

Bruce Budowle

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

247
papers

6,823
citations

44
h-index

71
g-index

262
ext. papers

7,780
ext. citations

3.9
avg, IF

6.09
L-index

#	Paper	IF	Citations
247	Validation of mitochondrial DNA sequencing for forensic casework analysis. <i>International Journal of Legal Medicine</i> , 1995 , 108, 68-74	3.1	281
246	Forensics and mitochondrial DNA: applications, debates, and foundations. <i>Annual Review of Genomics and Human Genetics</i> , 2003 , 4, 119-41	9.7	181
245	Forensically relevant SNP classes. <i>BioTechniques</i> , 2008 , 44, 603-8, 610	2.5	175
244	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. <i>Forensic Science International: Genetics</i> , 2014 , 12, 12-23	4.3	171
243	Evaluation of the Illumina () Beta Version ForenSeq DNA Signature Prep Kit for use in genetic profiling. <i>Forensic Science International: Genetics</i> , 2016 , 20, 20-29	4.3	151
242	Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements. <i>Forensic Science International: Genetics</i> , 2016 , 22, 54-63	4.3	148
241	Population Data on the Thirteen CODIS Core Short Tandem Repeat Loci in African Americans, U.S. Caucasians, Hispanics, Bahamians, Jamaicans, and Trinidadians. <i>Journal of Forensic Sciences</i> , 1999 , 44, 14601J	1.8	147
240	Validity of low copy number typing and applications to forensic science. <i>Croatian Medical Journal</i> , 2009 , 50, 207-17	1.6	144
239	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, 128-35	4.3	139
238	DNA methylation-based forensic tissue identification. <i>Forensic Science International: Genetics</i> , 2011 , 5, 517-24	4.3	129
237	Typing of Deoxyribonucleic Acid (DNA) Extracted from Compact Bone from Human Remains. <i>Journal of Forensic Sciences</i> , 1991 , 36, 13189J	1.8	128
236	Epidemiology. DNA identifications after the 9/11 World Trade Center attack. <i>Science</i> , 2005 , 310, 1122-3	33.3	120
235	Mitochondrial DNA regions HVI and HVII population data. <i>Forensic Science International</i> , 1999 , 103, 23-35	2.6	114
234	Public health. Building microbial forensics as a response to bioterrorism. <i>Science</i> , 2003 , 301, 1852-3	33.3	110
233	CODIS STR Loci Data from 41 Sample Populations. <i>Journal of Forensic Sciences</i> , 2001 , 46, 14996J	1.8	108
232	Forensic aspects of mass disasters: strategic considerations for DNA-based human identification. <i>Legal Medicine</i> , 2005 , 7, 230-43	1.9	106
231	Mixture interpretation: defining the relevant features for guidelines for the assessment of mixed DNA profiles in forensic casework. <i>Journal of Forensic Sciences</i> , 2009 , 54, 810-21	1.8	104

230	Characterization of genetic sequence variation of 58 STR loci in four major population groups. <i>Forensic Science International: Genetics</i> , 2016 , 25, 214-226	4.3	104
229	Single nucleotide polymorphism typing with massively parallel sequencing for human identification. <i>International Journal of Legal Medicine</i> , 2013 , 127, 1079-86	3.1	102
228	Validation of Short Tandem Repeats (STRs) for Forensic Usage: Performance Testing of Fluorescent Multiplex STR Systems and Analysis of Authentic and Simulated Forensic Samples. <i>Journal of Forensic Sciences</i> , 2001 , 46, 15018J	1.8	93
227	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, 409-17	4.3	84
226	An assessment of whether SNPs will replace STRs in national DNA databases--joint considerations of the DNA working group of the European Network of Forensic Science Institutes (ENFSI) and the Scientific Working Group on DNA Analysis Methods (SWGDM). <i>Science and Justice - Journal of the Forensic Science Society</i> , 2004 , 44, 51-3	2	81
225	A perspective on errors, bias, and interpretation in the forensic sciences and direction for continuing advancement. <i>Journal of Forensic Sciences</i> , 2009 , 54, 798-809	1.8	77
224	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, 533-40	3.1	74
223	STR primer concordance study. <i>Forensic Science International</i> , 2001 , 124, 47-54	2.6	73
222	Identification of a D8S1179 primer binding site mutation and the validation of a primer designed to recover null alleles. <i>Forensic Science International</i> , 2003 , 133, 220-7	2.6	68
221	High sensitivity multiplex short tandem repeat loci analyses with massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2015 , 16, 38-47	4.3	59
220	Extracting evidence from forensic DNA analyses: future molecular biology directions. <i>BioTechniques</i> , 2009 , 46, 339-40, 342-50	2.5	58
219	Twelve short tandem repeat loci Y chromosome haplotypes: genetic analysis on populations residing in North America. <i>Forensic Science International</i> , 2005 , 150, 1-15	2.6	58
218	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	4.3	56
217	Fast STR allele identification with STRait Razor 3.0. <i>Forensic Science International: Genetics</i> , 2017 , 30, 18-23	4.3	56
216	Population genetic analyses of the NGM STR loci. <i>International Journal of Legal Medicine</i> , 2011 , 125, 101-9	3.1	55
215	Mutation rates at Y chromosome short tandem repeats in Texas populations. <i>Forensic Science International: Genetics</i> , 2009 , 3, 179-84	4.3	54
214	STRait Razor v2.0: the improved STR Allele Identification Tool--Razor. <i>Forensic Science International: Genetics</i> , 2015 , 14, 182-6	4.3	53
213	STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci. <i>Forensic Science International: Genetics</i> , 2017 , 31, 111-117	4.3	52

212	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	4.3	50
211	Expansion of Microbial Forensics. <i>Journal of Clinical Microbiology</i> , 2016 , 54, 1964-74	9.7	49
210	Recommendations for consistent treatment of length variants in the human mitochondrial DNA control region. <i>Forensic Science International</i> , 2002 , 129, 35-42	2.6	49
209	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	4.3	48
208	Validation of high throughput sequencing and microbial forensics applications. <i>Investigative Genetics</i> , 2014 , 5, 9		46
207	Developing criteria and data to determine best options for expanding the core CODIS loci. <i>Investigative Genetics</i> , 2012 , 3, 1		46
206	Forensic Human Identification Using Skin Microbiomes. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	46
205	Quantification of human mitochondrial DNA using synthesized DNA standards. <i>Journal of Forensic Sciences</i> , 2011 , 56, 1457-63	1.8	46
204	Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. <i>Forensic Science International: Genetics</i> , 2018 , 32, 50-61	4.3	44
203	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	4.3	44
202	Concordance Study on Population Database Samples Using the PowerPlex [®] 16 Kit and AmpFSTR [®] Profiler Plus [™] Kit and AmpFSTR [®] COfiler [™] Kit. <i>Journal of Forensic Sciences</i> , 2001 , 46, 1501-6J	1.8	44
201	Evaluation of forensic DNA mixture evidence: protocol for evaluation, interpretation, and statistical calculations using the combined probability of inclusion. <i>BMC Genetics</i> , 2016 , 17, 125	2.6	44
200	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	4.3	42
199	Current state-of-art of STR sequencing in forensic genetics. <i>Electrophoresis</i> , 2018 , 39, 2655-2668	3.6	41
198	Choosing relatives for DNA identification of missing persons. <i>Journal of Forensic Sciences</i> , 2011 , 56 Suppl 1, S23-8	1.8	41
197	Comparisons of familial DNA database searching strategies. <i>Journal of Forensic Sciences</i> , 2011 , 56, 1448-56		41
196	More comprehensive forensic genetic marker analyses for accurate human remains identification using massively parallel DNA sequencing. <i>BMC Genomics</i> , 2016 , 17, 750	4.5	40
195	First all-in-one diagnostic tool for DNA intelligence: genome-wide inference of biogeographic ancestry, appearance, relatedness, and sex with the Identitas v1 Forensic Chip. <i>International Journal of Legal Medicine</i> , 2013 , 127, 559-72	3.1	38

194	Assessing a novel room temperature DNA storage medium for forensic biological samples. <i>Forensic Science International: Genetics</i> , 2012 , 6, 31-40	4.3	38
193	Direct PCR amplification of DNA from human bloodstains, saliva, and touch samples collected with microFLOQ swabs. <i>Forensic Science International: Genetics</i> , 2018 , 32, 80-87	4.3	36
192	Haplotype block: a new type of forensic DNA markers. <i>International Journal of Legal Medicine</i> , 2010 , 124, 353-61	3.1	36
191	Criteria for validation of methods in microbial forensics. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 5599-607	4.8	35
190	Blind study evaluation illustrates utility of the Ion PGM3 system for use in human identity DNA typing. <i>Croatian Medical Journal</i> , 2015 , 56, 218-29	1.6	33
189	Accurate, rapid and high-throughput detection of strain-specific polymorphisms in <i>Bacillus anthracis</i> and <i>Yersinia pestis</i> by next-generation sequencing. <i>Investigative Genetics</i> , 2010 , 1, 5		33
188	Increasing the reference populations for the 55 AISNP panel: the need and benefits. <i>International Journal of Legal Medicine</i> , 2017 , 131, 913-917	3.1	32
187	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	4.3	32
186	Underlying Data for Sequencing the Mitochondrial Genome with the Massively Parallel Sequencing Platform Ion Torrent PGM. <i>BMC Genomics</i> , 2015 , 16 Suppl 1, S4	4.5	32
185	Prototype PowerPlex Y23 System: A concordance study. <i>Forensic Science International: Genetics</i> , 2013 , 7, 204-8	4.3	32
184	Future directions of forensic DNA databases. <i>Croatian Medical Journal</i> , 2014 , 55, 163-6	1.6	32
183	Base composition profiling of human mitochondrial DNA using polymerase chain reaction and direct automated electrospray ionization mass spectrometry. <i>Analytical Chemistry</i> , 2009 , 81, 7515-26	7.8	32
182	DNA quality and quantity from up to 16 years old post-mortem blood stored on FTA cards. <i>Forensic Science International</i> , 2016 , 261, 148-53	2.6	31
181	An evaluation of the transfer of saliva-derived DNA. <i>International Journal of Legal Medicine</i> , 2012 , 126, 851-61	3.1	31
180	Texas population substructure and its impact on estimating the rarity of Y STR haplotypes from DNA evidence*. <i>Journal of Forensic Sciences</i> , 2009 , 54, 1016-21	1.8	31
179	Reconstructing the population history of Nicaragua by means of mtDNA, Y-chromosome STRs, and autosomal STR markers. <i>American Journal of Physical Anthropology</i> , 2010 , 143, 591-600	2.5	31
178	SNP typing strategies. <i>Forensic Science International</i> , 2004 , 146 Suppl, S139-42	2.6	31
177	Massively parallel sequencing-enabled mixture analysis of mitochondrial DNA samples. <i>International Journal of Legal Medicine</i> , 2018 , 132, 1263-1272	3.1	30

176	An evaluation of the RapidHIT() system for reliably genotyping reference samples. <i>Forensic Science International: Genetics</i> , 2014 , 13, 104-11	4.3	30
175	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	4.3	29
174	Extraction platform evaluations: a comparison of AutoMate ExpressEZ1 Advanced XL, and Maxwell 16 Bench-top DNA extraction systems. <i>Legal Medicine</i> , 2012 , 14, 36-9	1.9	29
173	Evaluation and comparative analysis of direct amplification of STRs using PowerPlex 18D and Identifiler Direct systems. <i>Forensic Science International: Genetics</i> , 2012 , 6, 640-5	4.3	28
172	Forensic human identification with targeted microbiome markers using nearest neighbor classification. <i>Forensic Science International: Genetics</i> , 2019 , 38, 130-139	4.3	28
171	Whole mitochondrial genome genetic diversity in an Estonian population sample. <i>International Journal of Legal Medicine</i> , 2016 , 130, 67-71	3.1	27
170	Strengthening forensic DNA decision making through a better understanding of the influence of cognitive bias. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2017 , 57, 415-420	2	27
169	Microbial forensics: application to bioterrorism preparedness and response. <i>Infectious Disease Clinics of North America</i> , 2006 , 20, 455-73, xi	6.5	27
168	A Comparison and Integration of MiSeq and MinION Platforms for Sequencing Single Source and Mixed Mitochondrial Genomes. <i>PLoS ONE</i> , 2016 , 11, e0167600	3.7	27
167	NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis. <i>Forensic Science International: Genetics</i> , 2018 , 37, 172-179	4.3	27
166	DNA identification by pedigree likelihood ratio accommodating population substructure and mutations. <i>Investigative Genetics</i> , 2010 , 1, 8		26
165	STRmix collaborative exercise on DNA mixture interpretation. <i>Forensic Science International: Genetics</i> , 2019 , 40, 1-8	4.3	26
164	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	4.3	25
163	Increasing the discrimination power of ancestry- and identity-informative SNP loci within the ForenSeqDNA Signature Prep Kit. <i>Forensic Science International: Genetics</i> , 2018 , 36, 60-76	4.3	25
162	European survey on forensic applications of massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2017 , 29, e23-e25	4.3	24
161	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	1.9	24
160	Novel Y-chromosome Short Tandem Repeat Variants Detected Through the Use of Massively Parallel Sequencing. <i>Genomics, Proteomics and Bioinformatics</i> , 2015 , 13, 250-7	6.5	24
159	The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity. <i>Journal of Forensic Sciences</i> , 2019 , 64, 393-405	1.8	23

158	Evaluation of circular DNA substrates for whole genome amplification prior to forensic analysis. <i>Forensic Science International: Genetics</i> , 2012 , 6, 185-90	4.3	23
157	US forensic Y-chromosome short tandem repeats database. <i>Legal Medicine</i> , 2010 , 12, 289-95	1.9	23
156	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, 123-7	1.9	22
155	Improved Y-STR typing for disaster victim identification, missing persons investigations, and historical human skeletal remains. <i>International Journal of Legal Medicine</i> , 2018 , 132, 1545-1553	3.1	22
154	Evaluation of mitogenome sequence concordance, heteroplasmy detection, and haplogrouping in a worldwide lineage study using the Precision ID mtDNA Whole Genome Panel. <i>Forensic Science International: Genetics</i> , 2019 , 42, 244-251	4.3	22
153	A high volume extraction and purification method for recovering DNA from human bone. <i>Forensic Science International: Genetics</i> , 2014 , 12, 155-60	4.3	22
152	Effects of the Ion PGM Hi-Q sequencing chemistry on sequence data quality. <i>International Journal of Legal Medicine</i> , 2016 , 130, 1169-80	3.1	21
151	Assessment of the role of DNA repair in damaged forensic samples. <i>International Journal of Legal Medicine</i> , 2014 , 128, 913-21	3.1	21
150	Privacy and genetic genealogy data. <i>Science</i> , 2018 , 361, 857	33.3	21
149	Massively parallel sequence data of 31 autosomal STR loci from 496 Spanish individuals revealed concordance with CE-STR technology and enhanced discrimination power. <i>Forensic Science International: Genetics</i> , 2019 , 42, 49-55	4.3	20
148	Massively parallel sequencing of forensically relevant single nucleotide polymorphisms using TruSeq Forensic amplicon. <i>International Journal of Legal Medicine</i> , 2015 , 129, 31-6	3.1	20
147	Automated analysis of sequence polymorphism in STR alleles by PCR and direct electrospray ionization mass spectrometry. <i>Forensic Science International: Genetics</i> , 2012 , 6, 594-606	4.3	20
146	Maternity exclusion with a very high autosomal STRs kinship index. <i>International Journal of Legal Medicine</i> , 2012 , 126, 645-8	3.1	20
145	The effects of Asian population substructure on Y STR forensic analyses. <i>Legal Medicine</i> , 2009 , 11, 64-9	1.9	20
144	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	4.3	20
143	Selection of highly informative SNP markers for population affiliation of major US populations. <i>International Journal of Legal Medicine</i> , 2016 , 130, 341-52	3.1	19
142	Increasing the reach of forensic genetics with massively parallel sequencing. <i>Forensic Science, Medicine, and Pathology</i> , 2017 , 13, 342-349	1.5	19
141	Interpreting Y chromosome STR haplotype mixture. <i>Legal Medicine</i> , 2010 , 12, 137-43	1.9	19

140	mitoSAVE: mitochondrial sequence analysis of variants in Excel. <i>Forensic Science International: Genetics</i> , 2014 , 12, 122-5	4.3	18
139	D5S2500 is an ambiguously characterized STR: Identification and description of forensic microsatellites in the genomics age. <i>Forensic Science International: Genetics</i> , 2016 , 23, 19-24	4.3	18
138	Comparative tolerance of two massively parallel sequencing systems to common PCR inhibitors. <i>International Journal of Legal Medicine</i> , 2018 , 132, 983-995	3.1	18
137	Development and validation of a novel multiplexed DNA analysis system, InnoTyper 21. <i>Forensic Science International: Genetics</i> , 2017 , 29, 80-99	4.3	17
136	Variants observed for STR locus SE33: a concordance study. <i>Forensic Science International: Genetics</i> , 2012 , 6, 494-7	4.3	17
135	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, 749-55	3.1	17
134	Utility of the Ion S5 and MiSeq FGx sequencing platforms to characterize challenging human remains. <i>Legal Medicine</i> , 2019 , 41, 101623	1.9	16
133	Flanking Variation Influences Rates of Stutter in Simple Repeats. <i>Genes</i> , 2017 , 8,	4.2	16
132	Modified DOP-PCR for improved STR typing of degraded DNA from human skeletal remains and bloodstains. <i>Legal Medicine</i> , 2016 , 18, 7-12	1.9	16
131	Reduction of stutter ratios in short tandem repeat loci typing of low copy number DNA samples. <i>Forensic Science International: Genetics</i> , 2014 , 8, 213-8	4.3	16
130	Population studies on three Native Alaska population groups using STR loci. <i>Forensic Science International</i> , 2002 , 129, 51-7	2.6	16
129	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	3.1	16
128	Aircraft-Assisted Pilot Suicides: Lessons to be Learned. <i>Aviation, Space, and Environmental Medicine</i> , 2014 , 85, 841-6		15
127	A validation study of the Nucleix DSI-Semen kit--a methylation-based assay for semen identification. <i>International Journal of Legal Medicine</i> , 2013 , 127, 299-308	3.1	15
126	Analysis of Short Tandem Repeat and Single Nucleotide Polymorphism Loci From Single-Source Samples Using a Custom HaloPlex Target Enrichment System Panel. <i>American Journal of Forensic Medicine and Pathology</i> , 2016 , 37, 99-107	1	15
125	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	4.3	14
124	Internal validation of the RapidHIT ID system. <i>Forensic Science International: Genetics</i> , 2017 , 31, 180-188	4.3	13
123	A technique for setting analytical thresholds in massively parallel sequencing-based forensic DNA analysis. <i>PLoS ONE</i> , 2017 , 12, e0178005	3.7	13

122	Identification and analysis of mtDNA genomes attributed to Finns reveal long-stagnant demographic trends obscured in the total diversity. <i>Scientific Reports</i> , 2017 , 7, 6193	4.9	13
121	INNULs: A novel design amplification strategy for retrotransposable elements for studying population variation. <i>Human Heredity</i> , 2012 , 74, 27-35	1.1	13
120	Enhancing resolution and statistical power by utilizing mass spectrometry for detection of SNPs within the short tandem repeats. <i>Forensic Science International: Genetics Supplement Series</i> , 2009 , 2, 529-531	0.5	13
119	Distinguishing mitochondrial DNA and NUMT sequences amplified with the precision ID mtDNA whole genome panel. <i>Mitochondrion</i> , 2020 , 55, 122-133	4.9	13
118	Native American population data based on the Globalfiler(®) autosomal STR loci. <i>Forensic Science International: Genetics</i> , 2016 , 24, e12-e13	4.3	13
117	Working towards implementation of whole genome mitochondrial DNA sequencing into routine casework. <i>Forensic Science International: Genetics Supplement Series</i> , 2017 , 6, e388-e389	0.5	12
116	Utility of amplification enhancers in low copy number DNA analysis. <i>International Journal of Legal Medicine</i> , 2015 , 129, 43-52	3.1	12
115	Results of a collaborative study on DNA identification of aged bone samples. <i>Croatian Medical Journal</i> , 2017 , 58, 203-213	1.6	12
114	Use of forensic methods under exigent circumstances without full validation. <i>Science Translational Medicine</i> , 2009 , 1, 8cm7	17.5	12
113	Forensic genetic investigation of human skeletal remains recovered from the La Belle shipwreck. <i>Forensic Science International</i> , 2020 , 306, 110050	2.6	12
112	Y-chromosomal analysis of Greek Cypriots reveals a primarily common pre-Ottoman paternal ancestry with Turkish Cypriots. <i>PLoS ONE</i> , 2017 , 12, e0179474	3.7	11
111	Investigation of the STR loci noise distributions of PowerSeq® Auto System. <i>Croatian Medical Journal</i> , 2017 , 58, 214-221	1.6	11
110	Potential highly polymorphic short tandem repeat markers for enhanced forensic identity testing. <i>Forensic Science International: Genetics</i> , 2018 , 37, 162-171	4.3	11
109	Kinship index variations among populations and thresholds for familial searching. <i>PLoS ONE</i> , 2012 , 7, e37474	3.7	11
108	Automated alignment and nomenclature for consistent treatment of polymorphisms in the human mitochondrial DNA control region. <i>Journal of Forensic Sciences</i> , 2010 , 55, 1190-5	1.8	11
107	Developmental Validation of a MPS Workflow with a PCR-Based Short Amplicon Whole Mitochondrial Genome Panel. <i>Genes</i> , 2020 , 11,	4.2	11
106	Forensic investigation approaches of searching relatives in DNA databases. <i>Journal of Forensic Sciences</i> , 2021 , 66, 430-443	1.8	11
105	A novel phylogenetic approach for de novo discovery of putative nuclear mitochondrial (pNumt) haplotypes. <i>Forensic Science International: Genetics</i> , 2019 , 43, 102146	4.3	10

104	Post-injection hybridization of complementary DNA strands on capillary electrophoresis platforms: a novel solution for dsDNA artifacts. <i>Forensic Science International: Genetics</i> , 2008 , 2, 257-73	4.3	9
103	Population genetic analyses of 15 STR loci from seven forensically-relevant populations residing in the state of Kuwait. <i>Forensic Science International: Genetics</i> , 2013 , 7, e106-7	4.3	8
102	Y-STR loci diversity in native Alaskan populations. <i>International Journal of Legal Medicine</i> , 2011 , 125, 559-63	3.3	8
101	How many familial relationship testing results could be wrong?. <i>PLoS Genetics</i> , 2020 , 16, e1008929	6	8
100	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	1.1	7
99	Microbial Forensic Investigation of the Anthrax-Letter Attacks 2011 , 15-25		7
98	Missing persons identification: genetics at work for society. <i>Science</i> , 2000 , 290, 2257-8	33.3	7
97	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	4.3	7
96	Empirical testing of a 23-AIMs panel of SNPs for ancestry evaluations in four major US populations. <i>International Journal of Legal Medicine</i> , 2016 , 130, 891-896	3.1	6
95	Pressure cycling technology (PCT) reduces effects of inhibitors of the PCR. <i>International Journal of Legal Medicine</i> , 2013 , 127, 321-33	3.1	6
94	Validation of the PLEX-ID [®] mass spectrometry mitochondrial DNA assay. <i>International Journal of Legal Medicine</i> , 2013 , 127, 277-86	3.1	6
93	Population genetic analyses of the STR loci of the AmpFISTR NGM Select [®] kit for Han population in Fujian Province, China. <i>International Journal of Legal Medicine</i> , 2013 , 127, 345-6	3.1	6
92	Correcting Inconsistencies and Errors in Bacterial Genome Metadata Using an Automated Curation Tool in Excel (AutoCurE). <i>Frontiers in Bioengineering and Biotechnology</i> , 2015 , 3, 138	5.8	6
91	A genetic overview of 23Y-STR markers in UAE population. <i>Forensic Science International: Genetics</i> , 2016 , 23, 150-152	4.3	6
90	The genetic structure of native Americans in North America based on the Globalfiler [®] STRs. <i>Legal Medicine</i> , 2016 , 23, 49-54	1.9	6
89	Compound stutter in D2S1338 and D12S391. <i>Forensic Science International: Genetics</i> , 2019 , 39, 50-56	4.3	6
88	A Continuous Statistical Phasing Framework for the Analysis of Forensic Mitochondrial DNA Mixtures. <i>Genes</i> , 2021 , 12,	4.2	6
87	International Wildlife Trafficking: A perspective on the challenges and potential forensic genetics solutions. <i>Forensic Science International: Genetics</i> , 2021 , 54, 102551	4.3	6

86	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	0.5	5
85	Postmortem medicolegal genetic diagnostics also require reporting guidance. <i>European Journal of Human Genetics</i> , 2016 , 24, 329-30	5.3	5
84	Duty of Notification and Aviation Safety-A Study of Fatal Aviation Accidents in the United States in 2015. <i>International Journal of Environmental Research and Public Health</i> , 2018 , 15,	4.6	5
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