

Bruce Budowle

List of Publications by Year in descending order

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Version: 2024-02-01

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	Population data of 27 Y-chromosome STRs in Aymara population from Peru. <i>Australian Journal of Forensic Sciences</i> , 2022, 54, 596-610.	1.2	4
2	Validation of the Applied Biosystems RapidHIT ID instrument and ACE GlobalFiler Express sample cartridge. <i>International Journal of Legal Medicine</i> , 2022, 136, 13-41.	2.2	9
3	skater: an R package for SNP-based kinship analysis, testing, and evaluation. <i>F1000Research</i> , 2022, 11, 18.	1.6	5
4	Determining Informative Microbial Single Nucleotide Polymorphisms for Human Identification. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0005222.	3.1	5
5	Re: Riman et al. Examining performance and likelihood ratios for two likelihood ratio systems using the PROVEDIt dataset. <i>Forensic Science International: Genetics</i> , 2022, 59, 102709.	3.1	7
6	Genetic study with 21 autosomal STRs in five Peruvian macro regions for human identification purposes. <i>Legal Medicine</i> , 2022, 57, 102073.	1.3	3
7	Techniques for estimating genetically variable peptides and semi-continuous likelihoods from massively parallel sequencing data. <i>Forensic Science International: Genetics</i> , 2022, 59, 102719.	3.1	2
8	Forensic investigation approaches of searching relatives in DNA databases. <i>Journal of Forensic Sciences</i> , 2021, 66, 430-443.	1.6	32
9	Allelic frequencies with 23 autosomic STRs in the Aymara population of Peru. <i>International Journal of Legal Medicine</i> , 2021, 135, 779-781.	2.2	8
10	A Continuous Statistical Phasing Framework for the Analysis of Forensic Mitochondrial DNA Mixtures. <i>Genes</i> , 2021, 12, 128.	2.4	10
11	Reducing noise and stutter in short tandem repeat loci with unique molecular identifiers. <i>Forensic Science International: Genetics</i> , 2021, 51, 102459.	3.1	9
12	Linkage and linkage disequilibrium among the markers in the forensic MPS panels. <i>Journal of Forensic Sciences</i> , 2021, 66, 1637-1646.	1.6	2
13	STRait Razor Online: An enhanced user interface to facilitate interpretation of MPS data. <i>Forensic Science International: Genetics</i> , 2021, 52, 102463.	3.1	16
14	Autosomal STR and SNP characterization of populations from the Northeastern Peruvian Andes with the ForenSeq [®] , [®] DNA Signature Prep Kit. <i>Forensic Science International: Genetics</i> , 2021, 52, 102487.	3.1	13
15	Genetic study with autosomal STR markers in people of the Peruvian jungle for human identification purposes. <i>Journal of the Canadian Society of Forensic Science</i> , 2021, 54, 117-138.	0.9	5
16	Evaluation of Promega PowerSeq [®] , [®] Auto/Y systems prototype on an admixed sample of Rio de Janeiro, Brazil: Population data, sensitivity, stutter and mixture studies. <i>Forensic Science International: Genetics</i> , 2021, 53, 102516.	3.1	13
17	Enhanced mixture interpretation with macrohaplotypes based on long-read DNA sequencing. <i>International Journal of Legal Medicine</i> , 2021, 135, 2189-2198.	2.2	5
18	Population Informative Markers Selected Using Wright's Fixation Index and Machine Learning Improves Human Identification Using the Skin Microbiome. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0120821.	3.1	8

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19	International Wildlife Trafficking: A perspective on the challenges and potential forensic genetics solutions. <i>Forensic Science International: Genetics</i> , 2021, 54, 102551.	3.1	20
20	Reverse complement-PCR, an innovative and effective method for multiplexing forensically relevant single nucleotide polymorphism marker systems. <i>BioTechniques</i> , 2021, 71, 484-489.	1.8	6
21	MMDIT: A tool for the deconvolution and interpretation of mitochondrial DNA mixtures. <i>Forensic Science International: Genetics</i> , 2021, 55, 102568.	3.1	4
22	A novel approach to imaging and visualization of minute amounts of DNA in small volume samples. <i>Analyst, The</i> , 2021, 146, 6520-6527.	3.5	2
23	Graph Algorithms for Mixture Interpretation. <i>Genes</i> , 2021, 12, 185.	2.4	5
24	Association of whole mtDNA, an NADPH G11914A variant, and haplogroups with high physical performance in an elite military troop. <i>Brazilian Journal of Medical and Biological Research</i> , 2021, 54, e10317.	1.5	0
25	ProDerAl: reference position dependent alignment. <i>Bioinformatics</i> , 2021, 37, 2479-2480.	4.1	3
26	Precision DNA Mixture Interpretation with Single-Cell Profiling. <i>Genes</i> , 2021, 12, 1649.	2.4	8
27	PREVIOUS MILITARY PILOTS AND THEIR LATER FATAL CIVIL AVIATION ACCIDENTS. <i>Aviation</i> , 2021, 25, 182-186.	0.9	0
28	Reverse Complement PCR: A novel one-step PCR system for typing highly degraded DNA for human identification. <i>Forensic Science International: Genetics</i> , 2020, 44, 102201.	3.1	13
29	Forensic genetic investigation of human skeletal remains recovered from the La Belle shipwreck. <i>Forensic Science International</i> , 2020, 306, 110050.	2.2	16
30	Forensic human identification using skin microbiome genetic signatures. , 2020, , 155-169.		1
31	Select methods for microbial forensic nucleic acid analysis of trace and uncultivable specimens. , 2020, , 195-205.		2
32	Education and training in microbial forensics. , 2020, , 473-495.		0
33	Distinguishing mitochondrial DNA and NUMT sequences amplified with the precision ID mtDNA whole genome panel. <i>Mitochondrion</i> , 2020, 55, 122-133.	3.4	24
34	Are low LR's reliable?. <i>Forensic Science International: Genetics</i> , 2020, 49, 102350.	3.1	10
35	Developmental Validation of a MPS Workflow with a PCR-Based Short Amplicon Whole Mitochondrial Genome Panel. <i>Genes</i> , 2020, 11, 1345.	2.4	30
36	Evaluation of 16S rRNA Hypervariable Regions for Bioweapon Species Detection by Massively Parallel Sequencing. <i>International Journal of Microbiology</i> , 2020, 2020, 1-11.	2.3	2

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37	Population genetic study of a Peruvian population using human identification STRs. <i>International Journal of Legal Medicine</i> , 2020, 134, 2071-2073.	2.2	7
38	How many familial relationship testing results could be wrong?. <i>PLoS Genetics</i> , 2020, 16, e1008929.	3.5	15
39	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.	2.2	10
40	The lot-to-lot variability in the mitochondrial genome of controls. <i>Forensic Science International: Genetics</i> , 2020, 47, 102298.	3.1	6
41	An algorithm for random match probability calculation from peptide sequences. <i>Forensic Science International: Genetics</i> , 2020, 47, 102295.	3.1	4
42	Genetic assessment reveals no population substructure and divergent regional and sex-specific histories in the Chachapoyas from northeast Peru. <i>PLoS ONE</i> , 2020, 15, e0244497.	2.5	5
43	The Probabilistic Genotyping Software <scp>STR</scp>mix: Utility and Evidence for its Validity. <i>Journal of Forensic Sciences</i> , 2019, 64, 393-405.	1.6	33
44	Linkage, recombination, and mutation rate analyses of 19 X-chromosomal STR loci in Chinese Southern Han pedigrees. <i>International Journal of Legal Medicine</i> , 2019, 133, 1691-1698.	2.2	5
45	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.	3.1	37
46	A novel phylogenetic approach for de novo discovery of putative nuclear mitochondrial (pNumt) haplotypes. <i>Forensic Science International: Genetics</i> , 2019, 43, 102146.	3.1	15
47	Utility of the Ion S5â„¢ and MiSeq FGxâ„¢ sequencing platforms to characterize challenging human remains. <i>Legal Medicine</i> , 2019, 41, 101623.	1.3	23
48	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.	3.1	34
49	A pathway-driven predictive model of tramadol pharmacogenetics. <i>European Journal of Human Genetics</i> , 2019, 27, 1143-1156.	2.8	4
50	Supervised Classification of CYP2D6 Genotype and Metabolizer Phenotype With Postmortem Tramadol-Exposed Finns. <i>American Journal of Forensic Medicine and Pathology</i> , 2019, 40, 8-18.	0.8	8
51	Compound stutter in D2S1338 and D12S391. <i>Forensic Science International: Genetics</i> , 2019, 39, 50-56.	3.1	9
52	STRmixâ„¢ collaborative exercise on DNA mixture interpretation. <i>Forensic Science International: Genetics</i> , 2019, 40, 1-8.	3.1	39
53	Assessment of impact of DNA extraction methods on analysis of human remain samples on massively parallel sequencing success. <i>International Journal of Legal Medicine</i> , 2019, 133, 51-58.	2.2	22
54	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.	3.1	23

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55	Forensic human identification with targeted microbiome markers using nearest neighbor classification. <i>Forensic Science International: Genetics</i> , 2019, 38, 130-139.	3.1	45
56	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.	2.2	28
57	Massively parallel sequencing-enabled mixture analysis of mitochondrial DNA samples. <i>International Journal of Legal Medicine</i> , 2018, 132, 1263-1272.	2.2	36
58	Insertion within the flanking region of the D10S1237 locus. <i>Forensic Science International: Genetics</i> , 2018, 35, e4-e6.	3.1	2
59	Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. <i>Forensic Science International: Genetics</i> , 2018, 32, 50-61.	3.1	69
60	Direct PCR amplification of DNA from human bloodstains, saliva, and touch samples collected with microFLOQ A® swabs. <i>Forensic Science International: Genetics</i> , 2018, 32, 80-87.	3.1	53
61	Predicted activity of UGT2B7, ABCB1, OPRM1, and COMT using full-gene haplotypes and their association with the CYP2D6-inferred metabolizer phenotype. <i>Forensic Science International: Genetics</i> , 2018, 33, 48-58.	3.1	4
62	Comparative tolerance of two massively parallel sequencing systems to common PCR inhibitors. <i>International Journal of Legal Medicine</i> , 2018, 132, 983-995.	2.2	25
63	Aircraft-Assisted Pilot Suicides in the General Aviation Increased for One-Year Period after 11 September 2001 Attack in the United States. <i>International Journal of Environmental Research and Public Health</i> , 2018, 15, 2525.	2.6	6
64	NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis. <i>Forensic Science International: Genetics</i> , 2018, 37, 172-179.	3.1	35
65	Privacy and genetic genealogy data. <i>Science</i> , 2018, 361, 857-857.	12.6	26
66	Evaluation of the precision ID mtDNA whole genome panel on two massively parallel sequencing systems. <i>Forensic Science International: Genetics</i> , 2018, 36, 213-224.	3.1	35
67	Copycats in Pilot Aircraft-Assisted Suicides after the Germanwings Incident. <i>International Journal of Environmental Research and Public Health</i> , 2018, 15, 491.	2.6	6
68	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, 1258.	2.6	9
69	Current state-of-art of STR sequencing in forensic genetics. <i>Electrophoresis</i> , 2018, 39, 2655-2668.	2.4	68
70	Potential highly polymorphic short tandem repeat markers for enhanced forensic identity testing. <i>Forensic Science International: Genetics</i> , 2018, 37, 162-171.	3.1	13
71	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.	3.1	41
72	Increasing the reference populations for the 55 AISNP panel: the need and benefits. <i>International Journal of Legal Medicine</i> , 2017, 131, 913-917.	2.2	38

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73	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.	3.1	60
74	The factor of 10 in forensic DNA match probabilities. <i>Forensic Science International: Genetics</i> , 2017, 28, 178-187.	3.1	5
75	European survey on forensic applications of massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2017, 29, e23-e25.	3.1	32
76	Reiteration of the Statistical Basis of DNA Source Attribution Determinations in View of the Attorney General's Directive on "Reasonable Scientific Certainty" Statements. <i>Journal of Forensic Sciences</i> , 2017, 62, 1114-1115.	1.6	5
77	Bipolar Disorder in Aviation Medicine. <i>Aerospace Medicine and Human Performance</i> , 2017, 88, 42-47.	0.4	5
78	STRait Razor v2s: Advancing sequence-based STR allele reporting and beyond to other marker systems. <i>Forensic Science International: Genetics</i> , 2017, 29, 21-28.	3.1	39
79	Development and validation of a novel multiplexed DNA analysis system, InnoTyper [®] 21. <i>Forensic Science International: Genetics</i> , 2017, 29, 80-99.	3.1	23
80	Internal validation of the RapidHIT [®] ID system. <i>Forensic Science International: Genetics</i> , 2017, 31, 180-188.	3.1	23
81	Parsing apart the contributors of mitochondrial DNA mixtures with massively parallel sequencing data. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e439-e441.	0.3	5
82	Working towards implementation of whole genome mitochondrial DNA sequencing into routine casework. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e388-e389.	0.3	14
83	Comparison of standard capillary electrophoresis based genotyping method and ForenSeq DNA Signature Prep kit (Illumina) on a set of challenging samples. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e140-e142.	0.3	3
84	Forensic Human Identification Using Skin Microbiomes. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	74
85	STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci. <i>Forensic Science International: Genetics</i> , 2017, 31, 111-117.	3.1	77
86	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.	2.1	35
87	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.	3.3	17
88	Population and performance analyses of four major populations with Illumina [™] s FGx Forensic Genomics System. <i>Forensic Science International: Genetics</i> , 2017, 30, 81-92.	3.1	70
89	Increasing the reach of forensic genetics with massively parallel sequencing. <i>Forensic Science, Medicine, and Pathology</i> , 2017, 13, 342-349.	1.4	25
90	Paternity calculations in a di-spermy case. <i>International Journal of Legal Medicine</i> , 2017, 131, 339-343.	2.2	0

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91	Flanking Variation Influences Rates of Stutter in Simple Repeats. <i>Genes</i> , 2017, 8, 329.	2.4	19
92	A technique for setting analytical thresholds in massively parallel sequencing-based forensic DNA analysis. <i>PLoS ONE</i> , 2017, 12, e0178005.	2.5	16
93	Y-chromosomal analysis of Greek Cypriots reveals a primarily common pre-Ottoman paternal ancestry with Turkish Cypriots. <i>PLoS ONE</i> , 2017, 12, e0179474.	2.5	13
94	Attention-Deficit/Hyperactivity Disorder and Fatal Accidents in Aviation Medicine. <i>Aerospace Medicine and Human Performance</i> , 2017, 88, 871-875.	0.4	7
95	General Aviation Pilots Over 70 Years Old. <i>Aerospace Medicine and Human Performance</i> , 2017, 88, 142-145.	0.4	4
96	Investigation of the STR loci noise distributions of PowerSeq [®] , [®] Auto System. <i>Croatian Medical Journal</i> , 2017, 58, 214-221.	0.7	12
97	Results of a collaborative study on DNA identification of aged bone samples. <i>Croatian Medical Journal</i> , 2017, 58, 203-213.	0.7	12
98	Fast STR allele identification with STRait Razor 3.0. <i>Forensic Science International: Genetics</i> , 2017, 30, 18-23.	3.1	82
99	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.	0.8	16
100	Native American population data based on the Globalfiler [®] autosomal STR loci. <i>Forensic Science International: Genetics</i> , 2016, 24, e12-e13.	3.1	23
101	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
102	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.	3.1	21
103	A genetic overview of 23Y-STR markers in UAE population. <i>Forensic Science International: Genetics</i> , 2016, 23, 150-152.	3.1	6
104	The genetic structure of native Americans in North America based on the Globalfiler [®] STRs. <i>Legal Medicine</i> , 2016, 23, 49-54.	1.3	7
105	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.	3.1	29
106	Characterization of genetic sequence variation of 58 STR loci in four major population groups. <i>Forensic Science International: Genetics</i> , 2016, 25, 214-226.	3.1	138
107	More comprehensive forensic genetic marker analyses for accurate human remains identification using massively parallel DNA sequencing. <i>BMC Genomics</i> , 2016, 17, 750.	2.8	47
108	Definition and Purpose. <i>Security Science and Technology</i> , 2016, , 1-12.	0.5	1

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109	The Next State-of-the-Art Forensic Genetics Technology: Massively Parallel Sequencing. Security Science and Technology, 2016, , 249-291.	0.5	1
110	Molecular Autopsy. Security Science and Technology, 2016, , 377-413.	0.5	2
111	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
112	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
113	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
114	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
115	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
116	Expansion of Microbial Forensics. Journal of Clinical Microbiology, 2016, 54, 1964-1974.	3.9	72
117	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
118	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
119	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
120	Postmortem medicolegal genetic diagnostics also require reporting guidance. European Journal of Human Genetics, 2016, 24, 329-330.	2.8	8
121	Whole mitochondrial genome genetic diversity in an Estonian population sample. International Journal of Legal Medicine, 2016, 130, 67-71.	2.2	33
122	Handbook of Forensic Genetics. Security Science and Technology, 2016, , .	0.5	3
123	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
124	Enhancement of Pathologist's Routine Practice: Reuse of DNA Extracted from Immunostained Formalin-fixed Paraffin-embedded (FFPE) Slides in Downstream Molecular Analysis of Cancer. Cancer Genomics and Proteomics, 2016, 13, 399-406.	2.0	3
125	Authorsâ€™ Response. Journal of Forensic Sciences, 2015, 60, 1669-1670.	1.6	0
126	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

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127	On doctors'™ accountability and flight deck safety. Croatian Medical Journal, 2015, 56, 385-386.	0.7	4
128	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
129	Massively parallel sequencing of forensically relevant single nucleotide polymorphisms using TruSeq™,¢ forensic amplicon. International Journal of Legal Medicine, 2015, 129, 31-36.	2.2	23
130	Population genetics of 23 Y-STR markers in Kuwaiti population. Forensic Science International: Genetics, 2015, 16, 203-204.	3.1	6
131	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
132	Blind study evaluation illustrates utility of the Ion PGM™,¢ system for use in human identity DNA typing. Croatian Medical Journal, 2015, 56, 218-229.	0.7	37
133	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
134	Underlying Data for Sequencing the Mitochondrial Genome with the Massively Parallel Sequencing Platform Ion Torrent™,¢ PGM™,¢. BMC Genomics, 2015, 16, S4.	2.8	43
135	An evaluation of the PowerSeq™,¢ 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
136	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
137	High sensitivity multiplex short tandem repeat loci analyses with massively parallel sequencing. Forensic Science International: Genetics, 2015, 16, 38-47.	3.1	69
138	Utility of amplification enhancers in low copy number DNA analysis. International Journal of Legal Medicine, 2015, 129, 43-52.	2.2	17
139	STRait Razor v2.0: The improved STR Allele Identification Tool "Razor. Forensic Science International: Genetics, 2015, 14, 182-186.	3.1	55
140	Future directions of forensic DNA databases. Croatian Medical Journal, 2014, 55, 163-166.	0.7	47
141	Internal validation of the GlobalFiler™,¢ 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
142	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. Forensic Science International: Genetics, 2014, 12, 12-23.	3.1	214
143	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
144	A high volume extraction and purification method for recovering DNA from human bone. Forensic Science International: Genetics, 2014, 12, 155-160.	3.1	25

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145	Evaluation of a novel material, Diomics X-Swab [®] , for collection of DNA. <i>Forensic Science International: Genetics</i> , 2014, 12, 192-198.	3.1	7
146	An evaluation of the RapidHIT [®] system for reliably genotyping reference samples. <i>Forensic Science International: Genetics</i> , 2014, 13, 104-111.	3.1	38
147	Validation of high throughput sequencing and microbial forensics applications. <i>Investigative Genetics</i> , 2014, 5, 9.	3.3	59
148	Molecular genetic investigative leads to differentiate monozygotic twins. <i>Investigative Genetics</i> , 2014, 5, 11.	3.3	6
149	Modeling one complete versus triplicate analyses in low template DNA typing. <i>International Journal of Legal Medicine</i> , 2014, 128, 259-267.	2.2	5
150	High throughput whole mitochondrial genome sequencing by two platforms of massively parallel sequencing. <i>BMC Genomics</i> , 2014, 15, P7.	2.8	4
151	Reduction of stutter ratios in short tandem repeat loci typing of low copy number DNA samples. <i>Forensic Science International: Genetics</i> , 2014, 8, 213-218.	3.1	22
152	Autosomal and Y-STR analysis of degraded DNA from the 120-year-old skeletal remains of Ezekiel Harper. <i>Forensic Science International: Genetics</i> , 2014, 9, 33-41.	3.1	32
153	Nomenclature update and allele repeat structure for the markers DYS518 and DYS449. <i>Forensic Science International: Genetics</i> , 2014, 13, e3.	3.1	5
154	Assessment of the role of DNA repair in damaged forensic samples. <i>International Journal of Legal Medicine</i> , 2014, 128, 913-921.	2.2	25
155	High-quality and high-throughput massively parallel sequencing of the human mitochondrial genome using the Illumina MiSeq. <i>Forensic Science International: Genetics</i> , 2014, 12, 128-135.	3.1	155
156	Population data on 25 autosomal STRs for 500 unrelated Kuwaitis. <i>Forensic Science International: Genetics</i> , 2014, 12, 126-127.	3.1	3
157	mitoSAVE: Mitochondrial sequence analysis of variants in Excel. <i>Forensic Science International: Genetics</i> , 2014, 12, 122-125.	3.1	19
158	Developmental validation of the EX20+4 system. <i>Forensic Science International: Genetics</i> , 2014, 11, 207-213.	3.1	5
159	Differences of PCR efficiency between two-step PCR and standard three-step PCR protocols in short tandem repeat amplification. <i>Australian Journal of Forensic Sciences</i> , 2014, 46, 80-90.	1.2	8
160	Aircraft-Assisted Pilot Suicides: Lessons to be Learned. <i>Aviation, Space, and Environmental Medicine</i> , 2014, 85, 841-846.	0.5	17
161	Pressure cycling technology (PCT) reduces effects of inhibitors of the PCR. <i>International Journal of Legal Medicine</i> , 2013, 127, 321-333.	2.2	6
162	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.	2.2	51

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163	Validation of the PLEX-IDTM mass spectrometry mitochondrial DNA assay. <i>International Journal of Legal Medicine</i> , 2013, 127, 277-286.	2.2	8
164	Population genetic analyses of the STR loci of the AmpFISTR NGM SElectâ„¢ kit for Han population in Fujian Province, China. <i>International Journal of Legal Medicine</i> , 2013, 127, 345-346.	2.2	7
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