rare off-ladder allele of the D13S325 locus during paternity testing. Legal Medicine, 2014, 16, 48-51.	1.3	0