

R Wu

List of Publications by Year in descending order

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papers

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1039406

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265
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#	ARTICLE	IF	CITATIONS
1	Comparative evaluation of autosomal STRs and X-chromosome STRs as a complement of autosomal STRs in kinship testing in Southern Han Chinese. <i>Annals of Human Biology</i> , 2021, 48, 66-69.	0.4	2
2	Developmental validation of the MGIEasy Signature Identification Library Prep Kit, an all-in-one multiplex system for forensic applications. <i>International Journal of Legal Medicine</i> , 2021, 135, 739-753.	1.2	20
3	Noninvasive Prenatal Paternity Testing with a Combination of Well-Established SNP and STR Markers Using Massively Parallel Sequencing. <i>Genes</i> , 2021, 12, 454.	1.0	7
4	Pairwise kinship testing with microhaplotypes: Can advancements be made in kinship inference with these markers?. <i>Forensic Science International</i> , 2021, 325, 110875.	1.3	12
5	Development and validation of a new 18 Xâ€STR typing assay for forensic applications. <i>Electrophoresis</i> , 2021, 42, 766-773.	1.3	3
6	Identification and sequencing of 59 highly polymorphic microhaplotypes for analysis of DNA mixtures. <i>International Journal of Legal Medicine</i> , 2021, 135, 1137-1149.	1.2	15
7	Characterizing stutter variants in forensic STRs with massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2020, 45, 102225.	1.6	21
8	Identification of sequence polymorphisms at 58 STRs and 94 iiSNPs in a Tibetan population using massively parallel sequencing. <i>Scientific Reports</i> , 2020, 10, 12225.	1.6	20
9	Characterization of genetic polymorphisms in Nigerians residing in Guangzhou using massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2020, 48, 102323.	1.6	3
10	Genetic polymorphism and population structure of Torghut Mongols and comparison with a Mongolian population 3000 kilometers away. <i>Forensic Science International: Genetics</i> , 2019, 42, 235-243.	1.6	11
11	High polymorphism detected by massively parallel sequencing of autosomal STRs using old blood samples from a Chinese Han population. <i>Scientific Reports</i> , 2019, 9, 18959.	1.6	3
12	Identification of the new <i>HLAâ€DRB5*01:01:01:02</i> allele in a Chinese individual. <i>Hla</i> , 2019, 93, 56-57.	0.4	3
13	Improved pairwise kinship analysis using massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2019, 38, 77-85.	1.6	46
14	Revisiting the potential power of human leukocyte antigen (HLA) genes on relationship testing by massively parallel sequencing-based HLA typing in an extended family. <i>Journal of Human Genetics</i> , 2019, 64, 29-38.	1.1	7
15	The novel <i>HLAâ€DQB1*03:01:01:12</i> allele, identified by nextâ€generation sequencing in a Chinese family. <i>Hla</i> , 2018, 91, 221-222.	0.4	7
16	Integrated massively parallel sequencing of 15 autosomal STRs and Amelogenin using a simplified library preparation approach. <i>Electrophoresis</i> , 2018, 39, 1466-1473.	1.3	5
17	Nextâ€generation sequencingâ€based typing of a new allele <i>HLAâ€DQB1*03:01:01:20</i> in a Chinese family. <i>Hla</i> , 2018, 91, 223-224.	0.4	6
18	<i>HLAâ€CA*02:01:01:28</i>, a novel HLA allele identified by nextâ€generation sequencing in a Chinese family. <i>Hla</i> , 2018, 91, 195-196.	0.4	5

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19	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.	1.2	22
20	The new allele <i>HLA*DRB1*14:54:01:04</i> in a Chinese family identified using next-generation sequencing. <i>Hla</i> , 2018, 92, 320-321.	0.4	2
21	Tandem amino acid repeats in the green anole (<i>Anolis carolinensis</i>) and other squamates may have a role in increasing genetic variability. <i>BMC Genomics</i> , 2016, 17, 109.	1.2	1
22	Hox cluster characterization of Banna caecilian (<i>Ichthyophis bannanicus</i>) provides hints for slow evolution of its genome. <i>BMC Genomics</i> , 2015, 16, 468.	1.2	7
23	A general scenario of Hoxgene inventory variation among major sarcopterygian lineages. <i>BMC Evolutionary Biology</i> , 2011, 11, 25.	3.2	25