

Bruce Budowle

List of Publications by Year in descending order

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Version: 2024-02-01

251
papers

8,808
citations

41258

49
h-index

62479

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. <i>International Journal of Legal Medicine</i> , 1995, 108, 68-74.	1.2	318
2	Forensically relevant SNP classes. <i>BioTechniques</i> , 2008, 44, 603-610.	0.8	223
3	FORENSICS AND MITOCHONDRIAL DNA: Applications, Debates, and Foundations. <i>Annual Review of Genomics and Human Genetics</i> , 2003, 4, 119-141.	2.5	216
4	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. <i>Forensic Science International: Genetics</i> , 2014, 12, 12-23.	1.6	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. <i>Forensic Science International: Genetics</i> , 2016, 22, 54-63.	1.6	190
6	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.	1.6	185
7	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, 1277-1286.	0.9	181
8	Typing of Deoxyribonucleic Acid (DNA) Extracted from Compact Bone from Human Remains. <i>Journal of Forensic Sciences</i> , 1991, 36, 1649-1661.	0.9	173
9	Validity of Low Copy Number Typing and Applications to Forensic Science. <i>Croatian Medical Journal</i> , 2009, 50, 207-217.	0.2	172
10	DNA methylation-based forensic tissue identification. <i>Forensic Science International: Genetics</i> , 2011, 5, 517-524.	1.6	157
11	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.	1.6	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. <i>Journal of Forensic Sciences</i> , 2001, 46, 647-660.	0.9	149
13	EPIDEMIOLOGY: Enhanced: DNA Identifications After the 9/11 World Trade Center Attack. <i>Science</i> , 2005, 310, 1122-1123.	6.0	147
14	CODIS STR Loci Data from 41 Sample Populations. <i>Journal of Forensic Sciences</i> , 2001, 46, 453-489.	0.9	146
15	PUBLIC HEALTH: Building Microbial Forensics as a Response to Bioterrorism. <i>Science</i> , 2003, 301, 1852-1853.	6.0	145
16	Characterization of genetic sequence variation of 58 STR loci in four major population groups. <i>Forensic Science International: Genetics</i> , 2016, 25, 214-226.	1.6	138
17	Forensic aspects of mass disasters: Strategic considerations for DNA-based human identification. <i>Legal Medicine</i> , 2005, 7, 230-243.	0.6	130
18	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, 810-821.	0.9	126

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19	Mitochondrial DNA regions HVI and HVII population data. <i>Forensic Science International</i> , 1999, 103, 23-35.	1.3	125
20	Single nucleotide polymorphism typing with massively parallel sequencing for human identification. <i>International Journal of Legal Medicine</i> , 2013, 127, 1079-1086.	1.2	112
21	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.	0.9	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 (SWGDM). <i>Science and Justice - Journal of the Forensic Science Society</i> , 2004, 44, 51-53.	1.3	95
23	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.	1.6	94
24	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.	1.2	92
25	STR primer concordance study. <i>Forensic Science International</i> , 2001, 124, 47-54.	1.3	87
26	Fast STR allele identification with STRait Razor 3.0. <i>Forensic Science International: Genetics</i> , 2017, 30, 18-23.	1.6	82
27	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, 220-227.	1.3	80
28	STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci. <i>Forensic Science International: Genetics</i> , 2017, 31, 111-117.	1.6	77
29	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.	2.7	76
30	Forensic Human Identification Using Skin Microbiomes. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	74
31	Expansion of Microbial Forensics. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1964-1974.	1.8	72
32	Population and performance analyses of four major populations with Illumina® FGx Forensic Genomics System. <i>Forensic Science International: Genetics</i> , 2017, 30, 81-92.	1.6	70
33	High sensitivity multiplex short tandem repeat loci analyses with massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2015, 16, 38-47.	1.6	69
34	Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. <i>Forensic Science International: Genetics</i> , 2018, 32, 50-61.	1.6	69
35	Extracting evidence from forensic DNA analyses: future molecular biology directions. <i>BioTechniques</i> , 2009, 46, 339-350.	0.8	68
36	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.	1.6	68

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37	Current state of art of STR sequencing in forensic genetics. <i>Electrophoresis</i> , 2018, 39, 2655-2668.	1.3	68
38	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.	1.3	65
39	Mutation rates at Y chromosome short tandem repeats in Texas populations. <i>Forensic Science International: Genetics</i> , 2009, 3, 179-184.	1.6	65
40	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.	1.6	60
41	Validation of high throughput sequencing and microbial forensics applications. <i>Investigative Genetics</i> , 2014, 5, 9.	3.3	59
42	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.	1.6	59
43	Population genetic analyses of the NGM STR loci. <i>International Journal of Legal Medicine</i> , 2011, 125, 101-109.	1.2	58
44	Developing criteria and data to determine best options for expanding the core CODIS loci. <i>Investigative Genetics</i> , 2012, 3, 1.	3.3	58
45	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.	1.6	58
46	Choosing Relatives for DNA Identification of Missing Persons. <i>Journal of Forensic Sciences</i> , 2011, 56, S23-8.	0.9	56
47	STRait Razor v2.0: The improved STR Allele Identification Tool "Razor. <i>Forensic Science International: Genetics</i> , 2015, 14, 182-186.	1.6	55
48	Concordance Study on Population Database Samples Using the PowerPlex, 16 Kit and AmpF, STR, Profiler Plus, Kit and AmpF, STR, COfiler, Kit. <i>Journal of Forensic Sciences</i> , 2001, 46, 637-641.	0.9	55
49	Recommendations for consistent treatment of length variants in the human mitochondrial DNA control region. <i>Forensic Science International</i> , 2002, 129, 35-42.	1.3	53
50	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.	1.6	53
51	Comparisons of Familial DNA Database Searching Strategies. <i>Journal of Forensic Sciences</i> , 2011, 56, 1448-1456.	0.9	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. <i>International Journal of Legal Medicine</i> , 2013, 127, 559-572.	1.2	51
53	Quantification of Human Mitochondrial DNA Using Synthesized DNA Standards*. <i>Journal of Forensic Sciences</i> , 2011, 56, 1457-1463.	0.9	50
54	Future directions of forensic DNA databases. <i>Croatian Medical Journal</i> , 2014, 55, 163-166.	0.2	47

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55	More comprehensive forensic genetic marker analyses for accurate human remains identification using massively parallel DNA sequencing. <i>BMC Genomics</i> , 2016, 17, 750.	1.2	47
56	DNA quality and quantity from up to 16 years old post-mortem blood stored on FTA cards. <i>Forensic Science International</i> , 2016, 261, 148-153.	1.3	47
57	SNP Typing Strategies. <i>Forensic Science International</i> , 2004, 146, S139-S142.	1.3	45
58	Assessing a novel room temperature DNA storage medium for forensic biological samples. <i>Forensic Science International: Genetics</i> , 2012, 6, 31-40.	1.6	45
59	Forensic human identification with targeted microbiome markers using nearest neighbor classification. <i>Forensic Science International: Genetics</i> , 2019, 38, 130-139.	1.6	45
60	Underlying Data for Sequencing the Mitochondrial Genome with the Massively Parallel Sequencing Platform Ion Torrent, PGM, . <i>BMC Genomics</i> , 2015, 16, S4.	1.2	43
61	Criteria for Validation of Methods in Microbial Forensics. <i>Applied and Environmental Microbiology</i> , 2008, 74, 5599-5607.	1.4	42
62	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.	0.6	41
63	Increasing the discrimination power of ancestry- and identity-informative SNP loci within the ForenSeq DNA Signature Prep Kit. <i>Forensic Science International: Genetics</i> , 2018, 36, 60-76.	1.6	41
64	Haplotype block: a new type of forensic DNA markers. <i>International Journal of Legal Medicine</i> , 2010, 124, 353-361.	1.2	39
65	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.	3.3	39
66	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.	1.6	39
67	STRmix collaborative exercise on DNA mixture interpretation. <i>Forensic Science International: Genetics</i> , 2019, 40, 1-8.	1.6	39
68	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.	2.1	38
69	An evaluation of the transfer of saliva-derived DNA. <i>International Journal of Legal Medicine</i> , 2012, 126, 851-861.	1.2	38
70	An evaluation of the RapidHIT system for reliably genotyping reference samples. <i>Forensic Science International: Genetics</i> , 2014, 13, 104-111.	1.6	38
71	Increasing the reference populations for the 55 AISNP panel: the need and benefits. <i>International Journal of Legal Medicine</i> , 2017, 131, 913-917.	1.2	38
72	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.	0.6	37

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73	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.	0.2	37
74	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.	1.6	37
75	Massively parallel sequencing-enabled mixture analysis of mitochondrial DNA samples. <i>International Journal of Legal Medicine</i> , 2018, 132, 1263-1272.	1.2	36
76	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, 1016-1021.	0.9	35
77	Base Composition Profiling of Human Mitochondrial DNA Using Polymerase Chain Reaction and Direct Automated Electrospray Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 7515-7526.	3.2	35
78	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.	1.3	35
79	NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis. <i>Forensic Science International: Genetics</i> , 2018, 37, 172-179.	1.6	35
80	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.	1.6	35
81	Prototype PowerPlex [®] Y23 System: A concordance study. <i>Forensic Science International: Genetics</i> , 2013, 7, 204-208.	1.6	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. <i>Forensic Science International: Genetics</i> , 2019, 42, 49-55.	1.6	34
83	A Comparison and Integration of MiSeq and MinION Platforms for Sequencing Single Source and Mixed Mitochondrial Genomes. <i>PLoS ONE</i> , 2016, 11, e0167600.	1.1	34
84	Use of prior odds for missing persons identifications. <i>Investigative Genetics</i> , 2011, 2, 15.	3.3	33
85	Whole mitochondrial genome genetic diversity in an Estonian population sample. <i>International Journal of Legal Medicine</i> , 2016, 130, 67-71.	1.2	33
86	The Probabilistic Genotyping Software <scp>STR</scp>mix: Utility and Evidence for its Validity. <i>Journal of Forensic Sciences</i> , 2019, 64, 393-405.	0.9	33
87	DNA identification by pedigree likelihood ratio accommodating population substructure and mutations. <i>Investigative Genetics</i> , 2010, 1, 8.	3.3	32
88	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.	1.6	32
89	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.	1.6	32
90	European survey on forensic applications of massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2017, 29, e23-e25.	1.6	32

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91	Forensic investigation approaches of searching relatives in DNA databases. <i>Journal of Forensic Sciences</i> , 2021, 66, 430-443.	0.9	32
92	Microbial Forensics: Application to Bioterrorism Preparedness and Response. <i>Infectious Disease Clinics of North America</i> , 2006, 20, 455-473.	1.9	31
93	Selection of highly informative SNP markers for population affiliation of major US populations. <i>International Journal of Legal Medicine</i> , 2016, 130, 341-352.	1.2	30
94	Developmental Validation of a MPS Workflow with a PCR-Based Short Amplicon Whole Mitochondrial Genome Panel. <i>Genes</i> , 2020, 11, 1345.	1.0	30
95	US forensic Y-chromosome short tandem repeats database. <i>Legal Medicine</i> , 2010, 12, 289-295.	0.6	29
96	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.	1.6	29
97	Novel Y-chromosome Short Tandem Repeat Variants Detected Through the Use of Massively Parallel Sequencing. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 250-257.	3.0	28
98	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.	0.6	28
99	Effects of the Ion PGM [®] , [®] Hi-Q [®] , [®] sequencing chemistry on sequence data quality. <i>International Journal of Legal Medicine</i> , 2016, 130, 1169-1180.	1.2	28
100	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.	1.2	28
101	Evaluation of circular DNA substrates for whole genome amplification prior to forensic analysis. <i>Forensic Science International: Genetics</i> , 2012, 6, 185-190.	1.6	26
102	Privacy and genetic genealogy data. <i>Science</i> , 2018, 361, 857-857.	6.0	26
103	A high volume extraction and purification method for recovering DNA from human bone. <i>Forensic Science International: Genetics</i> , 2014, 12, 155-160.	1.6	25
104	Assessment of the role of DNA repair in damaged forensic samples. <i>International Journal of Legal Medicine</i> , 2014, 128, 913-921.	1.2	25
105	Increasing the reach of forensic genetics with massively parallel sequencing. <i>Forensic Science, Medicine, and Pathology</i> , 2017, 13, 342-349.	0.6	25
106	Comparative tolerance of two massively parallel sequencing systems to common PCR inhibitors. <i>International Journal of Legal Medicine</i> , 2018, 132, 983-995.	1.2	25
107	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.	1.6	24
108	Distinguishing mitochondrial DNA and NUMT sequences amplified with the precision ID mtDNA whole genome panel. <i>Mitochondrion</i> , 2020, 55, 122-133.	1.6	24

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109	Maternity exclusion with a very high autosomal STRs kinship index. <i>International Journal of Legal Medicine</i> , 2012, 126, 645-648.	1.2	23
110	Massively parallel sequencing of forensically relevant single nucleotide polymorphisms using TruSeq [®] , [®] forensic amplicon. <i>International Journal of Legal Medicine</i> , 2015, 129, 31-36.	1.2	23
111	Native American population data based on the Globalfiler [®] autosomal STR loci. <i>Forensic Science International: Genetics</i> , 2016, 24, e12-e13.	1.6	23
112	Development and validation of a novel multiplexed DNA analysis system, InnoTyper [®] 21. <i>Forensic Science International: Genetics</i> , 2017, 29, 80-99.	1.6	23
113	Internal validation of the RapidHIT [®] ID system. <i>Forensic Science International: Genetics</i> , 2017, 31, 180-188.	1.6	23
114	Utility of the Ion S5 [®] , [®] and MiSeq FG [®] , [®] sequencing platforms to characterize challenging human remains. <i>Legal Medicine</i> , 2019, 41, 101623.	0.6	23
115	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.	1.6	23
116	Population studies on three Native Alaska population groups using STR loci. <i>Forensic Science International</i> , 2002, 129, 51-57.	1.3	22
117	The effects of Asian population substructure on Y STR forensic analyses. <i>Legal Medicine</i> , 2009, 11, 64-69.	0.6	22
118	Interpreting Y chromosome STR haplotype mixture. <i>Legal Medicine</i> , 2010, 12, 137-143.	0.6	22
119	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.	1.6	22
120	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.	1.2	22
121	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.	1.6	21
122	International Wildlife Trafficking: A perspective on the challenges and potential forensic genetics solutions. <i>Forensic Science International: Genetics</i> , 2021, 54, 102551.	1.6	20
123	Variants observed for STR locus SE33: A concordance study. <i>Forensic Science International: Genetics</i> , 2012, 6, 494-497.	1.6	19
124	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.	1.2	19
125	mitoSAVE: Mitochondrial sequence analysis of variants in Excel. <i>Forensic Science International: Genetics</i> , 2014, 12, 122-125.	1.6	19
126	Flanking Variation Influences Rates of Stutter in Simple Repeats. <i>Genes</i> , 2017, 8, 329.	1.0	19

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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.	1.2	18
128	Modified DOP-PCR for improved STR typing of degraded DNA from human skeletal remains and bloodstains. <i>Legal Medicine</i> , 2016, 18, 7-12.	0.6	18
129	Aircraft-Assisted Pilot Suicides: Lessons to be Learned. <i>Aviation, Space, and Environmental Medicine</i> , 2014, 85, 841-846.	0.6	17
130	Utility of amplification enhancers in low copy number DNA analysis. <i>International Journal of Legal Medicine</i> , 2015, 129, 43-52.	1.2	17
131	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.	1.6	17
132	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.	0.4	16
133	A technique for setting analytical thresholds in massively parallel sequencing-based forensic DNA analysis. <i>PLoS ONE</i> , 2017, 12, e0178005.	1.1	16
134	Forensic genetic investigation of human skeletal remains recovered from the La Belle shipwreck. <i>Forensic Science International</i> , 2020, 306, 110050.	1.3	16
135	STRait Razor Online: An enhanced user interface to facilitate interpretation of MPS data. <i>Forensic Science International: Genetics</i> , 2021, 52, 102463.	1.6	16
136	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.	0.1	15
137	Kinship Index Variations among Populations and Thresholds for Familial Searching. <i>PLoS ONE</i> , 2012, 7, e37474.	1.1	15
138	A novel phylogenetic approach for de novo discovery of putative nuclear mitochondrial (pNumt) haplotypes. <i>Forensic Science International: Genetics</i> , 2019, 43, 102146.	1.6	15
139	How many familial relationship testing results could be wrong?. <i>PLoS Genetics</i> , 2020, 16, e1008929.	1.5	15
140	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, 257-273.	1.6	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. <i>Human Heredity</i> , 2012, 74, 27-35.	0.4	14
143	Working towards implementation of whole genome mitochondrial DNA sequencing into routine casework. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e388-e389.	0.1	14
144	Use of Forensic Methods Under Exigent Circumstances Without Full Validation. <i>Science Translational Medicine</i> , 2009, 1, 8cm7.	5.8	13

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145	Y-chromosomal analysis of Greek Cypriots reveals a primarily common pre-Ottoman paternal ancestry with Turkish Cypriots. <i>PLoS ONE</i> , 2017, 12, e0179474.	1.1	13
146	Potential highly polymorphic short tandem repeat markers for enhanced forensic identity testing. <i>Forensic Science International: Genetics</i> , 2018, 37, 162-171.	1.6	13
147	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.	1.6	13
148	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.	1.6	13
149	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.	1.6	13
150	Investigation of the STR loci noise distributions of PowerSeq [®] , [®] Auto System. <i>Croatian Medical Journal</i> , 2017, 58, 214-221.	0.2	12
151	Results of a collaborative study on DNA identification of aged bone samples. <i>Croatian Medical Journal</i> , 2017, 58, 203-213.	0.2	12
152	Automated Alignment and Nomenclature for Consistent Treatment of Polymorphisms in the Human Mitochondrial DNA Control Region. <i>Journal of Forensic Sciences</i> , 2010, 55, 1190-1195.	0.9	11
153	Reply to Comments by Buckleton and Gill on "Low copy number typing has yet to achieve general acceptance"™ by Budowle, B., et al., 2009. <i>Forensic Sci. Int.: Genet. Suppl. Series 2</i> , 551-552. <i>Forensic Science International: Genetics</i> , 2011, 5, 12-14.	1.6	11
154	Are low LRs reliable?. <i>Forensic Science International: Genetics</i> , 2020, 49, 102350.	1.6	10
155	A standalone humanitarian DNA identification database system to increase identification of human remains of foreign nationals. <i>International Journal of Legal Medicine</i> , 2020, 134, 2039-2044.	1.2	10
156	A Continuous Statistical Phasing Framework for the Analysis of Forensic Mitochondrial DNA Mixtures. <i>Genes</i> , 2021, 12, 128.	1.0	10
157	Response to Comment on "Low copy number typing has yet to achieve general acceptance"™ (Budowle) Tj ETQq1 1 0.784911 Prinz. <i>Forensic Science International: Genetics</i> , 2011, 5, 5-7.	1.6	9
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