

John S Buckleton

List of Publications by Year in descending order

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154
papers

4,739
citations

109321

35
h-index

128289

60
g-index

163
all docs

163
docs citations

163
times ranked

1323
citing authors

#	ARTICLE	IF	CITATIONS
1	An investigation of the rigor of interpretation rules for STRs derived from less than 100 pg of DNA. <i>Forensic Science International</i> , 2000, 112, 17-40.	2.2	510
2	The interpretation of single source and mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2013, 7, 516-528.	3.1	237
3	Interpreting low template DNA profiles. <i>Forensic Science International: Genetics</i> , 2009, 4, 1-10.	3.1	167
4	Developing allelic and stutter peak height models for a continuous method of DNA interpretation. <i>Forensic Science International: Genetics</i> , 2013, 7, 296-304.	3.1	130
5	Characterising stutter in forensic STR multiplexes. <i>Forensic Science International: Genetics</i> , 2012, 6, 58-63.	3.1	121
6	Developmental validation of STRmix [®] , expert software for the interpretation of forensic DNA profiles. <i>Forensic Science International: Genetics</i> , 2016, 23, 226-239.	3.1	110
7	Evidence evaluation: A response to the court of appeal judgment in <i>R v T</i> . <i>Science and Justice - Journal of the Forensic Science Society</i> , 2011, 51, 43-49.	2.1	87
8	Towards understanding the effect of uncertainty in the number of contributors to DNA stains. <i>Forensic Science International: Genetics</i> , 2007, 1, 20-28.	3.1	82
9	Interpreting DNA Mixtures in Structured Populations. <i>Journal of Forensic Sciences</i> , 1999, 44, 987-995.	1.6	82
10	Population data on the expanded CODIS core STR loci for eleven populations of significance for forensic DNA analyses in the United States. <i>Forensic Science International: Genetics</i> , 2016, 25, 175-181.	3.1	78
11	132,173-Cyclopheophorbide enol, the first porphyrin isolated from a sponge. <i>Tetrahedron Letters</i> , 1986, 27, 2177-2178.	1.4	77
12	A universal strategy to interpret DNA profiles that does not require a definition of low-copy-number. <i>Forensic Science International: Genetics</i> , 2010, 4, 221-227.	3.1	76
13	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
14	PENDULUM [®] a guideline-based approach to the interpretation of STR mixtures. <i>Forensic Science International</i> , 2005, 148, 181-189.	2.2	75
15	Internal validation of STRmix [®] for the interpretation of single source and mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2017, 29, 126-144.	3.1	74
16	Population-specific F values for forensic STR markers: A worldwide survey. <i>Forensic Science International: Genetics</i> , 2016, 23, 91-100.	3.1	73
17	Internal validation of STRmix [®] – A multi laboratory response to PCAST. <i>Forensic Science International: Genetics</i> , 2018, 34, 11-24.	3.1	72
18	Searching mixed DNA profiles directly against profile databases. <i>Forensic Science International: Genetics</i> , 2014, 9, 102-110.	3.1	62

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19	Validation and development of interpretation guidelines for low copy number (LCN) DNA profiling in New Zealand using the AmpFISTR® SGM Plus, multiplex. <i>Forensic Science International: Genetics</i> , 2010, 4, 305-310.	3.1	59
20	An evaluation of potential allelic association between the STRs vWA and D12S391: Implications in criminal casework and applications to short pedigrees. <i>Forensic Science International: Genetics</i> , 2012, 6, 477-486.	3.1	59
21	A discussion of the merits of random man not excluded and likelihood ratios. <i>Forensic Science International: Genetics</i> , 2008, 2, 343-348.	3.1	57
22	Degradation of forensic DNA profiles. <i>Australian Journal of Forensic Sciences</i> , 2013, 45, 445-449.	1.2	56
23	A comparison of statistical models for the analysis of complex forensic DNA profiles. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2014, 54, 66-70.	2.1	54
24	Synthesis and characterization of masked aminopyrazolecarboxylic acid synthons. <i>Journal of Organic Chemistry</i> , 1989, 54, 428-431.	3.2	51
25	Examination of the variability in mixed DNA profile parameters for the Identifiler, multiplex. <i>Forensic Science International: Genetics</i> , 2010, 4, 111-114.	3.1	51
26	Validating multiplexes for use in conjunction with modern interpretation strategies. <i>Forensic Science International: Genetics</i> , 2016, 20, 6-19.	3.1	50
27	Some aspects of the Bayesian approach to evidence evaluation. <i>Journal - Forensic Science Society</i> , 1989, 29, 317-324.	0.2	45
28	Is the 2p rule always conservative?. <i>Forensic Science International</i> , 2006, 159, 206-209.	2.2	45
29	The effect of the uncertainty in the number of contributors to mixed DNA profiles on profile interpretation. <i>Forensic Science International: Genetics</i> , 2014, 12, 208-214.	3.1	44
30	What is the magnitude of the subpopulation effect?. <i>Forensic Science International</i> , 2003, 135, 1-8.	2.2	43
31	Effectiveness of familial searches. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2008, 48, 164-167.	2.1	42
32	Interpreting forensic DNA profiling evidence without specifying the number of contributors. <i>Forensic Science International: Genetics</i> , 2014, 13, 269-280.	3.1	40
33	Testing likelihood ratios produced from complex DNA profiles. <i>Forensic Science International: Genetics</i> , 2015, 16, 165-171.	3.1	39
34	STRmix, collaborative exercise on DNA mixture interpretation. <i>Forensic Science International: Genetics</i> , 2019, 40, 1-8.	3.1	39
35	A Practical Guide for the Formulation of Propositions in the Bayesian Approach to DNA Evidence Interpretation in an Adversarial Environment. <i>Journal of Forensic Sciences</i> , 2016, 61, 186-195.	1.6	37
36	Comparison of the performance of different models for the interpretation of low level mixed DNA profiles. <i>Electrophoresis</i> , 2014, 35, 3125-3133.	2.4	36

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37	The "factor of two" issue in mixed DNA profiles. <i>Journal of Theoretical Biology</i> , 2014, 363, 300-306.	1.7	36
38	A series of recommended tests when validating probabilistic DNA profile interpretation software. <i>Forensic Science International: Genetics</i> , 2015, 14, 125-131.	3.1	36
39	Relatedness and DNA: are we taking it seriously enough?. <i>Forensic Science International</i> , 2005, 152, 115-119.	2.2	35
40	A comparison of stochastic variation in mixed and unmixed casework and synthetic samples. <i>Forensic Science International: Genetics</i> , 2012, 6, 180-184.	3.1	35
41	NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis. <i>Forensic Science International: Genetics</i> , 2018, 37, 172-179.	3.1	35
42	Validation issues around DNA typing of low level DNA. <i>Forensic Science International: Genetics</i> , 2009, 3, 255-260.	3.1	34
43	Composite profiles in DNA analysis. <i>Forensic Science International: Genetics</i> , 2012, 6, 317-321.	3.1	34
44	The interpretation of elemental composition measurements from forensic glass evidence: II. <i>Science and Justice - Journal of the Forensic Science Society</i> , 1997, 37, 245-249.	2.1	33
45	Modelling heterozygote balance in forensic DNA profiles. <i>Forensic Science International: Genetics</i> , 2012, 6, 729-734.	3.1	33
46	Uncertainty in the number of contributors in the proposed new CODIS set. <i>Forensic Science International: Genetics</i> , 2015, 19, 207-211.	3.1	33
47	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
48	Combating transnational organized crime by linking multiple large ivory seizures to the same dealer. <i>Science Advances</i> , 2018, 4, eaat0625.	10.3	31
49	The interpretation of low level DNA mixtures. <i>Forensic Science International: Genetics</i> , 2012, 6, 191-197.	3.1	30
50	Application of Random Match Probability Calculations to Mixed <scp>STR</scp> Profiles. <i>Journal of Forensic Sciences</i> , 2013, 58, 474-485.	1.6	30
51	Considering relatives when assessing the evidential strength of mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2014, 13, 259-263.	3.1	30
52	Inclusion Probabilities and Dropout. <i>Journal of Forensic Sciences</i> , 2010, 55, 1171-1173.	1.6	29
53	Determination of the variables affecting mixed MiniFiler [®] DNA profiles. <i>Forensic Science International: Genetics</i> , 2011, 5, 381-385.	3.1	29
54	The effect of linkage on the calculation of DNA match probabilities for siblings and half siblings. <i>Forensic Science International</i> , 2006, 160, 193-199.	2.2	28

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55	How reliable is the sub-population model in DNA testimony?. Forensic Science International, 2006, 157, 144-148.	2.2	27
56	Investigation into the performance of different models for predicting stutter. Forensic Science International: Genetics, 2013, 7, 422-427.	3.1	27
57	Helping formulate propositions in forensic DNA analysis. Science and Justice - Journal of the Forensic Science Society, 2014, 54, 258-261.	2.1	27
58	The variability in likelihood ratios due to different mechanisms. Forensic Science International: Genetics, 2015, 14, 187-190.	3.1	27
59	Relatedness calculations for linked loci incorporating subpopulation effects. Forensic Science International: Genetics, 2013, 7, 380-383.	3.1	26
60	Do low template DNA profiles have useful quantitative data?. Forensic Science International: Genetics, 2015, 16, 13-16.	3.1	26
61	Factors affecting peak height variability for short tandem repeat data. Forensic Science International: Genetics, 2016, 21, 126-133.	3.1	25
62	A sensitivity analysis to determine the robustness of STRmix [®] , [‡] with respect to laboratory calibration. Forensic Science International: Genetics, 2018, 35, 113-122.	3.1	25
63	A Review of Probabilistic Genotyping Systems: EuroForMix, DNASTatistX and STRmix [®] , [‡] . Genes, 2021, 12, 1559.	2.4	25
64	Decision-making in familial database searching: KI alone or not alone?. Forensic Science International: Genetics, 2013, 7, 52-54.	3.1	24
65	Investigating a common approach to DNA profile interpretation using probabilistic software. Forensic Science International: Genetics, 2015, 16, 121-131.	3.1	24
66	Empirical testing of estimated DNA frequencies. Forensic Science International: Genetics, 2007, 1, 267-272.	3.1	23
67	Utilising allelic dropout probabilities estimated by logistic regression in casework. Forensic Science International: Genetics, 2014, 9, 9-11.	3.1	23
68	Selective sequential demasking of the ester functions of 1-methyl-3,4,5-tris(methoxycarbonyl)pyrazole. Journal of Organic Chemistry, 1985, 50, 4736-4738.	3.2	22
69	Modeling forward stutter: Toward increased objectivity in forensic <scp>DNA</scp> interpretation. Electrophoresis, 2014, 35, 3152-3157.	2.4	22
70	Likelihood ratio development for mixed Y-STR profiles. Forensic Science International: Genetics, 2018, 35, 82-96.	3.1	22
71	Interpreting a major component from a mixed DNA profile with an unknown number of minor contributors. Forensic Science International: Genetics, 2019, 40, 150-159.	3.1	22
72	Characterising the STR locus D6S1043 and examination of its effect on stutter rates. Forensic Science International: Genetics, 2014, 8, 20-23.	3.1	21

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73	The effect of varying the number of contributors in the prosecution and alternate propositions. <i>Forensic Science International: Genetics</i> , 2019, 38, 225-231.	3.1	21
74	A comprehensive analysis of microsatellite diversity in Aboriginal Australians. <i>Journal of Human Genetics</i> , 2007, 52, 712-728.	2.3	19
75	Variability of mixed DNA profiles separated on a 3130 and 3500 capillary electrophoresis instrument. <i>Australian Journal of Forensic Sciences</i> , 2014, 46, 304-312.	1.2	19
76	A guide to results and diagnostics within a STRmix [®] report. <i>Wiley Interdisciplinary Reviews Forensic Science</i> , 2019, 1, .	2.1	18
77	Commentary on: Budowle B, Onorato AJ, Callaghan TF, Della Manna A, Gross AM, Guerrieri RA, Luttman JC, McClure DL. Mixture interpretation: defining the relevant features for guidelines for the assessment of mixed DNA profiles in forensic casework. <i>J Forensic Sci</i> 2009;54(4):810-821. PETER GILL AND JOHN BUCKLETON. <i>Journal of Forensic Sciences</i> , 2010, 55, 265-268.	1.6	17
78	The efficacy of DNA mixture to mixture matching. <i>Forensic Science International: Genetics</i> , 2019, 41, 64-71.	3.1	17
79	Estimating the number of contributors to a DNA profile using decision trees. <i>Forensic Science International: Genetics</i> , 2021, 50, 102407.	3.1	17
80	Implementation and validation of an improved allele specific stutter filtering method for electropherogram interpretation. <i>Forensic Science International: Genetics</i> , 2018, 35, 50-56.	3.1	16
81	An investigation into the performance of methods for adjusting for sampling uncertainty in DNA likelihood ratio calculations. <i>Forensic Science International: Genetics</i> , 2011, 5, 512-516.	3.1	15
82	The paradigm shift in DNA profile interpretation. <i>Forensic Science International: Genetics</i> , 2017, 31, e24-e32.	3.1	15
83	Uncertainty in the number of contributors for the European Standard Set of loci. <i>Forensic Science International: Genetics</i> , 2014, 11, 205-206.	3.1	14
84	Importance sampling allows Hd true tests of highly discriminating DNA profiles. <i>Forensic Science International: Genetics</i> , 2017, 27, 74-81.	3.1	14
85	Exploring the probative value of mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2019, 41, 1-10.	3.1	14
86	A comparison of likelihood ratios obtained from EuroForMix and STRmix [®] . <i>Journal of Forensic Sciences</i> , 2021, 66, 2138-2155.	1.6	14
87	DNA Profiling and Criminal Justice: A Contribution to a Changing Debate. <i>Australian Journal of Forensic Sciences</i> , 2004, 36, 34-43.	1.2	13
88	Use of subpopulation data in Australian forensic DNA casework. <i>Forensic Science International: Genetics</i> , 2007, 1, 238-246.	3.1	13
89	Modeling Forensic DNA Database Performance*. <i>Journal of Forensic Sciences</i> , 2010, 55, 1174-1183.	1.6	13
90	A fully continuous system of DNA profile evidence evaluation that can utilise STR profile data produced under different conditions within a single analysis. <i>Forensic Science International: Genetics</i> , 2017, 31, 149-154.	3.1	13

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91	Commentary: A "Source" of Error: Computer Code, Criminal Defendants, and the Constitution. <i>Frontiers in Genetics</i> , 2017, 8, 33.	2.3	13
92	When evaluating DNA evidence within a likelihood ratio framework, should the propositions be exhaustive?. <i>Forensic Science International: Genetics</i> , 2021, 50, 102406.	3.1	13
93	Dealing with allelic dropout when reporting the evidential value in DNA relatedness analysis. <i>Forensic Science International</i> , 2006, 160, 134-139.	2.2	12
94	The Impact of Māori Cultural Values on Forensic Science Practice in New Zealand. <i>Journal of Forensic Sciences</i> , 2008, 53, 380-383.	1.6	12
95	Comparing the growth and effectiveness of forensic DNA databases. <i>Forensic Science International: Genetics Supplement Series</i> , 2008, 1, 667-668.	0.3	12
96	A response to "Likelihood ratio as weight of evidence: A closer look" by Lund and Iyer. <i>Forensic Science International</i> , 2018, 288, e15-e19.	2.2	12
97	Comparing multiple POI to DNA mixtures. <i>Forensic Science International: Genetics</i> , 2021, 52, 102481.	3.1	12
98	Allele frequencies for the four major sub-populations of New Zealand for the 15 Identifiler loci. <i>Forensic Science International: Genetics</i> , 2010, 4, e65-e66.	3.1	11
99	Further Comment on "Low copy number typing has yet to achieve "general acceptance" by Budowle, B., et al, 2009. <i>Forensic Sci. Int. Genetics: Supplement Series 2</i> , 551-552. <i>Forensic Science International: Genetics</i> , 2011, 5, 7-11.	3.1	11
100	The interpretation of shoeprint comparison class correspondences. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2012, 52, 243-248.	2.1	11
101	Does the use of probabilistic genotyping change the way we should view sub-threshold data?. <i>Australian Journal of Forensic Sciences</i> , 2017, 49, 78-92.	1.2	11
102	Modelling the dependence structure of Y-STR haplotypes using graphical models. <i>Forensic Science International: Genetics</i> , 2018, 37, 29-36.	3.1	11
103	A review of likelihood ratios in forensic science based on a critique of Stiffelman "No longer the Gold standard: Probabilistic genotyping is changing the nature of DNA evidence in criminal trials". <i>Forensic Science International</i> , 2020, 310, 110251.	2.2	11
104	Identifying and modelling the drivers of stutter in forensic DNA profiles. <i>Australian Journal of Forensic Sciences</i> , 2014, 46, 194-203.	1.2	10
105	A more straightforward derivation of the LR for a database search. <i>Forensic Science International: Genetics</i> , 2015, 14, 156-160.	3.1	10
106	Are low LR's reliable?. <i>Forensic Science International: Genetics</i> , 2020, 49, 102350.	3.1	10
107	Modelling PowerPlex [®] Y stutter and artefacts. <i>Forensic Science International: Genetics</i> , 2014, 11, 126-136.	3.1	9
108	Using probabilistic theory to develop interpretation guidelines for Y-STR profiles. <i>Forensic Science International: Genetics</i> , 2016, 21, 22-34.	3.1	9

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109	Performance of a method for weighting a range in the number of contributors in probabilistic genotyping. <i>Forensic Science International: Genetics</i> , 2020, 48, 102352.	3.1	9
110	Empirical support for the reliability of DNA interpretation in Croatia. <i>Forensic Science International: Genetics</i> , 2008, 3, 50-53.	3.1	8
111	Empirical support for the reliability of DNA evidence interpretation in Australia and New Zealand. <i>Australian Journal of Forensic Sciences</i> , 2008, 40, 99-108.	1.2	8
112	The interpretation of mixed DNA profiles from a mother, father, and child trio. <i>Forensic Science International: Genetics</i> , 2020, 44, 102175.	3.1	8
113	Modeling allelic analyte signals for aSTRs in NGS DNA profiles. <i>Journal of Forensic Sciences</i> , 2021, 66, 1234-1245.	1.6	8
114	Streamlining the decision-making process for international DNA kinship matching using Worldwide allele frequencies and tailored cutoff log ₁₀ LR thresholds. <i>Forensic Science International: Genetics</i> , 2022, 57, 102634.	3.1	8
115	The appropriate use of subpopulation corrections for differences in endogamous communities. <i>Forensic Science International</i> , 2007, 168, 106-111.	2.2	7
116	Testing whether stutter and low-level DNA peaks are additive. <i>Forensic Science International: Genetics</i> , 2019, 43, 102166.	3.1	7
117	Inter-sample contamination detection using mixture deconvolution comparison. <i>Forensic Science International: Genetics</i> , 2019, 40, 160-167.	3.1	7
118	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
119	A Logical Framework for Forensic DNA Interpretation. <i>Genes</i> , 2022, 13, 957.	2.4	7
120	Forensic DNA profiling: The importance of giving accurate answers to the right questions. <i>Criminal Law Forum</i> , 1997, 8, 445-459.	0.4	6
121	Combining autosomal and Y chromosome match probabilities using coalescent theory. <i>Forensic Science International: Genetics</i> , 2014, 11, 52-55.	3.1	6
122	Comment on "DNA mixtures interpretation" A proof-of-concept multi-software comparison highlighting different probabilistic methods' performances on challenging samples by Alladio et al.. <i>Forensic Science International: Genetics</i> , 2019, 40, e248-e251.	3.1	6
123	Validation of a top-down DNA profile analysis for database searching using a fully continuous probabilistic genotyping model. <i>Forensic Science International: Genetics</i> , 2021, 52, 102479.	3.1	6
124	Experimental design for acquiring relevant data to address the issue of comparing consecutively manufactured tools and firearms. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2008, 48, 178-181.	2.1	5
125	Database crime to crime match rate calculation. <i>Forensic Science International: Genetics</i> , 2009, 3, 200-201.	3.1	5
126	Low copy number typing"Where next?. <i>Forensic Science International: Genetics Supplement Series</i> , 2009, 2, 553-555.	0.3	5

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127	Interpreting lineage markers in view of subpopulation effects. Forensic Science International: Genetics, 2012, 6, 393-397.	3.1	5
128	The factor of 10 in forensic DNA match probabilities. Forensic Science International: Genetics, 2017, 28, 178-187.	3.1	5
129	Variability and additivity of read counts for aSTRs in NGS DNA profiles. Forensic Science International: Genetics, 2020, 48, 102351.	3.1	5
130	Re: Comments on "Interpreting Y chromosome STR haplotype mixture". Legal Medicine, 2011, 13, 52-53.	1.3	4
131	Examining the additivity of peak heights in forensic DNA profiles. Australian Journal of Forensic Sciences, 2020, , 1-15.	1.2	4
132	Relaxing the assumption of unrelatedness in the numerator and denominator of likelihood ratios for DNA mixtures. Forensic Science International: Genetics, 2021, 51, 102434.	3.1	4
133	A mixed DNA profile controversy revisited. Journal of Forensic Sciences, 2021, , .	1.6	4
134	Evidence in support of self-declaration as a sampling method for the formation of sub-population DNA databases. Journal of Forensic Sciences, 2003, 48, 1091-3.	1.6	4
135	The extent of substructure in the indigenous Australian population and its impact on DNA evidence interpretation. International Congress Series, 2006, 1288, 382-384.	0.2	3
136	Consideration of the probative value of single donor 15-plex STR profiles in UK populations and its presentation in UK courts II. Science and Justice - Journal of the Forensic Science Society, 2013, 53, 371.	2.1	3
137	Letter to editor in response to editorial by Risinger et al.. Science and Justice - Journal of the Forensic Science Society, 2014, 54, 510.	2.1	3
138	Investigation into the effect of mixtures comprising related people on non-donor likelihood ratios, and potential practises to mitigate providing misleading opinions. Forensic Science International: Genetics, 2022, 59, 102691.	3.1	3
139	Response to: Commentary on: Bright et al. (2018) Internal validation of STRmix, "A multi laboratory response to PCAST, Forensic Science International: Genetics, 34: 11-24. Forensic Science International: Genetics, 2020, 44, 102198.	3.1	2
140	The interpretation of forensic DNA profiles: an historical perspective. Journal of the Royal Society of New Zealand, 2020, 50, 211-225.	1.9	2
141	Western Australian sub-population data for the thirteen AMPFISTR Profiler Plus and COfiler STR loci. Journal of Forensic Sciences, 2002, 47, 1149-53.	1.6	2
142	Weight-of-Evidence for Forensic DNA Profiles, by David J. Balding: John Wiley and Sons, Ltd., 2005; 198 pp.. Law, Probability and Risk, 2005, 4, 191-193.	2.4	1
143	Geographical variation of shoeprint comparison class correspondences. Science and Justice - Journal of the Forensic Science Society, 2014, 54, 335-337.	2.1	1
144	What can forensic probabilistic genotyping software developers learn from significant non-forensic software failures?. Wiley Interdisciplinary Reviews Forensic Science, 2021, 3, .	2.1	1

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145	The effect of a user selected number of contributors within the LR assignment. Australian Journal of Forensic Sciences, 0, , 1-14.	1.2	1
146	Can a reference "match" an evidence profile if these have no loci in common?. Forensic Science International: Genetics, 2021, 53, 102520.	3.1	1
147	Re: Sign mistake in allele sharing probability formulae of Curran, et al.. Forensic Science International: Genetics, 2010, 4, 215-217.	3.1	0
148	Corrigendum to "Relatedness calculations for linked loci incorporating subpopulation effects" [Forensic Sci. Int: Genet., 7 (2013), 380-383]. Forensic Science International: Genetics, 2013, 7, 565.	3.1	0
149	Investigation into stutter ratio variance. Australian Journal of Forensic Sciences, 2014, 46, 313-316.	1.2	0
150	Authors' Response. Journal of Forensic Sciences, 2015, 60, 1669-1670.	1.6	0
151	The effect of wild card designations and rare alleles in forensic DNA database searches. Forensic Science International: Genetics, 2015, 16, 98-104.	3.1	0
152	Likelihood ratio formulae for disputed parentage when the product of conception is trisomic. International Journal of Legal Medicine, 2017, 131, 1513-1521.	2.2	0
153	Response to Lander's response to the ANZFSS Council Statement on the President's Council of Advisors on Science and Technology Report. Australian Journal of Forensic Sciences, 2018, 50, 453-454.	1.2	0
154	Probabilistic interpretation of the Amelogenin locus. Forensic Science International: Genetics, 2021, 52, 102462.	3.1	0