Jennifer Churchill Cihlar

List of Publications by Year
in descending order

28	1,124	471371 17	477173 29
papers	citations	h-index	g-index

30	30	30	1019
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Validation of the Applied Biosystems RapidHIT ID instrument and ACE GlobalFiler Express sample cartridge. International Journal of Legal Medicine, 2022, 136, 13-41.	1.2	9
2	Evolution of singleâ€nucleotide polymorphism use in forensic genetics. Wiley Interdisciplinary Reviews Forensic Science, 2022, 4, .	1.2	5
3	A Continuous Statistical Phasing Framework for the Analysis of Forensic Mitochondrial DNA Mixtures. Genes, 2021, 12, 128.	1.0	10
4	International Wildlife Trafficking: A perspective on the challenges and potential forensic genetics solutions. Forensic Science International: Genetics, 2021, 54, 102551.	1.6	20
5	Distinguishing mitochondrial DNA and NUMT sequences amplified with the precision ID mtDNA whole genome panel. Mitochondrion, 2020, 55, 122-133.	1.6	24
6	Developmental Validation of a MPS Workflow with a PCR-Based Short Amplicon Whole Mitochondrial Genome Panel. Genes, 2020, 11, 1345.	1.0	30
7	Numt identification and removal with RtN!. Bioinformatics, 2020, 36, 5115-5116.	1.8	18
8	The lot-to-lot variability in the mitochondrial genome of controls. Forensic Science International: Genetics, 2020, 47, 102298.	1.6	6
9	Evaluation of mitogenome sequence concordance, heteroplasmy detection, and haplogrouping in a worldwide lineage study using the Precision ID mtDNA Whole Genome Panel. Forensic Science International: Genetics, 2019, 42, 244-251.	1.6	37
10	Massively parallel sequencing-enabled mixture analysis of mitochondrial DNA samples. International Journal of Legal Medicine, 2018, 132, 1263-1272.	1.2	36
11	Increasing the discrimination power of ancestry- and identity-informative SNP loci within the ForenSeqâ„¢ DNA Signature Prep Kit. Forensic Science International: Genetics, 2018, 36, 60-76.	1.6	41
12	Flanking region variation of ForenSeqâ„¢ DNA Signature Prep Kit STR and SNP loci in Yavapai Native Americans. Forensic Science International: Genetics, 2017, 28, 146-154.	1.6	60
13	Parsing apart the contributors of mitochondrial DNA mixtures with massively parallel sequencing data. Forensic Science International: Genetics Supplement Series, 2017, 6, e439-e441.	0.1	5
14	Working towards implementation of whole genome mitochondrial DNA sequencing into routine casework. Forensic Science International: Genetics Supplement Series, 2017, 6, e388-e389.	0.1	14
15	Population and performance analyses of four major populations with Illuminaâ€™s FGx Forensic Genomics System. Forensic Science International: Genetics, 2017, 30, 81-92.	1.6	70
16	Analysis of Short Tandem Repeat and Single Nucleotide Polymorphism Loci From Single-Source Samples Using a Custom HaloPlex Target Enrichment System Panel. American Journal of Forensic Medicine and Pathology, 2016, 37, 99-107.	0.4	16
17	Massively parallel sequencing of 68 insertion/deletion markers identifies novel microhaplotypes for utility in human identity testing. Forensic Science International: Genetics, 2016, 25, 198-209.	1.6	29
18	Characterization of genetic sequence variation of 58 STR loci in four major population groups. Forensic Science International: Genetics, 2016, 25, 214-226.	1.6	138

#	Article	IF	Citations
19	More comprehensive forensic genetic marker analyses for accurate human remains identification using massively parallel DNA sequencing. BMC Genomics, 2016, 17, 750.	1.2	47
20	The Next State-of-the-Art Forensic Genetics Technology: Massively Parallel Sequencing. Security Science and Technology, 2016, , 249-291.	0.5	1
21	Genetic analysis of the Yavapai Native Americans from West-Central Arizona using the Illumina MiSeq FGxâ„¢ forensic genomics system. Forensic Science International: Genetics, 2016, 24, 18-23.	1.6	68
22	Effects of the Ion PGMâ„¢ Hi-Qâ„¢ sequencing chemistry on sequence data quality. International Journal of Legal Medicine, 2016, 130, 1169-1180.	1.2	28
23	Evaluation of the Illumina Â® Beta Version ForenSeqâ„¢ DNA Signature Prep Kit for use in genetic profiling. Forensic Science International: Genetics, 2016, 20, 20-29.	1.6	185
24	Empirical testing of a 23-AIMs panel of SNPs for ancestry evaluations in four major US populations. International Journal of Legal Medicine, 2016, 130, 891-896.	1.2	8
25	Novel Y-chromosome Short Tandem Repeat Variants Detected Through the Use of Massively Parallel Sequencing. Genomics, Proteomics and Bioinformatics, 2015, 13, 250-257.	3.0	28
26	Blind study evaluation illustrates utility of the Ion PGMâ„¢ system for use in human identity DNA typing. Croatian Medical Journal, 2015, 56, 218-229.	0.2	37
27	Exome-Based Mapping and Variant Prioritization for Inherited Mendelian Disorders. American Journal of Human Genetics, 2014, 94, 373-384.	2.6	37
28	Mutations in the X-Linked Retinitis Pigmentosa GenesRPGRandRP2Found in 8.5% of Families with a Provisional Diagnosis of Autosomal Dominant Retinitis Pigmentosa. , 2013, 54, 1411.		113