

Rebecca Just

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

1,280
citations

430874
18
h-index

395702
33
g-index

33
all docs

33
docs citations

33
times ranked

1038
citing authors

#	ARTICLE	IF	CITATIONS
1	Single nucleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians. <i>International Journal of Legal Medicine</i> , 2004, 118, 137-146.	2.2	195
2	A multiplex allele-specific primer extension assay for forensically informative SNPs distributed throughout the mitochondrial genome. <i>International Journal of Legal Medicine</i> , 2004, 118, 147-157.	2.2	125
3	Mitochondrial DNA heteroplasmy in the emerging field of massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2015, 18, 131-139.	3.1	118
4	Full mtGenome reference data: Development and characterization of 588 forensic-quality haplotypes representing three U.S. populations. <i>Forensic Science International: Genetics</i> , 2015, 14, 141-155.	3.1	78
5	Performance and concordance of the ForenSeq [®] system for autosomal and Y chromosome short tandem repeat sequencing of reference-type specimens. <i>Forensic Science International: Genetics</i> , 2017, 28, 1-9.	3.1	76
6	Internal validation of STRmix [®] for the interpretation of single source and mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2017, 29, 126-144.	3.1	74
7	Short tandem repeat typing on the 454 platform: Strategies and considerations for targeted sequencing of common forensic markers. <i>Forensic Science International: Genetics</i> , 2014, 12, 107-119.	3.1	68
8	Development and expansion of high-quality control region databases to improve forensic mtDNA evidence interpretation. <i>Forensic Science International: Genetics</i> , 2007, 1, 154-157.	3.1	49
9	Validation of NGS for mitochondrial DNA casework at the FBI Laboratory. <i>Forensic Science International: Genetics</i> , 2020, 44, 102151.	3.1	48
10	Complete mitochondrial genome sequences for 265 African American and U.S. "Hispanic" individuals. <i>Forensic Science International: Genetics</i> , 2008, 2, e45-e48.	3.1	38
11	DNA Identification of "Earthquake McGoon" 50 Years Postmortem. <i>Journal of Forensic Sciences</i> , 2007, 52, 1115-1118.	1.6	37
12	Effective strategies for forensic analysis in the mitochondrial DNA coding region. <i>International Journal of Legal Medicine</i> , 2006, 120, 27-32.	2.2	34
13	A closer look at Verogen's ForenSeq [®] DNA Signature Prep kit autosomal and Y-STR data for streamlined analysis of routine reference samples. <i>Electrophoresis</i> , 2018, 39, 2685-2693.	2.4	34
14	mtGenome reference population databases and the future of forensic mtDNA analysis. <i>Forensic Science International: Genetics</i> , 2011, 5, 222-225.	3.1	33
15	The Use of Mitochondrial DNA Single Nucleotide Polymorphisms to Assist in the Resolution of Three Challenging Forensic Cases. <i>Journal of Forensic Sciences</i> , 2009, 54, 887-891.	1.6	32
16	Use of the LUS in sequence allele designations to facilitate probabilistic genotyping of NGS-based STR typing results. <i>Forensic Science International: Genetics</i> , 2018, 34, 197-205.	3.1	29
17	Questioning the prevalence and reliability of human mitochondrial DNA heteroplasmy from massively parallel sequencing data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4546-7.	7.1	25
18	Assessing the potential of next generation sequencing technologies for missing persons identification efforts. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e447-e448.	0.3	19

#	ARTICLE	IF	CITATIONS
19	Short tandem repeat sequencing on the 454 platform. Forensic Science International: Genetics Supplement Series, 2011, 3, e357-e358.	0.3	18
20	Characterization of a modified amplification approach for improved STR recovery from severely degraded skeletal elements. Forensic Science International: Genetics, 2012, 6, 578-587.	3.1	18
21	Development of forensic-quality full mtGenome haplotypes: Success rates with low template specimens. Forensic Science International: Genetics, 2014, 10, 73-79.	3.1	18
22	Titanic's unknown child: The critical role of the mitochondrial DNA coding region in a re-identification effort. Forensic Science International: Genetics, 2011, 5, 231-235.	3.1	17
23	Mitochondrial control region sequences from a U.S. "Hispanic" population sample. Forensic Science International: Genetics, 2008, 2, e19-e23.	3.1	15
24	Mitochondrial control region sequences from an African American population sample. Forensic Science International: Genetics, 2009, 4, e45-e52.	3.1	15
25	Identification of West Eurasian mitochondrial haplogroups by mtDNA SNP screening: Results of the 2006-2007 EDNAP collaborative exercise. Forensic Science International: Genetics, 2008, 2, 61-68.	3.1	13
26	Sequence-based autosomal STR characterization in four US populations using PowerSeq [®] , [®] Auto/Y system. Forensic Science International: Genetics, 2020, 48, 102311.	3.1	11
27	The mitochondrial landscape of African Americans: An examination of more than 2500 control region haplotypes from 22 U.S. locations. Forensic Science International: Genetics, 2016, 22, 139-148.	3.1	10
28	An examination of STR nomenclatures, filters and models for MPS mixture interpretation. Forensic Science International: Genetics, 2020, 48, 102319.	3.1	10
29	Modeling allelic analyte signals for aSTRs in NGS DNA profiles. Journal of Forensic Sciences, 2021, 66, 1234-1245.	1.6	8
30	Variability and additivity of read counts for aSTRs in NGS DNA profiles. Forensic Science International: Genetics, 2020, 48, 102351.	3.1	5
31	The application of mtDNA SNPs to a forensic case. Forensic Science International: Genetics Supplement Series, 2008, 1, 295-297.	0.3	4
32	Evaluation of automatable silica-based extraction methods for low quantity samples. Forensic Science International: Genetics Supplement Series, 2011, 3, e504-e505.	0.3	4
33	Automation of high volume MPS mixture interpretation using CaseSolver. Forensic Science International: Genetics Supplement Series, 2019, 7, 14-15.	0.3	2