Jonathan L King

List of Publications by Year
in descending order

91 papers	3,073 citations	147801 31 h-index	182427 51 g-index
96 all docs	96 docs citations	96 times ranked	1596 citing authors

#	Article	IF	Citations
1	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
2	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.	3.1	185
3	High-quality and high-throughput massively parallel sequencing of the human mitochondrial genome using the Illumina MiSeq. Forensic Science International: Genetics, 2014, 12, 128-135.	3.1	155
4	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
5	Single nucleotide polymorphism typing with massively parallel sequencing for human identification. International Journal of Legal Medicine, 2013, 127, 1079-1086.	2.2	112
6	STRait Razor: A length-based forensic STR allele-calling tool for use with second generation sequencing data. Forensic Science International: Genetics, 2013, 7, 409-417.	3.1	94
7	A validation study of the Qiagen Investigator DIPplexÂ® kit; an INDEL-based assay for human identification. International Journal of Legal Medicine, 2012, 126, 533-540.	2.2	92
8	Fast STR allele identification with STRait Razor 3.0. Forensic Science International: Genetics, 2017, 30, 18-23.	3.1	82
9	STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci. Forensic Science International: Genetics, 2017, 31, 111-117.	3.1	77
10	â€œThe devilâ€™s in the detailâ€: Release of an expanded, enhanced and dynamically revised forensic STR Sequence Guide. Forensic Science International: Genetics, 2018, 34, 162-169.	3.1	73
11	Population and performance analyses of four major populations with Illuminaâ€™s FGx Forensic Genomics System. Forensic Science International: Genetics, 2017, 30, 81-92.	3.1	70
12	High sensitivity multiplex short tandem repeat loci analyses with massively parallel sequencing. Forensic Science International: Genetics, 2015, 16, 38-47.	3.1	69
13	Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. Forensic Science International: Genetics, 2018, 32, 50-61.	3.1	69
14	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.	3.1	68
15	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.	3.1	60
16	An evaluation of the PowerSeqâ„¢ Auto System: A multiplex short tandem repeat marker kit compatible with massively parallel sequencing. Forensic Science International: Genetics, 2015, 19, 172-179.	3.1	59
17	Internal validation of the GlobalFilerâ„¢ Express PCR Amplification Kit for the direct amplification of reference DNA samples on a high-throughput automated workflow. Forensic Science International: Genetics, 2014, 10, 33-39.	3.1	58
18	STRait Razor v2.0: The improved STR Allele Identification Tool â€“ Razor. Forensic Science International: Genetics, 2015, 14, 182-186.	3.1	55

#	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.	2.8	47
20	Underlying Data for Sequencing the Mitochondrial Genome with the Massively Parallel Sequencing Platform Ion Torrentâ„¢ PGMâ„¢. BMC Genomics, 2015, 16, S4.	2.8	43
21	Extraction platform evaluations: A comparison of Automate Expressâ„¢, EZ1Â® Advanced XL, and MaxwellÂ® 16 Bench-top DNA extraction systems. Legal Medicine, 2012, 14, 36-39.	1.3	41
22	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.	3.1	41
23	STRait Razor v2s: Advancing sequence-based STR allele reporting and beyond to other marker systems. Forensic Science International: Genetics, 2017, 29, 21-28.	3.1	39
24	An evaluation of the transfer of saliva-derived DNA. International Journal of Legal Medicine, 2012, 126, 851-861.	2.2	38
25	An evaluation of the RapidHITÂ® system for reliably genotyping reference samples. Forensic Science International: Genetics, 2014, 13, 104-111.	3.1	38
26	Characterization of 114 insertion/deletion (INDEL) polymorphisms, and selection for a global INDEL panel for human identification. Legal Medicine, 2014, 16, 26-32.	1.3	37
27	Blind study evaluation illustrates utility of the Ion PGMâ„¢ system for use in human identity DNA typing. Croatian Medical Journal, 2015, 56, 218-229.	0.7	37
28	Massively parallel sequencing-enabled mixture analysis of mitochondrial DNA samples. International Journal of Legal Medicine, 2018, 132, 1263-1272.	2.2	36
29	Evaluation of the precision ID mtDNA whole genome panel on two massively parallel sequencing systems. Forensic Science International: Genetics, 2018, 36, 213-224.	3.1	35
30	Whole mitochondrial genome genetic diversity in an Estonian population sample. International Journal of Legal Medicine, 2016, 130, 67-71.	2.2	33
31	Evaluation and comparative analysis of direct amplification of STRs using PowerPlexÂ® 18D and IdentifilerÂ® Direct systems. Forensic Science International: Genetics, 2012, 6, 640-645.	3.1	32
32	Autosomal and Y-STR analysis of degraded DNA from the 120-year-old skeletal remains of Ezekiel Harper. Forensic Science International: Genetics, 2014, 9, 33-41.	3.1	32
33	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
34	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
35	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
36	Sequencing the hypervariable regions of human mitochondrial DNA using massively parallel sequencing: Enhanced data acquisition for DNA samples encountered in forensic testing. Legal Medicine, 2015, 17, 123-127.	1.3	28

#	Article	IF	Citations
37	Effects of the Ion PGMâ„¢ Hi-Qâ„¢ sequencing chemistry on sequence data quality. International Journal of Legal Medicine, 2016, 130, 1169-1180.	2.2	28
38	A high volume extraction and purification method for recovering DNA from human bone. Forensic Science International: Genetics, 2014, 12, 155-160.	3.1	25
39	Assessment of the role of DNA repair in damaged forensic samples. International Journal of Legal Medicine, 2014, 128, 913-921.	2.2	25
40	Comparative tolerance of two massively parallel sequencing systems to common PCR inhibitors. International Journal of Legal Medicine, 2018, 132, 983-995.	2.2	25
41	Massively parallel sequencing of forensically relevant single nucleotide polymorphisms using TruSeqâ„¢ forensic amplicon. International Journal of Legal Medicine, 2015, 129, 31-36.	2.2	23
42	Development and validation of a novel multiplexed DNA analysis system, InnoTyperÂ® 21. Forensic Science International: Genetics, 2017, 29, 80-99.	3.1	23
43	Utility of the Ion S5â„¢ and MiSeq FGxâ„¢ sequencing platforms to characterize challenging human remains. Legal Medicine, 2019, 41, 101623.	1.3	23
44	Reduction of stutter ratios in short tandem repeat loci typing of low copy number DNA samples. Forensic Science International: Genetics, 2014, 8, 213-218.	3.1	22
45	Assessment of impact of DNA extraction methods on analysis of human remain samples on massively parallel sequencing success. International Journal of Legal Medicine, 2019, 133, 51-58.	2.2	22
46	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
47	Variants observed for STR locus SE33: A concordance study. Forensic Science International: Genetics, 2012, 6, 494-497.	3.1	19
48	Effective removal of co-purified inhibitors from extracted DNA samples using synchronous coefficient of drag alteration (SCODA) technology. International Journal of Legal Medicine, 2013, 127, 749-755.	2.2	19
49	mitoSAVE: Mitochondrial sequence analysis of variants in Excel. Forensic Science International: Genetics, 2014, 12, 122-125.	3.1	19
50	Flanking Variation Influences Rates of Stutter in Simple Repeats. Genes, 2017, 8, 329.	2.4	19
51	A validation study of the Nucleix DSI-Semen kitâ€”a methylation-based assay for semen identification. International Journal of Legal Medicine, 2013, 127, 299-308.	2.2	18
52	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
53	Utility of amplification enhancers in low copy number DNA analysis. International Journal of Legal Medicine, 2015, 129, 43-52.	2.2	17
54	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

#	Article	IF	Citations
55	A technique for setting analytical thresholds in massively parallel sequencing-based forensic DNA analysis. PLoS ONE, 2017, 12, e0178005.	2.5	16
56	Forensic genetic investigation of human skeletal remains recovered from the La Belle shipwreck. Forensic Science International, 2020, 306, 110050.	2.2	16
57	STRait Razor Online: An enhanced user interface to facilitate interpretation of MPS data. Forensic Science International: Genetics, 2021, 52, 102463.	3.1	16
58	INNULs: A Novel Design Amplification Strategy for Retrotransposable Elements for Studying Population Variation. Human Heredity, 2012, 74, 27-35.	0.8	14
59	Y-chromosomal analysis of Greek Cypriots reveals a primarily common pre-Ottoman paternal ancestry with Turkish Cypriots. PLoS ONE, 2017, 12, e0179474.	2.5	13
60	Copan microFLOQÂ® Direct Swab collection of bloodstains, saliva, and semen on cotton cloth. International Journal of Legal Medicine, 2020, 134, 45-54.	2.2	13
61	Reverse Complement PCR: A novel one-step PCR system for typing highly degraded DNA for human identification. Forensic Science International: Genetics, 2020, 44, 102201.	3.1	13
62	Autosomal STR and SNP characterization of populations from the Northeastern Peruvian Andes with the ForenSeqâ„¢ DNA Signature Prep Kit. Forensic Science International: Genetics, 2021, 52, 102487.	3.1	13
63	Evaluation of Promega PowerSeqâ„¢ Auto/Y systems prototype on an admixed sample of Rio de Janeiro, Brazil: Population data, sensitivity, stutter and mixture studies. Forensic Science International: Genetics, 2021, 53, 102516.	3.1	13
64	Investigation of the STR loci noise distributions of PowerSeqâ„¢ Auto System. Croatian Medical Journal, 2017, 58, 214-221.	0.7	12
65	Massively parallel sequencing of 12 autosomal STRs in Cannabis sativa. Electrophoresis, 2018, 39, 2906-2911.	2.4	11
66	A Continuous Statistical Phasing Framework for the Analysis of Forensic Mitochondrial DNA Mixtures. Genes, 2021, 12, 128.	2.4	10
67	High-throughput DNA isolation method for detection of Xylella fastidiosa in plant and insect samples. Journal of Microbiological Methods, 2011, 86, 310-312.	1.6	9
68	Improvement of short tandem repeat analysis of samples highly contaminated by humic acid. Journal of Clinical Forensic and Legal Medicine, 2013, 20, 922-928.	1.0	9
69	Compound stutter in D2S1338 and D12S391. Forensic Science International: Genetics, 2019, 39, 50-56.	3.1	9
70	Reducing noise and stutter in short tandem repeat loci with unique molecular identifiers. Forensic Science International: Genetics, 2021, 51, 102459.	3.1	9
71	Y-STR loci diversity in native Alaskan populations. International Journal of Legal Medicine, 2011, 125, 559-563.	2.2	8
72	Validation of the PLEX-IDTM mass spectrometry mitochondrial DNA assay. International Journal of Legal Medicine, 2013, 127, 277-286.	2.2	8

#	Article	IF	Citations
73	Differences of PCR efficiency between two-step PCR and standard three-step PCR protocols in short tandem repeat amplification. Australian Journal of Forensic Sciences, 2014, 46, 80-90.	1.2	8
74	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
75	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
76	Precision DNA Mixture Interpretation with Single-Cell Profiling. Genes, 2021, 12, 1649.	2.4	8
77	Evaluation of a novel material, Diomics X-Swabâ„¢, for collection of DNA. Forensic Science International: Genetics, 2014, 12, 192-198.	3.1	7
78	Pressure cycling technology (PCT) reduces effects of inhibitors of the PCR. International Journal of Legal Medicine, 2013, 127, 321-333.	2.2	6
79	Evaluation of InnoTyperÂ® 21 in a sample of Rio de Janeiro population as an alternative forensic panel. International Journal of Legal Medicine, 2018, 132, 149-151.	2.2	6
80	Reverse complement-PCR, an innovative and effective method for multiplexing forensically relevant single nucleotide polymorphismÂmarker systems. BioTechniques, 2021, 71, 484-489.	1.8	6
81	Parsing apart the contributors of mitochondrial DNA mixtures with massively parallel sequencing data. Forensic Science International: Genetics Supplement Series, 2017, 6, e439-e441.	0.3	5
82	Enhanced mixture interpretation with macrohaplotypes based on long-read DNA sequencing. International Journal of Legal Medicine, 2021, 135, 2189-2198.	2.2	5
83	Graph Algorithms for Mixture Interpretation. Genes, 2021, 12, 185.	2.4	5
84	Genetic assessment reveals no population substructure and divergent regional and sex-specific histories in the Chachapoyas from northeast Peru. PLoS ONE, 2020, 15, e0244497.	2.5	5
85	High throughput whole mitochondrial genome sequencing by two platforms of massively parallel sequencing. BMC Genomics, 2014, 15, P7.	2.8	4
86	Evaluation of a 49 InDel Marker HID panel in two specific populations of South America and one population of Northern Africa. International Journal of Legal Medicine, 2015, 129, 245-249.	2.2	4
87	MMDIT: A tool for the deconvolution and interpretation of mitochondrial DNA mixtures. Forensic Science International: Genetics, 2021, 55, 102568.	3.1	4
88	A genome-wide association study of tramadol metabolism from post-mortem samples. Pharmacogenomics Journal, 2020, 20, 94-103.	2.0	3
89	Allele frequencies for 15 autosomal STR loci and haplotype data for 17 Y-STR loci in a population from Belize. International Journal of Legal Medicine, 2015, 129, 1217-1218.	2.2	1
90	The Next State-of-the-Art Forensic Genetics Technology: Massively Parallel Sequencing. Security Science and Technology, 2016, , 249-291.	0.5	1

#	Article	IF	Citations
91	Association of whole mtDNA, an NADPH G11914A variant, and haplogroups with high physical performance in an elite military troop. Brazilian Journal of Medical and Biological Research, 2021, 54, e10317.	1.5	0