

Jonathan L King

List of Publications by Year in descending order

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91
papers

3,073
citations

147801

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96
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docs citations

96
times ranked

1596
citing authors

#	ARTICLE	IF	CITATIONS
1	A Continuous Statistical Phasing Framework for the Analysis of Forensic Mitochondrial DNA Mixtures. <i>Genes</i> , 2021, 12, 128.	2.4	10
2	Reducing noise and stutter in short tandem repeat loci with unique molecular identifiers. <i>Forensic Science International: Genetics</i> , 2021, 51, 102459.	3.1	9
3	STRait Razor Online: An enhanced user interface to facilitate interpretation of MPS data. <i>Forensic Science International: Genetics</i> , 2021, 52, 102463.	3.1	16
4	Autosomal STR and SNP characterization of populations from the Northeastern Peruvian Andes with the ForenSeq [®] , [®] DNA Signature Prep Kit. <i>Forensic Science International: Genetics</i> , 2021, 52, 102487.	3.1	13
5	Evaluation of Promega PowerSeq [®] , [®] Auto/Y systems prototype on an admixed sample of Rio de Janeiro, Brazil: Population data, sensitivity, stutter and mixture studies. <i>Forensic Science International: Genetics</i> , 2021, 53, 102516.	3.1	13
6	Enhanced mixture interpretation with macrohaplotypes based on long-read DNA sequencing. <i>International Journal of Legal Medicine</i> , 2021, 135, 2189-2198.	2.2	5
7	Reverse complement-PCR, an innovative and effective method for multiplexing forensically relevant single nucleotide polymorphism [®] marker systems. <i>BioTechniques</i> , 2021, 71, 484-489.	1.8	6
8	MMDIT: A tool for the deconvolution and interpretation of mitochondrial DNA mixtures. <i>Forensic Science International: Genetics</i> , 2021, 55, 102568.	3.1	4
9	Graph Algorithms for Mixture Interpretation. <i>Genes</i> , 2021, 12, 185.	2.4	5
10	Association of whole mtDNA, an NADPH G11914A variant, and haplogroups with high physical performance in an elite military troop. <i>Brazilian Journal of Medical and Biological Research</i> , 2021, 54, e10317.	1.5	0
11	Precision DNA Mixture Interpretation with Single-Cell Profiling. <i>Genes</i> , 2021, 12, 1649.	2.4	8
12	A genome-wide association study of tramadol metabolism from post-mortem samples. <i>Pharmacogenomics Journal</i> , 2020, 20, 94-103.	2.0	3
13	Copan microFLOQ [®] Direct Swab collection of bloodstains, saliva, and semen on cotton cloth. <i>International Journal of Legal Medicine</i> , 2020, 134, 45-54.	2.2	13
14	Reverse Complement PCR: A novel one-step PCR system for typing highly degraded DNA for human identification. <i>Forensic Science International: Genetics</i> , 2020, 44, 102201.	3.1	13
15	Forensic genetic investigation of human skeletal remains recovered from the La Belle shipwreck. <i>Forensic Science International</i> , 2020, 306, 110050.	2.2	16
16	Genetic assessment reveals no population substructure and divergent regional and sex-specific histories in the Chachapoyas from northeast Peru. <i>PLoS ONE</i> , 2020, 15, e0244497.	2.5	5
17	Utility of the Ion S5 [®] , [®] and MiSeq FG [®] , [®] sequencing platforms to characterize challenging human remains. <i>Legal Medicine</i> , 2019, 41, 101623.	1.3	23
18	Compound stutter in D2S1338 and D12S391. <i>Forensic Science International: Genetics</i> , 2019, 39, 50-56.	3.1	9

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19	Assessment of impact of DNA extraction methods on analysis of human remain samples on massively parallel sequencing success. <i>International Journal of Legal Medicine</i> , 2019, 133, 51-58.	2.2	22
20	Massively parallel sequencing-enabled mixture analysis of mitochondrial DNA samples. <i>International Journal of Legal Medicine</i> , 2018, 132, 1263-1272.	2.2	36
21	“The devil’s in the detail”: Release of an expanded, enhanced and dynamically revised forensic STR Sequence Guide. <i>Forensic Science International: Genetics</i> , 2018, 34, 162-169.	3.1	73
22	Evaluation of InnoTyper® 21 in a sample of Rio de Janeiro population as an alternative forensic panel. <i>International Journal of Legal Medicine</i> , 2018, 132, 149-151.	2.2	6
23	Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. <i>Forensic Science International: Genetics</i> , 2018, 32, 50-61.	3.1	69
24	Comparative tolerance of two massively parallel sequencing systems to common PCR inhibitors. <i>International Journal of Legal Medicine</i> , 2018, 132, 983-995.	2.2	25
25	Massively parallel sequencing of 12 autosomal STRs in <i>Cannabis sativa</i> . <i>Electrophoresis</i> , 2018, 39, 2906-2911.	2.4	11
26	Evaluation of the precision ID mtDNA whole genome panel on two massively parallel sequencing systems. <i>Forensic Science International: Genetics</i> , 2018, 36, 213-224.	3.1	35
27	Increasing the discrimination power of ancestry- and identity-informative SNP loci within the ForenSeq™,ϕ DNA Signature Prep Kit. <i>Forensic Science International: Genetics</i> , 2018, 36, 60-76.	3.1	41
28	Flanking region variation of ForenSeq™,ϕ DNA Signature Prep Kit STR and SNP loci in Yavapai Native Americans. <i>Forensic Science International: Genetics</i> , 2017, 28, 146-154.	3.1	60
29	STRait Razor v2s: Advancing sequence-based STR allele reporting and beyond to other marker systems. <i>Forensic Science International: Genetics</i> , 2017, 29, 21-28.	3.1	39
30	Development and validation of a novel multiplexed DNA analysis system, InnoTyper® 21. <i>Forensic Science International: Genetics</i> , 2017, 29, 80-99.	3.1	23
31	Parsing apart the contributors of mitochondrial DNA mixtures with massively parallel sequencing data. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e439-e441.	0.3	5
32	STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci. <i>Forensic Science International: Genetics</i> , 2017, 31, 111-117.	3.1	77
33	Population and performance analyses of four major populations with Illumina®™s FGx Forensic Genomics System. <i>Forensic Science International: Genetics</i> , 2017, 30, 81-92.	3.1	70
34	Flanking Variation Influences Rates of Stutter in Simple Repeats. <i>Genes</i> , 2017, 8, 329.	2.4	19
35	A technique for setting analytical thresholds in massively parallel sequencing-based forensic DNA analysis. <i>PLoS ONE</i> , 2017, 12, e0178005.	2.5	16
36	Y-chromosomal analysis of Greek Cypriots reveals a primarily common pre-Ottoman paternal ancestry with Turkish Cypriots. <i>PLoS ONE</i> , 2017, 12, e0179474.	2.5	13

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37	Investigation of the STR loci noise distributions of PowerSeq [®] , [®] Auto System. Croatian Medical Journal, 2017, 58, 214-221.	0.7	12
38	Fast STR allele identification with STRait Razor 3.0. Forensic Science International: Genetics, 2017, 30, 18-23.	3.1	82
39	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.	0.8	16
40	D5S2500 is an ambiguously characterized STR: Identification and description of forensic microsatellites in the genomics age.. Forensic Science International: Genetics, 2016, 23, 19-24.	3.1	21
41	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.	3.1	29
42	Characterization of genetic sequence variation of 58 STR loci in four major population groups. Forensic Science International: Genetics, 2016, 25, 214-226.	3.1	138
43	More comprehensive forensic genetic marker analyses for accurate human remains identification using massively parallel DNA sequencing. BMC Genomics, 2016, 17, 750.	2.8	47
44	The Next State-of-the-Art Forensic Genetics Technology: Massively Parallel Sequencing. Security Science and Technology, 2016, , 249-291.	0.5	1
45	Genetic analysis of the Yavapai Native Americans from West-Central Arizona using the Illumina MiSeq FG [®] , [®] forensic genomics system. Forensic Science International: Genetics, 2016, 24, 18-23.	3.1	68
46	Effects of the Ion PGM [®] , [®] Hi-Q [®] , [®] sequencing chemistry on sequence data quality. International Journal of Legal Medicine, 2016, 130, 1169-1180.	2.2	28
47	Evaluation of the Illumina [®] Beta Version ForenSeq [®] , [®] DNA Signature Prep Kit for use in genetic profiling. Forensic Science International: Genetics, 2016, 20, 20-29.	3.1	185
48	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.	2.2	8
49	Modified DOP-PCR for improved STR typing of degraded DNA from human skeletal remains and bloodstains. Legal Medicine, 2016, 18, 7-12.	1.3	18
50	Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements. Forensic Science International: Genetics, 2016, 22, 54-63.	3.1	190
51	Selection of highly informative SNP markers for population affiliation of major US populations. International Journal of Legal Medicine, 2016, 130, 341-352.	2.2	30
52	Whole mitochondrial genome genetic diversity in an Estonian population sample. International Journal of Legal Medicine, 2016, 130, 67-71.	2.2	33
53	Correcting Inconsistencies and Errors in Bacterial Genome Metadata Using an Automated Curation Tool in Excel (AutoCurE). Frontiers in Bioengineering and Biotechnology, 2015, 3, 138.	4.1	8
54	Novel Y-chromosome Short Tandem Repeat Variants Detected Through the Use of Massively Parallel Sequencing. Genomics, Proteomics and Bioinformatics, 2015, 13, 250-257.	6.9	28

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55	Massively parallel sequencing of forensically relevant single nucleotide polymorphisms using TruSeq [®] , [®] forensic amplicon. <i>International Journal of Legal Medicine</i> , 2015, 129, 31-36.	2.2	23
56	Allele frequencies for 15 autosomal STR loci and haplotype data for 17 Y-STR loci in a population from Belize. <i>International Journal of Legal Medicine</i> , 2015, 129, 1217-1218.	2.2	1
57	Blind study evaluation illustrates utility of the Ion PGM [®] , [®] system for use in human identity DNA typing. <i>Croatian Medical Journal</i> , 2015, 56, 218-229.	0.7	37
58	Evaluation of a 49 InDel Marker HID panel in two specific populations of South America and one population of Northern Africa. <i>International Journal of Legal Medicine</i> , 2015, 129, 245-249.	2.2	4
59	Underlying Data for Sequencing the Mitochondrial Genome with the Massively Parallel Sequencing Platform Ion Torrent [®] , [®] PGM [®] , [®] . <i>BMC Genomics</i> , 2015, 16, S4.	2.8	43
60	An evaluation of the PowerSeq [®] , [®] Auto System: A multiplex short tandem repeat marker kit compatible with massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2015, 19, 172-179.	3.1	59
61	Sequencing the hypervariable regions of human mitochondrial DNA using massively parallel sequencing: Enhanced data acquisition for DNA samples encountered in forensic testing. <i>Legal Medicine</i> , 2015, 17, 123-127.	1.3	28
62	High sensitivity multiplex short tandem repeat loci analyses with massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2015, 16, 38-47.	3.1	69
63	Utility of amplification enhancers in low copy number DNA analysis. <i>International Journal of Legal Medicine</i> , 2015, 129, 43-52.	2.2	17
64	STRait Razor v2.0: The improved STR Allele Identification Tool “Razor”. <i>Forensic Science International: Genetics</i> , 2015, 14, 182-186.	3.1	55
65	Internal validation of the GlobalFiler [®] , [®] Express PCR Amplification Kit for the direct amplification of reference DNA samples on a high-throughput automated workflow. <i>Forensic Science International: Genetics</i> , 2014, 10, 33-39.	3.1	58
66	Characterization of 114 insertion/deletion (INDEL) polymorphisms, and selection for a global INDEL panel for human identification. <i>Legal Medicine</i> , 2014, 16, 26-32.	1.3	37
67	A high volume extraction and purification method for recovering DNA from human bone. <i>Forensic Science International: Genetics</i> , 2014, 12, 155-160.	3.1	25
68	Evaluation of a novel material, Diomics X-Swab [®] , [®] , for collection of DNA. <i>Forensic Science International: Genetics</i> , 2014, 12, 192-198.	3.1	7
69	An evaluation of the RapidHIT [®] system for reliably genotyping reference samples. <i>Forensic Science International: Genetics</i> , 2014, 13, 104-111.	3.1	38
70	High throughput whole mitochondrial genome sequencing by two platforms of massively parallel sequencing. <i>BMC Genomics</i> , 2014, 15, P7.	2.8	4
71	Reduction of stutter ratios in short tandem repeat loci typing of low copy number DNA samples. <i>Forensic Science International: Genetics</i> , 2014, 8, 213-218.	3.1	22
72	Autosomal and Y-STR analysis of degraded DNA from the 120-year-old skeletal remains of Ezekiel Harper. <i>Forensic Science International: Genetics</i> , 2014, 9, 33-41.	3.1	32

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73	Assessment of the role of DNA repair in damaged forensic samples. <i>International Journal of Legal Medicine</i> , 2014, 128, 913-921.	2.2	25
74	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.	3.1	155
75	mitoSAVE: Mitochondrial sequence analysis of variants in Excel. <i>Forensic Science International: Genetics</i> , 2014, 12, 122-125.	3.1	19
76	Differences of PCR efficiency between two-step PCR and standard three-step PCR protocols in short tandem repeat amplification. <i>Australian Journal of Forensic Sciences</i> , 2014, 46, 80-90.	1.2	8
77	Pressure cycling technology (PCT) reduces effects of inhibitors of the PCR. <i>International Journal of Legal Medicine</i> , 2013, 127, 321-333.	2.2	6
78	Validation of the PLEX-IDTM mass spectrometry mitochondrial DNA assay. <i>International Journal of Legal Medicine</i> , 2013, 127, 277-286.	2.2	8
79	Improvement of short tandem repeat analysis of samples highly contaminated by humic acid. <i>Journal of Clinical Forensic and Legal Medicine</i> , 2013, 20, 922-928.	1.0	9
80	STRait Razor: A length-based forensic STR allele-calling tool for use with second generation sequencing data. <i>Forensic Science International: Genetics</i> , 2013, 7, 409-417.	3.1	94
81	Effective removal of co-purified inhibitors from extracted DNA samples using synchronous coefficient of drag alteration (SCODA) technology. <i>International Journal of Legal Medicine</i> , 2013, 127, 749-755.	2.2	19
82	Single nucleotide polymorphism typing with massively parallel sequencing for human identification. <i>International Journal of Legal Medicine</i> , 2013, 127, 1079-1086.	2.2	112
83	A validation study of the Nucleix DSI-Semen kit's a methylation-based assay for semen identification. <i>International Journal of Legal Medicine</i> , 2013, 127, 299-308.	2.2	18
84	An evaluation of the transfer of saliva-derived DNA. <i>International Journal of Legal Medicine</i> , 2012, 126, 851-861.	2.2	38
85	Variants observed for STR locus SE33: A concordance study. <i>Forensic Science International: Genetics</i> , 2012, 6, 494-497.	3.1	19
86	Evaluation and comparative analysis of direct amplification of STRs using PowerPlex® 18D and Identifiler® Direct systems. <i>Forensic Science International: Genetics</i> , 2012, 6, 640-645.	3.1	32
87	INNULs: A Novel Design Amplification Strategy for Retrotransposable Elements for Studying Population Variation. <i>Human Heredity</i> , 2012, 74, 27-35.	0.8	14
88	A validation study of the Qiagen Investigator DIPplex® kit; an INDEL-based assay for human identification. <i>International Journal of Legal Medicine</i> , 2012, 126, 533-540.	2.2	92
89	Extraction platform evaluations: A comparison of Automate Express®, EZ1® Advanced XL, and Maxwell® 16 Bench-top DNA extraction systems. <i>Legal Medicine</i> , 2012, 14, 36-39.	1.3	41
90	High-throughput DNA isolation method for detection of <i>Xylella fastidiosa</i> in plant and insect samples. <i>Journal of Microbiological Methods</i> , 2011, 86, 310-312.	1.6	9

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91	Y-STR loci diversity in native Alaskan populations. International Journal of Legal Medicine, 2011, 125, 559-563.	2.2	8