

Nicole Mm Novroski

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

770
citations

858243

12
h-index

939365

18
g-index

19
all docs

19
docs citations

19
times ranked

664
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessing DNA recovery and profile determination from bloody snow. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2022, 62, 152-155.	1.3	0
2	Evolution of single nucleotide polymorphism use in forensic genetics. <i>Wiley Interdisciplinary Reviews Forensic Science</i> , 2022, 4, .	1.2	5
3	Microbial Forensics: A Present to Future Perspective on Genomic Targets, Bioinformatic Challenges, and Applications. <i>Forensic Genomics</i> , 2022, 2, 42-64.	0.3	3
4	Exploring new short tandem repeat markers for <scp>DNA</scp> mixture deconvolution. <i>Wiley Interdisciplinary Reviews Forensic Science</i> , 2021, 3, .	1.2	2
5	Identity informative SNP associations in the UK Biobank. <i>Forensic Science International: Genetics</i> , 2019, 42, 45-48.	1.6	10
6	Expanding beyond the current core STR loci: An exploration of 73 STR markers with increased diversity for enhanced DNA mixture deconvolution. <i>Forensic Science International: Genetics</i> , 2019, 38, 121-129.	1.6	23
7	Forensic human identification with targeted microbiome markers using nearest neighbor classification. <i>Forensic Science International: Genetics</i> , 2019, 38, 130-139.	1.6	45
8	Insertion within the flanking region of the D10S1237 locus. <i>Forensic Science International: Genetics</i> , 2018, 35, e4-e6.	1.6	2
9	Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. <i>Forensic Science International: Genetics</i> , 2018, 32, 50-61.	1.6	69
10	Potential highly polymorphic short tandem repeat markers for enhanced forensic identity testing. <i>Forensic Science International: Genetics</i> , 2018, 37, 162-171.	1.6	13
11	Increasing the discrimination power of ancestry- and identity-informative SNP loci within the ForenSeq [®] , [®] DNA Signature Prep Kit. <i>Forensic Science International: Genetics</i> , 2018, 36, 60-76.	1.6	41
12	Flanking region variation of ForenSeq [®] , [®] DNA Signature Prep Kit STR and SNP loci in Yavapai Native Americans. <i>Forensic Science International: Genetics</i> , 2017, 28, 146-154.	1.6	60
13	Population and performance analyses of four major populations with Illumina [®] FCx Forensic Genomics System. <i>Forensic Science International: Genetics</i> , 2017, 30, 81-92.	1.6	70
14	Massively parallel sequencing of 68 insertion/deletion markers identifies novel microhaplotypes for utility in human identity testing. <i>Forensic Science International: Genetics</i> , 2016, 25, 198-209.	1.6	29
15	Characterization of genetic sequence variation of 58 STR loci in four major population groups. <i>Forensic Science International: Genetics</i> , 2016, 25, 214-226.	1.6	138
16	Genetic analysis of the Yavapai Native Americans from West-Central Arizona using the Illumina MiSeq FGx [®] , [®] forensic genomics system. <i>Forensic Science International: Genetics</i> , 2016, 24, 18-23.	1.6	68
17	Novel Y-chromosome Short Tandem Repeat Variants Detected Through the Use of Massively Parallel Sequencing. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 250-257.	3.0	28
18	High-quality and high-throughput massively parallel sequencing of the human mitochondrial genome using the Illumina MiSeq. <i>Forensic Science International: Genetics</i> , 2014, 12, 128-135.	1.6	155

#	ARTICLE	IF	CITATIONS
19	The Evaluation of Possible False Positives with Detergents when Performing Amylase Serological Testing on Clothing. Journal of Forensic Sciences, 2013, 58, S183-5.	0.9	9