Bruce Budowle

List of Publications by Year
in descending order

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251 papers	8,808 citations	41344 49 h-index	62596 80 g-index
262 all docs	262 docs citations	262 times ranked	3844 citing authors

#	Article	IF	Citations
1	Validation of mitochondrial DNA sequencing for forensic casework analysis. International Journal of Legal Medicine, 1995, 108, 68-74.	2.2	318
2	Forensically relevant SNP classes. BioTechniques, 2008, 44, 603-610.	1.8	223
3	FORENSICS ANDMITOCHONDRIALDNA: Applications, Debates, and Foundations. Annual Review of Genomics and Human Genetics, 2003, 4, 119-141.	6.2	216
4	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. Forensic Science International: Genetics, 2014, 12, 12-23.	3.1	214
5	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
6	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
7	Population Data on the Thirteen CODIS Core Short Tandem Repeat Loci in African Americans, U.S. Caucasians, Hispanics, Bahamians, Jamaicans, and Trinidadians. Journal of Forensic Sciences, 1999, 44, 1277-1286.	1.6	181
8	Typing of Deoxyribonucleic Acid (DNA) Extracted from Compact Bone from Human Remains. Journal of Forensic Sciences, 1991, 36, 1649-1661.	1.6	173
9	Validity of Low Copy Number Typing and Applications to Forensic Science. Croatian Medical Journal, 2009, 50, 207-217.	0.7	172
10	DNA methylation-based forensic tissue identification. Forensic Science International: Genetics, 2011, 5, 517-524.	3.1	157
11	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
12	Validation of Short Tandem Repeats (STRs) for Forensic Usage: Performance Testing of Fluorescent Multiplex STR Systems and Analysis of Authentic and Simulated Forensic Samples. Journal of Forensic Sciences, 2001, 46, 647-660.	1.6	149
13	EPIDEMIOLOGY: Enhanced: DNA Identifications After the 9/11 World Trade Center Attack. Science, 2005, 310, 1122-1123.	12.6	147
14	CODIS STR Loci Data from 41 Sample Populations. Journal of Forensic Sciences, 2001, 46, 453-489.	1.6	146
15	PUBLIC HEALTH: Building Microbial Forensics as a Response to Bioterrorism. Science, 2003, 301, 1852-1853.	12.6	145
16	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
17	Forensic aspects of mass disasters: Strategic considerations for DNA-based human identification. Legal Medicine, 2005, 7, 230-243.	1.3	130
18	Mixture Interpretation: Defining the Relevant Features for Guidelines for the Assessment of Mixed DNA Profiles in Forensic Casework*. Journal of Forensic Sciences, 2009, 54, 810-821.	1.6	126

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19	Mitochondrial DNA regions HVI and HVII population data. Forensic Science International, 1999, 103, 23-35.	2.2	125
20	Single nucleotide polymorphism typing with massively parallel sequencing for human identification. International Journal of Legal Medicine, 2013, 127, 1079-1086.	2.2	112
21	A Perspective on Errors, Bias, and Interpretation in the Forensic Sciences and Direction for Continuing Advancement*. Journal of Forensic Sciences, 2009, 54, 798-809.	1.6	99
22	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 (SWGDAM). Science and Justice - Journal of the Forensic Science Society, 2004, 44, 51-53.	2.1	95
23	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
24	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
25	STR primer concordance study. Forensic Science International, 2001, 124, 47-54.	2.2	87
26	Fast STR allele identification with STRait Razor 3.0. Forensic Science International: Genetics, 2017, 30, 18-23.	3.1	82
27	Identification of a D8S1179 primer binding site mutation and the validation of a primer designed to recover null alleles. Forensic Science International, 2003, 133, 220-227.	2.2	80
28	STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci. Forensic Science International: Genetics, 2017, 31, 111-117.	3.1	77
29	Evaluation of forensic DNA mixture evidence: protocol for evaluation, interpretation, and statistical calculations using the combined probability of inclusion. BMC Genetics, 2016, 17, 125.	2.7	76
30	Forensic Human Identification Using Skin Microbiomes. Applied and Environmental Microbiology, 2017, 83, .	3.1	74
31	Expansion of Microbial Forensics. Journal of Clinical Microbiology, 2016, 54, 1964-1974.	3.9	72
32	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
33	High sensitivity multiplex short tandem repeat loci analyses with massively parallel sequencing. Forensic Science International: Genetics, 2015, 16, 38-47.	3.1	69
34	Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. Forensic Science International: Genetics, 2018, 32, 50-61.	3.1	69
35	Extracting evidence from forensic DNA analyses: future molecular biology directions. BioTechniques, 2009, 46, 339-350.	1.8	68
36	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

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37	Current stateâ€ofâ€art of STR sequencing in forensic genetics. Electrophoresis, 2018, 39, 2655-2668.	2.4	68
38	Twelve short tandem repeat loci Y chromosome haplotypes: Genetic analysis on populations residing in North America. Forensic Science International, 2005, 150, 1-15.	2.2	65
39	Mutation rates at Y chromosome short tandem repeats in Texas populations. Forensic Science International: Genetics, 2009, 3, 179-184.	3.1	65
40	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
41	Validation of high throughput sequencing and microbial forensics applications. Investigative Genetics, 2014, 5, 9.	3.3	59
42	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
43	Population genetic analyses of the NGM STR loci. International Journal of Legal Medicine, 2011, 125, 101-109.	2.2	58
44	Developing criteria and data to determine best options for expanding the core CODIS loci. Investigative Genetics, 2012, 3, 1.	3.3	58
45	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
46	Choosing Relatives for DNA Identification of Missing Persons. Journal of Forensic Sciences, 2011, 56, S23-8.	1.6	56
47	STRait Razor v2.0: The improved STR Allele Identification Tool â€“ Razor. Forensic Science International: Genetics, 2015, 14, 182-186.	3.1	55
48	Concordance Study on Population Database Samples Using the PowerPlexâ„¢ 16 Kit and AmpFâ„“STRÂ® Profiler Plusâ„¢ Kit and AmpFâ„“STRÂ® COfilerâ„¢ Kit. Journal of Forensic Sciences, 2001, 46, 637-641.	1.6	55
49	Recommendations for consistent treatment of length variants in the human mitochondrial DNA control region. Forensic Science International, 2002, 129, 35-42.	2.2	53
50	Direct PCR amplification of DNA from human bloodstains, saliva, and touch samples collected with microFLOQ Â® swabs. Forensic Science International: Genetics, 2018, 32, 80-87.	3.1	53
51	Comparisons of Familial DNA Database Searching Strategies. Journal of Forensic Sciences, 2011, 56, 1448-1456.	1.6	52
52	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. International Journal of Legal Medicine, 2013, 127, 559-572.	2.2	51
53	Quantification of Human Mitochondrial DNA Using Synthesized DNA Standards*. Journal of Forensic Sciences, 2011, 56, 1457-1463.	1.6	50
54	Future directions of forensic DNA databases. Croatian Medical Journal, 2014, 55, 163-166.	0.7	47

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55	More comprehensive forensic genetic marker analyses for accurate human remains identification using massively parallel DNA sequencing. BMC Genomics, 2016, 17, 750.	2.8	47
56	DNA quality and quantity from up to 16 years old post-mortem blood stored on FTA cards. Forensic Science International, 2016, 261, 148-153.	2.2	47
57	SNP Typing Strategies. Forensic Science International, 2004, 146, S139-S142.	2.2	45
58	Assessing a novel room temperature DNA storage medium for forensic biological samples. Forensic Science International: Genetics, 2012, 6, 31-40.	3.1	45
59	Forensic human identification with targeted microbiome markers using nearest neighbor classification. Forensic Science International: Genetics, 2019, 38, 130-139.	3.1	45
60	Underlying Data for Sequencing the Mitochondrial Genome with the Massively Parallel Sequencing Platform Ion Torrentâ„¢ PGMâ„¢. BMC Genomics, 2015, 16, S4.	2.8	43
61	Criteria for Validation of Methods in Microbial Forensics. Applied and Environmental Microbiology, 2008, 74, 5599-5607.	3.1	42
62	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
63	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
64	Haplotype block: a new type of forensic DNA markers. International Journal of Legal Medicine, 2010, 124, 353-361.	2.2	39
65	Accurate, rapid and high-throughput detection of strain-specific polymorphisms in Bacillus anthracis and Yersinia pestis by next-generation sequencing. Investigative Genetics, 2010, 1, 5.	3.3	39
66	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
67	STRmixâ„¢ collaborative exercise on DNA mixture interpretation. Forensic Science International: Genetics, 2019, 40, 1-8.	3.1	39
68	Reconstructing the population history of Nicaragua by means of mtDNA, Yâ€¢chromosome STRs, and autosomal STR markers. American Journal of Physical Anthropology, 2010, 143, 591-600.	2.1	38
69	An evaluation of the transfer of saliva-derived DNA. International Journal of Legal Medicine, 2012, 126, 851-861.	2.2	38
70	An evaluation of the RapidHITÂ® system for reliably genotyping reference samples. Forensic Science International: Genetics, 2014, 13, 104-111.	3.1	38
71	Increasing the reference populations for the 55 AISNP panel: the need and benefits. International Journal of Legal Medicine, 2017, 131, 913-917.	2.2	38
72	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

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73	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
74	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.	3.1	37
75	Massively parallel sequencing-enabled mixture analysis of mitochondrial DNA samples. International Journal of Legal Medicine, 2018, 132, 1263-1272.	2.2	36
76	Texas Population Substructure and Its Impact on Estimating the Rarity of Y STR Haplotypes from DNA Evidence*. Journal of Forensic Sciences, 2009, 54, 1016-1021.	1.6	35
77	Base Composition Profiling of Human Mitochondrial DNA Using Polymerase Chain Reaction and Direct Automated Electrospray Ionization Mass Spectrometry. Analytical Chemistry, 2009, 81, 7515-7526.	6.5	35
78	Strengthening forensic DNA decision making through a better understanding of the influence of cognitive bias. Science and Justice - Journal of the Forensic Science Society, 2017, 57, 415-420.	2.1	35
79	NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis. Forensic Science International: Genetics, 2018, 37, 172-179.	3.1	35
80	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
81	Prototype PowerPlexÂ® Y23 System: A concordance study. Forensic Science International: Genetics, 2013, 7, 204-208.	3.1	34
82	Massively parallel sequence data of 31 autosomal STR loci from 496 Spanish individuals revealed concordance with CE-STR technology and enhanced discrimination power. Forensic Science International: Genetics, 2019, 42, 49-55.	3.1	34
83	A Comparison and Integration of MiSeq and MinION Platforms for Sequencing Single Source and Mixed Mitochondrial Genomes. PLoS ONE, 2016, 11, e0167600.	2.5	34
84	Use of prior odds for missing persons identifications. Investigative Genetics, 2011, 2, 15.	3.3	33
85	Whole mitochondrial genome genetic diversity in an Estonian population sample. International Journal of Legal Medicine, 2016, 130, 67-71.	2.2	33
86	The Probabilistic Genotyping Software <scp>STR</scp>mix: Utility and Evidence for its Validity. Journal of Forensic Sciences, 2019, 64, 393-405.	1.6	33
87	DNA identification by pedigree likelihood ratio accommodating population substructure and mutations. Investigative Genetics, 2010, 1, 8.	3.3	32
88	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
89	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
90	European survey on forensic applications of massively parallel sequencing. Forensic Science International: Genetics, 2017, 29, e23-e25.	3.1	32

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91	Forensic investigation approaches of searching relatives in DNA databases. Journal of Forensic Sciences, 2021, 66, 430-443.	1.6	32
92	Microbial Forensics: Application to Bioterrorism Preparedness and Response. Infectious Disease Clinics of North America, 2006, 20, 455-473.	5.1	31
93	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
94	Developmental Validation of a MPS Workflow with a PCR-Based Short Amplicon Whole Mitochondrial Genome Panel. Genes, 2020, 11, 1345.	2.4	30
95	US forensic Y-chromosome short tandem repeats database. Legal Medicine, 2010, 12, 289-295.	1.3	29
96	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
97	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
98	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
99	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
100	Improved Y-STR typing for disaster victim identification, missing persons investigations, and historical human skeletal remains. International Journal of Legal Medicine, 2018, 132, 1545-1553.	2.2	28
101	Evaluation of circular DNA substrates for whole genome amplification prior to forensic analysis. Forensic Science International: Genetics, 2012, 6, 185-190.	3.1	26
102	Privacy and genetic genealogy data. Science, 2018, 361, 857-857.	12.6	26
103	A high volume extraction and purification method for recovering DNA from human bone. Forensic Science International: Genetics, 2014, 12, 155-160.	3.1	25
104	Assessment of the role of DNA repair in damaged forensic samples. International Journal of Legal Medicine, 2014, 128, 913-921.	2.2	25
105	Increasing the reach of forensic genetics with massively parallel sequencing. Forensic Science, Medicine, and Pathology, 2017, 13, 342-349.	1.4	25
106	Comparative tolerance of two massively parallel sequencing systems to common PCR inhibitors. International Journal of Legal Medicine, 2018, 132, 983-995.	2.2	25
107	Automated analysis of sequence polymorphism in STR alleles by PCR and direct electrospray ionization mass spectrometry. Forensic Science International: Genetics, 2012, 6, 594-606.	3.1	24
108	Distinguishing mitochondrial DNA and NUMT sequences amplified with the precision ID mtDNA whole genome panel. Mitochondrion, 2020, 55, 122-133.	3.4	24

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109	Maternity exclusion with a very high autosomal STRs kinship index. International Journal of Legal Medicine, 2012, 126, 645-648.	2.2	23
110	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
111	Native American population data based on the Globalfiler Â® autosomal STR loci. Forensic Science International: Genetics, 2016, 24, e12-e13.	3.1	23
112	Development and validation of a novel multiplexed DNA analysis system, InnoTyperÂ® 21. Forensic Science International: Genetics, 2017, 29, 80-99.	3.1	23
113	Internal validation of the RapidHIT Â® ID system. Forensic Science International: Genetics, 2017, 31, 180-188.	3.1	23
114	Utility of the Ion S5â„¢ and MiSeq FGxâ„¢ sequencing platforms to characterize challenging human remains. Legal Medicine, 2019, 41, 101623.	1.3	23
115	Expanding beyond the current core STR loci: An exploration of 73 STR markers with increased diversity for enhanced DNA mixture deconvolution. Forensic Science International: Genetics, 2019, 38, 121-129.	3.1	23
116	Population studies on three Native Alaska population groups using STR loci. Forensic Science International, 2002, 129, 51-57.	2.2	22
117	The effects of Asian population substructure on Y STR forensic analyses. Legal Medicine, 2009, 11, 64-69.	1.3	22
118	Interpreting Y chromosome STR haplotype mixture. Legal Medicine, 2010, 12, 137-143.	1.3	22
119	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
120	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
121	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
122	International Wildlife Trafficking: A perspective on the challenges and potential forensic genetics solutions. Forensic Science International: Genetics, 2021, 54, 102551.	3.1	20
123	Variants observed for STR locus SE33: A concordance study. Forensic Science International: Genetics, 2012, 6, 494-497.	3.1	19
124	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
125	mitoSAVE: Mitochondrial sequence analysis of variants in Excel. Forensic Science International: Genetics, 2014, 12, 122-125.	3.1	19
126	Flanking Variation Influences Rates of Stutter in Simple Repeats. Genes, 2017, 8, 329.	2.4	19

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127	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
128	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
129	Aircraft-Assisted Pilot Suicides: Lessons to be Learned. Aviation, Space, and Environmental Medicine, 2014, 85, 841-846.	0.5	17
130	Utility of amplification enhancers in low copy number DNA analysis. International Journal of Legal Medicine, 2015, 129, 43-52.	2.2	17
131	Identification and analysis of mtDNA genomes attributed to Finns reveal long-stagnant demographic trends obscured in the total diversity. Scientific Reports, 2017, 7, 6193.	3.3	17
132	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
133	A technique for setting analytical thresholds in massively parallel sequencing-based forensic DNA analysis. PLoS ONE, 2017, 12, e0178005.	2.5	16
134	Forensic genetic investigation of human skeletal remains recovered from the La Belle shipwreck. Forensic Science International, 2020, 306, 110050.	2.2	16
135	STRait Razor Online: An enhanced user interface to facilitate interpretation of MPS data. Forensic Science International: Genetics, 2021, 52, 102463.	3.1	16
136	Enhancing resolution and statistical power by utilizing mass spectrometry for detection of SNPs within the short tandem repeats. Forensic Science International: Genetics Supplement Series, 2009, 2, 529-531.	0.3	15
137	Kinship Index Variations among Populations and Thresholds for Familial Searching. PLoS ONE, 2012, 7, e37474.	2.5	15
138	A novel phylogenetic approach for de novo discovery of putative nuclear mitochondrial (pNumt) haplotypes. Forensic Science International: Genetics, 2019, 43, 102146.	3.1	15
139	How many familial relationship testing results could be wrong?. PLoS Genetics, 2020, 16, e1008929.	3.5	15
140	Post-injection hybridization of complementary DNA strands on capillary electrophoresis platforms: A novel solution for dsDNA artifacts. Forensic Science International: Genetics, 2008, 2, 257-273.	3.1	14
141	Microbial Forensic Investigation of the Anthrax-Letter Attacks. , 2011, , 15-25.		14
142	INNULs: A Novel Design Amplification Strategy for Retrotransposable Elements for Studying Population Variation. Human Heredity, 2012, 74, 27-35.	0.8	14
143	Working towards implementation of whole genome mitochondrial DNA sequencing into routine casework. Forensic Science International: Genetics Supplement Series, 2017, 6, e388-e389.	0.3	14
144	Use of Forensic Methods Under Exigent Circumstances Without Full Validation. Science Translational Medicine, 2009, 1, 8cm7.	12.4	13

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145	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
146	Potential highly polymorphic short tandem repeat markers for enhanced forensic identity testing. Forensic Science International: Genetics, 2018, 37, 162-171.	3.1	13
147	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
148	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
149	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
150	Investigation of the STR loci noise distributions of PowerSeqâ„¢ Auto System. Croatian Medical Journal, 2017, 58, 214-221.	0.7	12
151	Results of a collaborative study on DNA identification of aged bone samples. Croatian Medical Journal, 2017, 58, 203-213.	0.7	12
152	Automated Alignment and Nomenclature for Consistent Treatment of Polymorphisms in the Human Mitochondrial DNA Control Region. Journal of Forensic Sciences, 2010, 55, 1190-1195.	1.6	11
153	Reply to Comments by Buckleton and Gill on â€œLow copy number typing has yet to achieve â€˜general acceptanceâ€â€™ by Budowle, B., et al., 2009. Forensic Sci. Int.: Genet. Suppl. Series 2, 551â€“552. Forensic Science International: Genetics, 2011, 5, 12-14.	3.1	11
154	Are low LRs reliable?. Forensic Science International: Genetics, 2020, 49, 102350.	3.1	10
155	A standalone humanitarian DNA identification database system to increase identification of human remains of foreign nationals. International Journal of Legal Medicine, 2020, 134, 2039-2044.	2.2	10
156	A Continuous Statistical Phasing Framework for the Analysis of Forensic Mitochondrial DNA Mixtures. Genes, 2021, 12, 128.	2.4	10
157	Response to Comment on â€œLow copy number typing has yet to achieve â€œgeneral acceptanceâ€â€•(Budowle) Tj ETQq1 1 0.784 Prinz. Forensic Science International: Genetics, 2011, 5, 5-7.	3.1	9
158	Population genetic analyses of 15 STR loci from seven forensically-relevant populations residing in the state of Kuwait. Forensic Science International: Genetics, 2013, 7, e106-e107.	3.1	9
159	Duty of Notification and Aviation Safetyâ€”A Study of Fatal Aviation Accidents in the United States in 2015. International Journal of Environmental Research and Public Health, 2018, 15, 1258.	2.6	9
160	Compound stutter in D2S1338 and D12S391. Forensic Science International: Genetics, 2019, 39, 50-56.	3.1	9
161	Reducing noise and stutter in short tandem repeat loci with unique molecular identifiers. Forensic Science International: Genetics, 2021, 51, 102459.	3.1	9
162	Missing Persons Identification: Genetics at Work for Society. Science, 2000, 290, 2257-2258.	12.6	9

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163	Validation of the Applied Biosystems RapidHIT ID instrument and ACE GlobalFiler Express sample cartridge. International Journal of Legal Medicine, 2022, 136, 13-41.	2.2	9
164	Y-STR loci diversity in native Alaskan populations. International Journal of Legal Medicine, 2011, 125, 559-563.	2.2	8
165	A Case of Amelogenin Y-null: A simple primer binding site mutation or unusual genetic anomaly?. Legal Medicine, 2012, 14, 320-323.	1.3	8
166	Validation of the PLEX-IDTM mass spectrometry mitochondrial DNA assay. International Journal of Legal Medicine, 2013, 127, 277-286.	2.2	8
167	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
168	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
169	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
170	Postmortem medicolegal genetic diagnostics also require reporting guidance. European Journal of Human Genetics, 2016, 24, 329-330.	2.8	8
171	Supervised Classification of CYP2D6 Genotype and Metabolizer Phenotype With Postmortem Tramadol-Exposed Finns. American Journal of Forensic Medicine and Pathology, 2019, 40, 8-18.	0.8	8
172	Allelic frequencies with 23 autosomic STRS in the Aymara population of Peru. International Journal of Legal Medicine, 2021, 135, 779-781.	2.2	8
173	Population Informative Markers Selected Using Wright's Fixation Index and Machine Learning Improves Human Identification Using the Skin Microbiome. Applied and Environmental Microbiology, 2021, 87, e0120821.	3.1	8
174	Precision DNA Mixture Interpretation with Single-Cell Profiling. Genes, 2021, 12, 1649.	2.4	8
175	Pedigree likelihood ratio for lineage markers. International Journal of Legal Medicine, 2011, 125, 519-525.	2.2	7
176	Population genetic analyses of the STR loci of the AmpFlSTR NGM SElectâ„¢ kit for Han population in Fujian Province, China. International Journal of Legal Medicine, 2013, 127, 345-346.	2.2	7
177	Evaluation of a novel material, Diomics X-Swabâ„¢, for collection of DNA. Forensic Science International: Genetics, 2014, 12, 192-198.	3.1	7
178	The genetic structure of native Americans in North America based on the GlobalfilerÂ® STRs. Legal Medicine, 2016, 23, 49-54.	1.3	7
179	Attention-Deficit/Hyperactivity Disorder and Fatal Accidents in Aviation Medicine. Aerospace Medicine and Human Performance, 2017, 88, 871-875.	0.4	7
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