

# Kimberly Sturk-Andreaggi

## List of Publications by Year in descending order

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Version: 2024-02-01

29  
papers

632  
citations

516561

16  
h-index

610775

24  
g-index

30  
all docs

30  
docs citations

30  
times ranked

467  
citing authors

#	ARTICLE	IF	CITATIONS
1	Extended kinship analysis of historical remains using SNP capture. <i>Forensic Science International: Genetics</i> , 2022, 57, 102636.	1.6	26
2	Ancient DNA Methods Improve Forensic DNA Profiling of Korean War and World War II Unknowns. <i>Genes</i> , 2022, 13, 129.	1.0	22
3	The Value of Whole-Genome Sequencing for Mitochondrial DNA Population Studies: Strategies and Criteria for Extracting High-Quality Mitogenome Haplotypes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2244.	1.8	4
4	Capture enrichment and massively parallel sequencing for human identification. <i>Forensic Science International: Genetics</i> , 2021, 53, 102496.	1.6	19
5	The FORCE Panel: An All-in-One SNP Marker Set for Confirming Investigative Genetic Genealogy Leads and for General Forensic Applications. <i>Genes</i> , 2021, 12, 1968.	1.0	27
6	Impact of the sequencing method on the detection and interpretation of mitochondrial DNA length heteroplasmy. <i>Forensic Science International: Genetics</i> , 2020, 44, 102205.	1.6	25
7	Next generation sequencing of STR artifacts produced from historical bone samples. <i>Forensic Science International: Genetics</i> , 2020, 49, 102397.	1.6	2
8	Pathogenic Variant Filtering for Mitochondrial Genome Haplotype Reporting. <i>Genes</i> , 2020, 11, 1140.	1.0	6
9	Platinum-Quality Mitogenome Haplotypes from United States Populations. <i>Genes</i> , 2020, 11, 1290.	1.0	17
10	A Forensic Genomics Approach for the Identification of Sister Marija Crucifiksa Kozulić. <i>Genes</i> , 2020, 11, 938.	1.0	4
11	Mitochondrial DNA haplogrouping to assist with the identification of unknown service members from the World War II Battle of Tarawa. <i>Forensic Science International: Genetics</i> , 2020, 47, 102291.	1.6	8
12	Resolving mitochondrial haplogroups B2 and B4 with next-generation mitogenome sequencing to distinguish Native American from Asian haplotypes. <i>Forensic Science International: Genetics</i> , 2019, 43, 102143.	1.6	7
13	Mitochondrial DNA control region variation in Lebanon, Jordan, and Bahrain. <i>Forensic Science International: Genetics</i> , 2019, 42, 99-102.	1.6	6
14	Advancing mitochondrial genome data interpretation in missing persons casework. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 721-723.	0.1	2
15	Developmental validation of a Nextera XT mitogenome Illumina MiSeq sequencing method for high-quality samples. <i>Forensic Science International: Genetics</i> , 2018, 34, 25-36.	1.6	35
16	Repair of DNA damage caused by cytosine deamination in mitochondrial DNA of forensic case samples. <i>Forensic Science International: Genetics</i> , 2018, 34, 257-264.	1.6	38
17	Bioinformatic removal of NUMT-associated variants in mitotyping next-generation sequencing data from whole blood samples. <i>Electrophoresis</i> , 2018, 39, 2785-2797.	1.3	32
18	A performance evaluation of Nextera XT and KAPA HyperPlus for rapid Illumina library preparation of long-range mitogenome amplicons. <i>Forensic Science International: Genetics</i> , 2017, 29, 174-180.	1.6	38

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19	AQME: A forensic mitochondrial DNA analysis tool for next-generation sequencing data. <i>Forensic Science International: Genetics</i> , 2017, 31, 189-197.	1.6	27
20	Performance evaluation of a mitogenome capture and Illumina sequencing protocol using non-probative, case-type skeletal samples: Implications for the use of a positive control in a next-generation sequencing procedure. <i>Forensic Science International: Genetics</i> , 2017, 31, 198-206.	1.6	63
21	Concordance and reproducibility of a next generation mtGenome sequencing method for high-quality samples using the Illumina MiSeq. <i>Forensic Science International: Genetics</i> , 2016, 24, 103-111.	1.6	40
22	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.	1.6	78
23	Mitochondrial control region variation in a Korean population sample. <i>International Journal of Legal Medicine</i> , 2014, 128, 745-746.	1.2	3
24	Development of forensic-quality full mtGenome haplotypes: Success rates with low template specimens. <i>Forensic Science International: Genetics</i> , 2014, 10, 73-79.	1.6	18
25	A high-throughput Sanger strategy for human mitochondrial genome sequencing. <i>BMC Genomics</i> , 2013, 14, 881.	1.2	37
26	Mitochondrial DNA control region variation from samples of the Moroccan population. <i>International Journal of Legal Medicine</i> , 2013, 127, 757-759.	1.2	9
27	Evaluation of automatable silica-based extraction methods for low quantity samples. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e504-e505.	0.1	4
28	Titanic's unknown child: The critical role of the mitochondrial DNA coding region in a re-identification effort. <i>Forensic Science International: Genetics</i> , 2011, 5, 231-235.	1.6	17
29	Mitochondrial DNA control region variation in a Kuwaiti population sample. <i>Forensic Science International: Genetics</i> , 2011, 5, e112-e113.	1.6	18