John S Buckleton

List of Publications by Year
in descending order

154 papers	4,739 citations	109264 35 h-index	128225 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. Forensic Science International, 2000, 112, 17-40.	1.3	510
2	The interpretation of single source and mixed DNA profiles. Forensic Science International: Genetics, 2013, 7, 516-528.	1.6	237
3	Interpreting low template DNA profiles. Forensic Science International: Genetics, 2009, 4, 1-10.	1.6	167
4	Developing allelic and stutter peak height models for a continuous method of DNA interpretation. Forensic Science International: Genetics, 2013, 7, 296-304.	1.6	130
5	Characterising stutter in forensic STR multiplexes. Forensic Science International: Genetics, 2012, 6, 58-63.	1.6	121
6	Developmental validation of STRmixâ„¢, expert software for the interpretation of forensic DNA profiles. Forensic Science International: Genetics, 2016, 23, 226-239.	1.6	110
7	Evidence evaluation: A response to the court of appeal judgment in R v T. Science and Justice - Journal of the Forensic Science Society, 2011, 51, 43-49.	1.3	87
8	Towards understanding the effect of uncertainty in the number of contributors to DNA stains. Forensic Science International: Genetics, 2007, 1, 20-28.	1.6	82
9	Interpreting DNA Mixtures in Structured Populations. Journal of Forensic Sciences, 1999, 44, 987-995.	0.9	82
10	Population data on the expanded CODIS core STR loci for eleven populations of significance for forensic DNA analyses in the United States. Forensic Science International: Genetics, 2016, 25, 175-181.	1.6	78
11	132,173-Cyclopheophorbide enol, the first porphyrin isolated from a sponge. Tetrahedron Letters, 1986, 27, 2177-2178.	0.7	77
12	A universal strategy to interpret DNA profiles that does not require a definition of low-copy-number. Forensic Science International: Genetics, 2010, 4, 221-227.	1.6	76
13	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
14	PENDULUMâ€"a guideline-based approach to the interpretation of STR mixtures. Forensic Science International, 2005, 148, 181-189.	1.3	75
15	Internal validation of STRmixâ„¢ for the interpretation of single source and mixed DNA profiles. Forensic Science International: Genetics, 2017, 29, 126-144.	1.6	74
16	Population-specific F values for forensic STR markers: A worldwide survey. Forensic Science International: Genetics, 2016, 23, 91-100.	1.6	73
17	Internal validation of STRmixâ„¢ â€" A multi laboratory response to PCAST. Forensic Science International: Genetics, 2018, 34, 11-24.	1.6	72
18	Searching mixed DNA profiles directly against profile databases. Forensic Science International: Genetics, 2014, 9, 102-110.	1.6	62

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19	Validation and development of interpretation guidelines for low copy number (LCN) DNA profiling in New Zealand using the AmpFlSTRÂ® SGM Plusâ„¢ multiplex. Forensic Science International: Genetics, 2010, 4, 305-310.	1.6	59
20	An evaluation of potential allelic association between the STRs vWA and D12S391: Implications in criminal casework and applications to short pedigrees. Forensic Science International: Genetics, 2012, 6, 477-486.	1.6	59
21	A discussion of the merits of random man not excluded and likelihood ratios. Forensic Science International: Genetics, 2008, 2, 343-348.	1.6	57
22	Degradation of forensic DNA profiles. Australian Journal of Forensic Sciences, 2013, 45, 445-449.	0.7	56
23	A comparison of statistical models for the analysis of complex forensic DNA profiles. Science and Justice - Journal of the Forensic Science Society, 2014, 54, 66-70.	1.3	54
24	Synthesis and characterization of masked aminopyrazolecarboxylic acid synthons. Journal of Organic Chemistry, 1989, 54, 428-431.	1.7	51
25	Examination of the variability in mixed DNA profile parameters for the Identifilerâ„¢ multiplex. Forensic Science International: Genetics, 2010, 4, 111-114.	1.6	51
26	Validating multiplexes for use in conjunction with modern interpretation strategies. Forensic Science International: Genetics, 2016, 20, 6-19.	1.6	50
27	Some aspects of the Bayesian approach to evidence evaluation. Journal - Forensic Science Society, 1989, 29, 317-324.	0.3	45
28	Is the 2p rule always conservative?. Forensic Science International, 2006, 159, 206-209.	1.3	45
29	The effect of the uncertainty in the number of contributors to mixed DNA profiles on profile interpretation. Forensic Science International: Genetics, 2014, 12, 208-214.	1.6	44
30	What is the magnitude of the subpopulation effect?. Forensic Science International, 2003, 135, 1-8.	1.3	43
31	Effectiveness of familial searches. Science and Justice - Journal of the Forensic Science Society, 2008, 48, 164-167.	1.3	42
32	Interpreting forensic DNA profiling evidence without specifying the number of contributors. Forensic Science International: Genetics, 2014, 13, 269-280.	1.6	40
33	Testing likelihood ratios produced from complex DNA profiles. Forensic Science International: Genetics, 2015, 16, 165-171.	1.6	39
34	STRmixâ„¢ collaborative exercise on DNA mixture interpretation. Forensic Science International: Genetics, 2019, 40, 1-8.	1.6	39
35	A Practical Guide for the Formulation of Propositions in the Bayesian Approach to DNA Evidence Interpretation in an Adversarial Environment. Journal of Forensic Sciences, 2016, 61, 186-195.	0.9	37
36	Comparison of the performance of different models for the interpretation of low level mixed <scp>DNA</scp> profiles. Electrophoresis, 2014, 35, 3125-3133.	1.3	36

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37	The 'factor of two' issue in mixed DNA profiles. Journal of Theoretical Biology, 2014, 363, 300-306.	0.8	36
38	A series of recommended tests when validating probabilistic DNA profile interpretation software. Forensic Science International: Genetics, 2015, 14, 125-131.	1.6	36
39	Relatedness and DNA: are we taking it seriously enough?. Forensic Science International, 2005, 152, 115-119.	1.3	35
40	A comparison of stochastic variation in mixed and unmixed casework and synthetic samples. Forensic Science International: Genetics, 2012, 6, 180-184.	1.6	35
41	NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis. Forensic Science International: Genetics, 2018, 37, 172-179.	1.6	35
42	Validation issues around DNA typing of low level DNA. Forensic Science International: Genetics, 2009, 3, 255-260.	1.6	34
43	Composite profiles in DNA analysis. Forensic Science International: Genetics, 2012, 6, 317-321.	1.6	34
44	The interpretation of elemental composition measurements from forensic glass evidence: II. Science and Justice - Journal of the Forensic Science Society, 1997, 37, 245-249.	1.3	33
45	Modelling heterozygote balance in forensic DNA profiles. Forensic Science International: Genetics, 2012, 6, 729-734.	1.6	33
46	Uncertainty in the number of contributors in the proposed new CODIS set. Forensic Science International: Genetics, 2015, 19, 207-211.	1.6	33
47	The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity. Journal of Forensic Sciences, 2019, 64, 393-405.	0.9	33
48	Combating transnational organized crime by linking multiple large ivory seizures to the same dealer. Science Advances, 2018, 4, eaat0625.	4.7	31
49	The interpretation of low level DNA mixtures. Forensic Science International: Genetics, 2012, 6, 191-197.	1.6	30
50	Application of Random Match Probability Calculations to Mixed STR Profiles. Journal of Forensic Sciences, 2013, 58, 474-485.	0.9	30
51	Considering relatives when assessing the evidential strength of mixed DNA profiles. Forensic Science International: Genetics, 2014, 13, 259-263.	1.6	30
52	Inclusion Probabilities and Dropout. Journal of Forensic Sciences, 2010, 55, 1171-1173.	0.9	29
53	Determination of the variables affecting mixed MiniFiler™ DNA profiles. Forensic Science International: Genetics, 2011, 5, 381-385.	1.6	29
54	The effect of linkage on the calculation of DNA match probabilities for siblings and half siblings. Forensic Science International, 2006, 160, 193-199.	1.3	28

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55	How reliable is the sub-population model in DNA testimony?. Forensic Science International, 2006, 157, 144-148.	1.3	27
56	Investigation into the performance of different models for predicting stutter. Forensic Science International: Genetics, 2013, 7, 422-427.	1.6	27
57	Helping formulate propositions in forensic DNA analysis. Science and Justice - Journal of the Forensic Science Society, 2014, 54, 258-261.	1.3	27
58	The variability in likelihood ratios due to different mechanisms. Forensic Science International: Genetics, 2015, 14, 187-190.	1.6	27
59	Relatedness calculations for linked loci incorporating subpopulation effects. Forensic Science International: Genetics, 2013, 7, 380-383.	1.6	26
60	Do low template DNA profiles have useful quantitative data?. Forensic Science International: Genetics, 2015, 16, 13-16.	1.6	26
61	Factors affecting peak height variability for short tandem repeat data. Forensic Science International: Genetics, 2016, 21, 126-133.	1.6	25
62	A sensitivity analysis to determine the robustness of STRmixâ„¢ with respect to laboratory calibration. Forensic Science International: Genetics, 2018, 35, 113-122.	1.6	25
63	A Review of Probabilistic Genotyping Systems: EuroForMix, DNAStatistX and STRmixâ„¢. Genes, 2021, 12, 1559.	1.0	25
64	Decision-making in familial database searching: KI alone or not alone?. Forensic Science International: Genetics, 2013, 7, 52-54.	1.6	24
65	Investigating a common approach to DNA profile interpretation using probabilistic software. Forensic Science International: Genetics, 2015, 16, 121-131.	1.6	24
66	Empirical testing of estimated DNA frequencies. Forensic Science International: Genetics, 2007, 1, 267-272.	1.6	23
67	Utilising allelic dropout probabilities estimated by logistic regression in casework. Forensic Science International: Genetics, 2014, 9, 9-11.	1.6	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.	1.7	22
69	Modeling forward stutter: Toward increased objectivity in forensic <scp>DNA</scp> interpretation. Electrophoresis, 2014, 35, 3152-3157.	1.3	22
70	Likelihood ratio development for mixed Y-STR profiles. Forensic Science International: Genetics, 2018, 35, 82-96.	1.6	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.	1.6	22
72	Characterising the STR locus D6S1043 and examination of its effect on stutter rates. Forensic Science International: Genetics, 2014, 8, 20-23.	1.6	21

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73	The effect of varying the number of contributors in the prosecution and alternate propositions. Forensic Science International: Genetics, 2019, 38, 225-231.	1.6	21
74	A comprehensive analysis of microsatellite diversity in Aboriginal Australians. Journal of Human Genetics, 2007, 52, 712-728.	1.1	19
75	Variability of mixed DNA profiles separated on a 3130 and 3500 capillary electrophoresis instrument. Australian Journal of Forensic Sciences, 2014, 46, 304-312.	0.7	19
76	A guide to results and diagnostics within a STRmixâ„¢ report. Wiley Interdisciplinary Reviews Forensic Science, 2019, 1, .	1.2	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. J Forensic Sci 2009;54(4):810â€21â€PETER GILL AND JOHN BUCKLETON. Journal of Forensic Sciences, 2010, 55, 265-268.	0.9	17
78	The efficacy of DNA mixture to mixture matching. Forensic Science International: Genetics, 2019, 41, 64-71.	1.6	17
79	Estimating the number of contributors to a DNA profile using decision trees. Forensic Science International: Genetics, 2021, 50, 102407.	1.6	17
80	Implementation and validation of an improved allele specific stutter filtering method for electropherogram interpretation. Forensic Science International: Genetics, 2018, 35, 50-56.	1.6	16
81	An investigation into the performance of methods for adjusting for sampling uncertainty in DNA likelihood ratio calculations. Forensic Science International: Genetics, 2011, 5, 512-516.	1.6	15
82	The paradigm shift in DNA profile interpretation. Forensic Science International: Genetics, 2017, 31, e24-e32.	1.6	15
83	Uncertainty in the number of contributors for the European Standard Set of loci. Forensic Science International: Genetics, 2014, 11, 205-206.	1.6	14
84	Importance sampling allows Hd true tests of highly discriminating DNA profiles. Forensic Science International: Genetics, 2017, 27, 74-81.	1.6	14
85	Exploring the probative value of mixed DNA profiles. Forensic Science International: Genetics, 2019, 41, 1-10.	1.6	14
86	A comparison of likelihood ratios obtained from EuroForMix and STRmixâ„¢. Journal of Forensic Sciences, 2021, 66, 2138-2155.	0.9	14
87	DNA Profiling and Criminal Justice: A Contribution to a Changing Debate. Australian Journal of Forensic Sciences, 2004, 36, 34-43.	0.7	13
88	Use of subpopulation data in Australian forensic DNA casework. Forensic Science International: Genetics, 2007, 1, 238-246.	1.6	13
89	Modeling Forensic DNA Database Performance*. Journal of Forensic Sciences, 2010, 55, 1174-1183.	0.9	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. Forensic Science International: Genetics, 2017, 31, 149-154.	1.6	13

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91	Commentary: A "Source" of Error: Computer Code, Criminal Defendants, and the Constitution. Frontiers in Genetics, 2017, 8, 33.	1.1	13
92	When evaluating DNA evidence within a likelihood ratio framework, should the propositions be exhaustive?. Forensic Science International: Genetics, 2021, 50, 102406.	1.6	13
93	Dealing with allelic dropout when reporting the evidential value in DNA relatedness analysis. Forensic Science International, 2006, 160, 134-139.	1.3	12
94	The Impact of Māori Cultural Values on Forensic Science Practice in New Zealand. Journal of Forensic Sciences, 2008, 53, 380-383.	0.9	12
95	Comparing the growth and effectiveness of forensic DNA databases. Forensic Science International: Genetics Supplement Series, 2008, 1, 667-668.	0.1	12
96	A response to "Likelihood ratio as weight of evidence: A closer look" by Lund and Iyer. Forensic Science International, 2018, 288, e15-e19.	1.3	12
97	Comparing multiple POI to DNA mixtures. Forensic Science International: Genetics, 2021, 52, 102481.	1.6	12
98	Allele frequencies for the four major sub-populations of New Zealand for the 15 Identifiler loci. Forensic Science International: Genetics, 2010, 4, e65-e66.	1.6	11
99	Further Comment on "Low copy number typing has yet to achieve "general acceptance"" by Budowle, B., et al, 2009. Forensic Sci. Int. Genetics: Supplement Series 2, 551–552. Forensic Science International: Genetics, 2011, 5, 7-11.	1.6	11
100	The interpretation of shoeprint comparison class correspondences. Science and Justice - Journal of the Forensic Science Society, 2012, 52, 243-248.	1.3	11
101	Does the use of probabilistic genotyping change the way we should view sub-threshold data?. Australian Journal of Forensic Sciences, 2017, 49, 78-92.	0.7	11
102	Modelling the dependence structure of Y-STR haplotypes using graphical models. Forensic Science International: Genetics, 2018, 37, 29-36.	1.6	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". Forensic Science International, 2020, 310, 110251.	1.3	11
104	Identifying and modelling the drivers of stutter in forensic DNA profiles. Australian Journal of Forensic Sciences, 2014, 46, 194-203.	0.7	10
105	A more straightforward derivation of the LR for a database search. Forensic Science International: Genetics, 2015, 14, 156-160.	1.6	10
106	Are low LRs reliable?. Forensic Science International: Genetics, 2020, 49, 102350.	1.6	10
107	Modelling PowerPlex® Y stutter and artefacts. Forensic Science International: Genetics, 2014, 11, 126-136.	1.6	9
108	Using probabilistic theory to develop interpretation guidelines for Y-STR profiles. Forensic Science International: Genetics, 2016, 21, 22-34.	1.6	9

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109	Performance of a method for weighting a range in the number of contributors in probabilistic genotyping. Forensic Science International: Genetics, 2020, 48, 102352.	1.6	9
110	Empirical support for the reliability of DNA interpretation in Croatia. Forensic Science International: Genetics, 2008, 3, 50-53.	1.6	8
111	Empirical support for the reliability of DNA evidence interpretation in Australia and New Zealand. Australian Journal of Forensic Sciences, 2008, 40, 99-108.	0.7	8
112	The interpretation of mixed DNA profiles from a mother, father, and child trio. Forensic Science International: Genetics, 2020, 44, 102175.	1.6	8
113	Modeling allelic analyte signals for aSTRs in NGS DNA profiles. Journal of Forensic Sciences, 2021, 66, 1234-1245.	0.9	8
114	Streamlining the decision-making process for international DNA kinship matching using Worldwide allele frequencies and tailored cutoff log10LR thresholds. Forensic Science International: Genetics, 2022, 57, 102634.	1.6	8
115	The appropriate use of subpopulation corrections for differences in endogamous communities. Forensic Science International, 2007, 168, 106-111.	1.3	7
116	Testing whether stutter and low-level DNA peaks are additive. Forensic Science International: Genetics, 2019, 43, 102166.	1.6	7
117	Inter-sample contamination detection using mixture deconvolution comparison. Forensic Science International: Genetics, 2019, 40, 160-167.	1.6	7
118	Re: Riman et al. Examining performance and likelihood ratios for two likelihood ratio systems using the PROVEDIt dataset. Forensic Science International: Genetics, 2022, 59, 102709.	1.6	7
119	A Logical Framework for Forensic DNA Interpretation. Genes, 2022, 13, 957.	1.0	7
120	Forensic DNA profiling: The importance of giving accurate answers to the right questions. Criminal Law Forum, 1997, 8, 445-459.	0.2	6
121	Combining autosomal and Y chromosome match probabilities using coalescent theory. Forensic Science International: Genetics, 2014, 11, 52-55.	1.6	6
122	Comment on â€œDNA mixtures interpretation â€“ A proof-of-concept multi-software comparison highlighting different probabilistic methodsâ€™ performances on challenging samplesâ€•by Alladio et al.. Forensic Science International: Genetics, 2019, 40, e248-e251.	1.6	6
123	Validation of a top-down DNA profile analysis for database searching using a fully continuous probabilistic genotyping model. Forensic Science International: Genetics, 2021, 52, 102479.	1.6	6
124	Experimental design for acquiring relevant data to address the issue of comparing consecutively manufactured tools and firearms. Science and Justice - Journal of the Forensic Science Society, 2008, 48, 178-181.	1.3	5
125	Database crime to crime match rate calculation. Forensic Science International: Genetics, 2009, 3, 200-201.	1.6	5
126	Low copy number typingâ€"Where next?. Forensic Science International: Genetics Supplement Series, 2009, 2, 553-555.	0.1	5

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127	Interpreting lineage markers in view of subpopulation effects. Forensic Science International: Genetics, 2012, 6, 393-397.	1.6	5
128	The factor of 10 in forensic DNA match probabilities. Forensic Science International: Genetics, 2017, 28, 178-187.	1.6	5
129	Variability and additivity of read counts for aSTRs in NGS DNA profiles. Forensic Science International: Genetics, 2020, 48, 102351.	1.6	5
130	Re: Comments on â€˜â€˜Interpreting Y chromosome STR haplotype mixtureâ€• Legal Medicine, 2011, 13, 52-53.	0.6	4
131	Examining the additivity of peak heights in forensic DNA profiles. Australian Journal of Forensic Sciences, 2020, , 1-15.	0.7	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.	1.6	4
133	A mixed DNA profile controversy revisited. Journal of Forensic Sciences, 2021, , .	0.9	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.	0.9	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.	1.3	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.	1.3	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.	1.6	3
139	Response to: Commentary on: Bright et al. (2018) Internal validation of STRmixâ„¢ â€" A multi laboratory response to PCAST, Forensic Science International: Genetics, 34: 11â€"24. Forensic Science International: Genetics, 2020, 44, 102198.	1.6	2
140	The interpretation of forensic DNA profiles: an historical perspective. Journal of the Royal Society of New Zealand, 2020, 50, 211-225.	1.0	2
141	Western Australian sub-population data for the thirteen AMPFlSTR Profiler Plus and COfiler STR loci. Journal of Forensic Sciences, 2002, 47, 1149-53.	0.9	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.	1.2	1
143	Geographical variation of shoeprint comparison class correspondences. Science and Justice - Journal of the Forensic Science Society, 2014, 54, 335-337.	1.3	1
144	What can forensic probabilistic genotyping software developers learn from significant nonâ€forensic software failures?. Wiley Interdisciplinary Reviews Forensic Science, 2021, 3, .	1.2	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.	0.7	1
146	Can a reference 'match' an evidence profile if these have no loci in common?. Forensic Science International: Genetics, 2021, 53, 102520.	1.6	1
147	Re: Sign mistake in allele sharing probability formulae of Curran, et al.. Forensic Science International: Genetics, 2010, 4, 215-217.	1.6	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.	1.6	0
149	Investigation into stutter ratio variance. Australian Journal of Forensic Sciences, 2014, 46, 313-316.	0.7	0
150	Authors' Response. Journal of Forensic Sciences, 2015, 60, 1669-1670.	0.9	0
151	The effect of wild card designations and rare alleles in forensic DNA database searches. Forensic Science International: Genetics, 2015, 16, 98-104.	1.6	0
152	Likelihood ratio formulae for disputed parentage when the product of conception is trisomic. International Journal of Legal Medicine, 2017, 131, 1513-1521.	1.2	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.	0.7	0
154	Probabilistic interpretation of the Amelogenin locus. Forensic Science International: Genetics, 2021, 52, 102462.	1.6	0