

# R Wu

## List of Publications by Year in descending order

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23  
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docs citations

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times ranked

265  
citing authors

#	ARTICLE	IF	CITATIONS
1	Improved pairwise kinship analysis using massively parallel sequencing. Forensic Science International: Genetics, 2019, 38, 77-85.	1.6	46
2	A general scenario of Hoxgene inventory variation among major sarcopterygian lineages. BMC Evolutionary Biology, 2011, 11, 25.	3.2	25
3	SNP typing using the HID-Ion AmpliSeq <sup>®</sup> Identity Panel in a southern Chinese population. International Journal of Legal Medicine, 2018, 132, 997-1006.	1.2	22
4	Characterizing stutter variants in forensic STRs with massively parallel sequencing. Forensic Science International: Genetics, 2020, 45, 102225.	1.6	21
5	Identification of sequence polymorphisms at 58 STRs and 94 iSNPs in a Tibetan population using massively parallel sequencing. Scientific Reports, 2020, 10, 12225.	1.6	20
6	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.	1.2	20
7	Identification and sequencing of 59 highly polymorphic microhaplotypes for analysis of DNA mixtures. International Journal of Legal Medicine, 2021, 135, 1137-1149.	1.2	15
8	Pairwise kinship testing with microhaplotypes: Can advancements be made in kinship inference with these markers?. Forensic Science International, 2021, 325, 110875.	1.3	12
9	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.	1.6	11
10	Hox cluster characterization of Banna caecilian ( <i>Ichthyophis bannanicus</i> ) provides hints for slow evolution of its genome. BMC Genomics, 2015, 16, 468.	1.2	7
11	The novel <i>HLA-DQB1*03:01:01:12</i> allele, identified by next-generation sequencing in a Chinese family. Hla, 2018, 91, 221-222.	0.4	7
12	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.	1.1	7
13	Noninvasive Prenatal Paternity Testing with a Combination of Well-Established SNP and STR Markers Using Massively Parallel Sequencing. Genes, 2021, 12, 454.	1.0	7
14	Next-generation sequencing-based typing of a new allele <i>HLA-DQB1*03:01:01:20</i> in a Chinese family. Hla, 2018, 91, 223-224.	0.4	6
15	Integrated massively parallel sequencing of 15 autosomal STRs and Amelogenin using a simplified library preparation approach. Electrophoresis, 2018, 39, 1466-1473.	1.3	5
16	<i>HLA-CA*02:01:01:28</i> , a novel HLA allele identified by next-generation sequencing in a Chinese family. Hla, 2018, 91, 195-196.	0.4	5
17	High polymorphism detected by massively parallel sequencing of autosomal STRs using old blood samples from a Chinese Han population. Scientific Reports, 2019, 9, 18959.	1.6	3
18	Identification of the new <i>HLA-DRB5*01:01:01:02</i> allele in a Chinese individual. Hla, 2019, 93, 56-57.	0.4	3

#	ARTICLE	IF	CITATIONS
19	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
20	Development and validation of a new 18 X-STR typing assay for forensic applications. <i>Electrophoresis</i> , 2021, 42, 766-773.	1.3	3
21	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
22	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
23	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