

John S Buckleton

List of Publications by Citations

Source: <https://exaly.com/author-pdf/9268065/john-s-buckleton-publications-by-citations.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

153
papers

3,662
citations

32
h-index

54
g-index

163
ext. papers

4,358
ext. citations

3.4
avg, IF

5.64
L-index

#	Paper	IF	Citations
153	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	2.6	446
152	The interpretation of single source and mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2013 , 7, 516-28	4.3	187
151	Interpreting low template DNA profiles. <i>Forensic Science International: Genetics</i> , 2009 , 4, 1-10	4.3	139
150	Developing allelic and stutter peak height models for a continuous method of DNA interpretation. <i>Forensic Science International: Genetics</i> , 2013 , 7, 296-304	4.3	113
149	Characterising stutter in forensic STR multiplexes. <i>Forensic Science International: Genetics</i> , 2012 , 6, 58-63	4.3	103
148	Evidence evaluation: a response to the court of appeal judgment in R v T. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2011 , 51, 43-9	2	79
147	132,173-Cyclophosphoramide enol, the first porphyrin isolated from a sponge. <i>Tetrahedron Letters</i> , 1986 , 27, 2177-2178	2	74
146	Developmental validation of STRmix [®] expert software for the interpretation of forensic DNA profiles. <i>Forensic Science International: Genetics</i> , 2016 , 23, 226-239	4.3	71
145	Towards understanding the effect of uncertainty in the number of contributors to DNA stains. <i>Forensic Science International: Genetics</i> , 2007 , 1, 20-8	4.3	70
144	PENDULUM—a guideline-based approach to the interpretation of STR mixtures. <i>Forensic Science International</i> , 2005 , 148, 181-9	2.6	66
143	Interpreting DNA Mixtures in Structured Populations. <i>Journal of Forensic Sciences</i> , 1999 , 44, 12028J	1.8	62
142	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, 221-7	4.3	59
141	Internal validation of STRmix [®] for the interpretation of single source and mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2017 , 29, 126-144	4.3	58
140	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	4.3	58
139	Internal validation of STRmix [®] A multi laboratory response to PCAST. <i>Forensic Science International: Genetics</i> , 2018 , 34, 11-24	4.3	55
138	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, 477-86	4.3	54
137	Population-specific FST values for forensic STR markers: A worldwide survey. <i>Forensic Science International: Genetics</i> , 2016 , 23, 91-100	4.3	52

136	Searching mixed DNA profiles directly against profile databases. <i>Forensic Science International: Genetics</i> , 2014 , 9, 102-10	4.3	51
135	A discussion of the merits of random man not excluded and likelihood ratios. <i>Forensic Science International: Genetics</i> , 2008 , 2, 343-8	4.3	50
134	Validation and development of interpretation guidelines for low copy number (LCN) DNA profiling in New Zealand using the AmpFSTR SGM Plus multiplex. <i>Forensic Science International: Genetics</i> , 2010 , 4, 305-10	4.3	47
133	Examination of the variability in mixed DNA profile parameters for the Identifiler multiplex. <i>Forensic Science International: Genetics</i> , 2010 , 4, 111-4	4.3	46
132	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	44
131	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	2.6	44
130	Synthesis and characterization of masked aminopyrazolecarboxylic acid synthons. <i>Journal of Organic Chemistry</i> , 1989 , 54, 428-431	4.2	43
129	Degradation of forensic DNA profiles. <i>Australian Journal of Forensic Sciences</i> , 2013 , 45, 445-449	1.1	41
128	Validating multiplexes for use in conjunction with modern interpretation strategies. <i>Forensic Science International: Genetics</i> , 2016 , 20, 6-19	4.3	39
127	Some aspects of the Bayesian approach to evidence evaluation. <i>Journal - Forensic Science Society</i> , 1989 , 29, 317-324		39
126	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, 208-14	4.3	36
125	Is the 2p rule always conservative?. <i>Forensic Science International</i> , 2006 , 159, 206-9	2.6	36
124	A series of recommended tests when validating probabilistic DNA profile interpretation software. <i>Forensic Science International: Genetics</i> , 2015 , 14, 125-31	4.3	32
123	A comparison of stochastic variation in mixed and unmixed casework and synthetic samples. <i>Forensic Science International: Genetics</i> , 2012 , 6, 180-4	4.3	32
122	Effectiveness of familial searches. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2008 , 48, 164-7	2	32
121	What is the magnitude of the subpopulation effect?. <i>Forensic Science International</i> , 2003 , 135, 1-8	2.6	32
120	Modelling heterozygote balance in forensic DNA profiles. <i>Forensic Science International: Genetics</i> , 2012 , 6, 729-34	4.3	30
119	Uncertainty in the number of contributors in the proposed new CODIS set. <i>Forensic Science International: Genetics</i> , 2015 , 19, 207-211	4.3	29

118	Testing likelihood ratios produced from complex DNA profiles. <i>Forensic Science International: Genetics</i> , 2015 , 16, 165-171	4.3	29
117	Validation issues around DNA typing of low level DNA. <i>Forensic Science International: Genetics</i> , 2009 , 3, 255-60	4.3	29
116	Relatedness and DNA: are we taking it seriously enough?. <i>Forensic Science International</i> , 2005 , 152, 115-2.6	2.6	29
115	Comparison of the performance of different models for the interpretation of low level mixed DNA profiles. <i>Electrophoresis</i> , 2014 , 35, 3125-33	3.6	28
114	Interpreting forensic DNA profiling evidence without specifying the number of contributors. <i>Forensic Science International: Genetics</i> , 2014 , 13, 269-80	4.3	27
113	Determination of the variables affecting mixed MiniFiler DNA profiles. <i>Forensic Science International: Genetics</i> , 2011 , 5, 381-5	4.3	27
112	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, 186-95	1.8	27
111	NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis. <i>Forensic Science International: Genetics</i> , 2018 , 37, 172-179	4.3	27
110	The effect of linkage on the calculation of DNA match probabilities for siblings and half siblings. <i>Forensic Science International</i> , 2006 , 160, 193-9	2.6	26
109	STRmix collaborative exercise on DNA mixture interpretation. <i>Forensic Science International: Genetics</i> , 2019 , 40, 1-8	4.3	26
108	Inclusion probabilities and dropout. <i>Journal of Forensic Sciences</i> , 2010 , 55, 1171-3	1.8	25
107	Investigation into the performance of different models for predicting stutter. <i>Forensic Science International: Genetics</i> , 2013 , 7, 422-7	4.3	24
106	The 'factor of two' issue in mixed DNA profiles. <i>Journal of Theoretical Biology</i> , 2014 , 363, 300-6	2.3	24
105	Composite profiles in DNA analysis. <i>Forensic Science International: Genetics</i> , 2012 , 6, 317-21	4.3	24
104	The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity. <i>Journal of Forensic Sciences</i> , 2019 , 64, 393-405	1.8	23
103	Application of random match probability calculations to mixed STR profiles. <i>Journal of Forensic Sciences</i> , 2013 , 58, 474-85	1.8	23
102	The interpretation of low level DNA mixtures. <i>Forensic Science International: Genetics</i> , 2012 , 6, 191-7	4.3	22
101	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	22

100	Investigating a common approach to DNA profile interpretation using probabilistic software. <i>Forensic Science International: Genetics</i> , 2015 , 16, 121-131	4.3	21
99	Combating transnational organized crime by linking multiple large ivory seizures to the same dealer. <i>Science Advances</i> , 2018 , 4, eaat0625	14.3	21
98	Do low template DNA profiles have useful quantitative data?. <i>Forensic Science International: Genetics</i> , 2015 , 16, 13-16	4.3	20
97	Helping formulate propositions in forensic DNA analysis. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2014 , 54, 258-61	2	20
96	Characterising the STR locus D6S1043 and examination of its effect on stutter rates. <i>Forensic Science International: Genetics</i> , 2014 , 8, 20-3	4.3	20
95	How reliable is the sub-population model in DNA testimony?. <i>Forensic Science International</i> , 2006 , 157, 144-8	2.6	20
94	The variability in likelihood ratios due to different mechanisms. <i>Forensic Science International: Genetics</i> , 2015 , 14, 187-90	4.3	19
93	Considering relatives when assessing the evidential strength of mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2014 , 13, 259-63	4.3	19
92	Relatedness calculations for linked loci incorporating subpopulation effects. <i>Forensic Science International: Genetics</i> , 2013 , 7, 380-3	4.3	19
91	Utilising allelic dropout probabilities estimated by logistic regression in casework. <i>Forensic Science International: Genetics</i> , 2014 , 9, 9-11	4.3	18
90	A sensitivity analysis to determine the robustness of STRmix with respect to laboratory calibration. <i>Forensic Science International: Genetics</i> , 2018 , 35, 113-122	4.3	17
89	Modeling forward stutter: toward increased objectivity in forensic DNA interpretation. <i>Electrophoresis</i> , 2014 , 35, 3152-7	3.6	17
88	Decision-making in familial database searching: KI alone or not alone?. <i>Forensic Science International: Genetics</i> , 2013 , 7, 52-4	4.3	17
87	Empirical testing of estimated DNA frequencies. <i>Forensic Science International: Genetics</i> , 2007 , 1, 267-72	4.3	17
86	Interpreting a major component from a mixed DNA profile with an unknown number of minor contributors. <i>Forensic Science International: Genetics</i> , 2019 , 40, 150-159	4.3	16
85	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	1.1	16
84	A comprehensive analysis of microsatellite diversity in Aboriginal Australians. <i>Journal of Human Genetics</i> , 2007 , 52, 712-728	4.3	16
83	Selective sequential demasking of the ester functions of 1-methyl-3,4,5-tris(methoxycarbonyl)pyrazole. <i>Journal of Organic Chemistry</i> , 1985 , 50, 4736-4738	4.2	15

82	Likelihood ratio development for mixed Y-STR profiles. <i>Forensic Science International: Genetics</i> , 2018 , 35, 82-96	4.3	13
81	Factors affecting peak height variability for short tandem repeat data. <i>Forensic Science International: Genetics</i> , 2016 , 21, 126-33	4.3	13
80	The paradigm shift in DNA profile interpretation. <i>Forensic Science International: Genetics</i> , 2017 , 31, e24-e33	4.3	12
79	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, 512-6	4.3	12
78	DNA Profiling and Criminal Justice: A Contribution to a Changing Debate. <i>Australian Journal of Forensic Sciences</i> , 2004 , 36, 34-43	1.1	12
77	Uncertainty in the number of contributors for the European Standard Set of loci. <i>Forensic Science International: Genetics</i> , 2014 , 11, 205-6	4.3	11
76	The interpretation of shoeprint comparison class correspondences. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2012 , 52, 243-8	2	11
75	Use of subpopulation data in Australian forensic DNA casework. <i>Forensic Science International: Genetics</i> , 2007 , 1, 238-46	4.3	11
74	The effect of varying the number of contributors in the prosecution and alternate propositions. <i>Forensic Science International: Genetics</i> , 2019 , 38, 225-231	4.3	11
73	The efficacy of DNA mixture to mixture matching. <i>Forensic Science International: Genetics</i> , 2019 , 41, 64-71	4.3	10
72	Comparing the growth and effectiveness of forensic DNA databases. <i>Forensic Science International: Genetics Supplement Series</i> , 2008 , 1, 667-668	0.5	10
71	The impact of Māori cultural values on forensic science practice in New Zealand. <i>Journal of Forensic Sciences</i> , 2008 , 53, 380-3	1.8	10
70	Dealing with allelic dropout when reporting the evidential value in DNA relatedness analysis. <i>Forensic Science International</i> , 2006 , 160, 134-9	2.6	10
69	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	1.1	9
68	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	4.3	9
67	Implementation and validation of an improved allele specific stutter filtering method for electropherogram interpretation. <i>Forensic Science International: Genetics</i> , 2018 , 35, 50-56	4.3	9
66	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):810-21. <i>Journal of Forensic Sciences</i> , 2010 , 55, 265-8; author reply 269-72	1.8	9
65	Modeling forensic DNA database performance. <i>Journal of Forensic Sciences</i> , 2010 , 55, 1174-83	1.8	9

64	Allele frequencies for the four major sub-populations of New Zealand for the 15 Identifier loci. <i>Forensic Science International: Genetics</i> , 2010 , 4, e65-6	4.3	9
63	Estimating the number of contributors to a DNA profile using decision trees. <i>Forensic Science International: Genetics</i> , 2021 , 50, 102407	4.3	9
62	Importance sampling allows H true tests of highly discriminating DNA profiles. <i>Forensic Science International: Genetics</i> , 2017 , 27, 74-81	4.3	8
61	Exploring the probative value of mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2019 , 41, 1-10	4.3	8
60	A guide to results and diagnostics within a STRmix report. <i>Wiley Interdisciplinary Reviews Forensic Science</i> , 2019 , 1,	2.6	8
59	Modelling PowerPlex Y stutter and artefacts. <i>Forensic Science International: Genetics</i> , 2014 , 11, 126-36	4.3	8
58	Identifying and modelling the drivers of stutter in forensic DNA profiles. <i>Australian Journal of Forensic Sciences</i> , 2014 , 46, 194-203	1.1	8
57	When evaluating DNA evidence within a likelihood ratio framework, should the propositions be exhaustive?. <i>Forensic Science International: Genetics</i> , 2021 , 50, 102406	4.3	8
56	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	2.6	8
55	Modelling the dependence structure of Y-STR haplotypes using graphical models. <i>Forensic Science International: Genetics</i> , 2018 , 37, 29-36	4.3	7
54	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	4.3	7
53	The appropriate use of subpopulation corrections for differences in endogamous communities. <i>Forensic Science International</i> , 2007 , 168, 106-11	2.6	7
52	A more straightforward derivation of the LR for a database search. <i>Forensic Science International: Genetics</i> , 2015 , 14, 156-60	4.3	6
51	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	2.6	6
50	Using probabilistic theory to develop interpretation guidelines for Y-STR profiles. <i>Forensic Science International: Genetics</i> , 2016 , 21, 22-34	4.3	5
49	Testing whether stutter and low-level DNA peaks are additive. <i>Forensic Science International: Genetics</i> , 2019 , 43, 102166	4.3	5
48	Interpreting lineage markers in view of subpopulation effects. <i>Forensic Science International: Genetics</i> , 2012 , 6, 393-7	4.3	5
47	Database crime to crime match rate calculation. <i>Forensic Science International: Genetics</i> , 2009 , 3, 200-1	4.3	5

46	Empirical support for the reliability of DNA interpretation in Croatia. <i>Forensic Science International: Genetics</i> , 2008 , 3, 50-3	4.3	5
45	Are low LR's reliable?. <i>Forensic Science International: Genetics</i> , 2020 , 49, 102350	4.3	5
44	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	4.3	5
43	Comparing multiple POI to DNA mixtures. <i>Forensic Science International: Genetics</i> , 2021 , 52, 102481	4.3	5
42	Inter-sample contamination detection using mixture deconvolution comparison. <i>Forensic Science International: Genetics</i> , 2019 , 40, 160-167	4.3	5
41	A comparison of likelihood ratios obtained from EuroForMix and STRmix. <i>Journal of Forensic Sciences</i> , 2021 , 66, 2138-2155	1.8	5
40	The factor of 10 in forensic DNA match probabilities. <i>Forensic Science International: Genetics</i> , 2017 , 28, 178-187	4.3	4
39	Low copy number typing. Where next?. <i>Forensic Science International: Genetics Supplement Series</i> , 2009 , 2, 553-555	0.5	4
38	Variability and additivity of read counts for aSTRs in NGS DNA profiles. <i>Forensic Science International: Genetics</i> , 2020 , 48, 102351	4.3	4
37	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	4.3	4
36	A Review of Probabilistic Genotyping Systems: , and. <i>Genes</i> , 2021 , 12,	4.2	4
35	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	4.3	3
34	Examining the additivity of peak heights in forensic DNA profiles. <i>Australian Journal of Forensic Sciences</i> , 2020 , 1-15	1.1	3
33	Commentary: A "Source" of Error: Computer Code, Criminal Defendants, and the Constitution. <i>Frontiers in Genetics</i> , 2017 , 8, 33	4.5	3
32	Re: Comments on Interpreting Y chromosome STR haplotype mixture. <i>Legal Medicine</i> , 2011 , 13, 52-53	1.9	3
31	Forensic DNA profiling: The importance of giving accurate answers to the right questions. <i>Criminal Law Forum</i> , 1997 , 8, 445-459	0.5	3
30	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	1.1	3
29	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, 178-81	2	3

28	The interpretation of mixed DNA profiles from a mother, father, and child trio. <i>Forensic Science International: Genetics</i> , 2020 , 44, 102175	4.3	3
27	Modeling allelic analyte signals for aSTRs in NGS DNA profiles. <i>Journal of Forensic Sciences</i> , 2021 , 66, 1234-1245	1.8	3
26	Combining autosomal and Y chromosome match probabilities using coalescent theory. <i>Forensic Science International: Genetics</i> , 2014 , 11, 52-5	4.3	2
25	Consideration of the probative value of single donor 15-plex STR profiles in UK populations and its presentation in UK courts II. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2013 , 53, 371	2	2
24	Letter to editor in response to editorial by Risinger et al. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2014 , 54, 510	2	2
23	The extent of substructure in the indigenous Australian population and its impact on DNA evidence interpretation. <i>International Congress Series</i> , 2006 , 1288, 382-384		2
22	Response to: Commentary on: Bright et al. (2018) Internal validation of STRmix [®] A multi laboratory response to PCAST, <i>Forensic Science International: Genetics</i> , 34: 11-24. <i>Forensic Science International: Genetics</i> , 2020 , 44, 102198	4.3	2
21	Relaxing the assumption of unrelatedness in the numerator and denominator of likelihood ratios for DNA mixtures. <i>Forensic Science International: Genetics</i> , 2021 , 51, 102434	4.3	2
20	Western Australian sub-population data for the thirteen AMPFISTR Profiler Plus and COfiler STR loci. <i>Journal of Forensic Sciences</i> , 2002 , 47, 1149-53	1.8	2
19	Evidence in support of self-declaration as a sampling method for the formation of sub-population DNA databases. <i>Journal of Forensic Sciences</i> , 2003 , 48, 1091-3	1.8	2
18	Geographical variation of shoeprint comparison class correspondences. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2014 , 54, 335-7	2	1
17	A mixed DNA profile controversy revisited. <i>Journal of Forensic Sciences</i> , 2021 ,	1.8	1
16	The interpretation of forensic DNA profiles: an historical perspective. <i>Journal of the Royal Society of New Zealand</i> , 2020 , 50, 211-225	2	1
15	What can forensic probabilistic genotyping software developers learn from significant non-forensic software failures?. <i>Wiley Interdisciplinary Reviews Forensic Science</i> , 2021 , 3,	2.6	1
14	The effect of a user selected number of contributors within the LR assignment. <i>Australian Journal of Forensic Sciences</i> , 1-14	1.1	1
13	A Logical Framework for Forensic DNA Interpretation. <i>Genes</i> , 2022 , 13, 957	4.2	1
12	Weight-of-Evidence for Forensic DNA Profiles, by David J. Balding John Wiley and Sons, Ltd., 2005; 198 pp.. <i>Law, Probability and Risk</i> , 2005 , 4, 191-193	0.6	0
11	Streamlining the decision-making process for international DNA kinship matching using Worldwide allele frequencies and tailored cutoff logLR thresholds. <i>Forensic Science International: Genetics</i> , 2021 , 57, 102634	4.3	0

10	Can a reference 'match' an evidence profile if these have no loci in common?. <i>Forensic Science International: Genetics</i> , 2021 , 53, 102520	4.3	○
9	Investigation into the effect of mixtures comprising related people on non-donor likelihood ratios, and potential practises to mitigate providing misleading opinions.. <i>Forensic Science International: Genetics</i> , 2022 , 59, 102691	4.3	○
8	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 , 102709	4.3	○
7	Likelihood ratio formulae for disputed parentage when the product of conception is trisomic. <i>International Journal of Legal Medicine</i> , 2017 , 131, 1513-1521	3.1	
6	Response to Lander's response to the ANZFSS Council Statement on the President's Council of Advisors on Science and Technology Report. <i>Australian Journal of Forensic Sciences</i> , 2018 , 50, 453-454	1.1	
5	Authors' Response. <i>Journal of Forensic Sciences</i> , 2015 , 60, 1669-70	1.8	
4	The effect of wild card designations and rare alleles in forensic DNA database searches. <i>Forensic Science International: Genetics</i> , 2015 , 16, 98-104	4.3	
3	Investigation into stutter ratio variance. <i>Australian Journal of Forensic Sciences</i> , 2014 , 46, 313-316	1.1	
2	Re: Sign mistake in allele sharing probability formulae of Curran, et al.. <i>Forensic Science International: Genetics</i> , 2010 , 4, 215-217	4.3	
1	Probabilistic interpretation of the Amelogenin locus. <i>Forensic Science International: Genetics</i> , 2021 , 52, 102462	4.3	