John S Buckleton

List of Publications by Year
in descending order

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	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.	3.1	8
2	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
3	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.	3.1	7
4	A Logical Framework for Forensic DNA Interpretation. Genes, 2022, 13, 957.	2.4	7
5	What can forensic probabilistic genotyping software developers learn from significant non‐forensic software failures?. Wiley Interdisciplinary Reviews Forensic Science, 2021, 3, .	2.1	1
6	When evaluating DNA evidence within a likelihood ratio framework, should the propositions be exhaustive?. Forensic Science International: Genetics, 2021, 50, 102406.	3.1	13
7	Estimating the number of contributors to a DNA profile using decision trees. Forensic Science International: Genetics, 2021, 50, 102407.	3.1	17
8	Modeling allelic analyte signals for aSTRs in NGS DNA profiles. Journal of Forensic Sciences, 2021, 66, 1234-1245.	1.6	8
9	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
10	Probabilistic interpretation of the Amelogenin locus. Forensic Science International: Genetics, 2021, 52, 102462.	3.1	0
11	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.	3.1	6
12	Comparing multiple POI to DNA mixtures. Forensic Science International: Genetics, 2021, 52, 102481.	3.1	12
13	Can a reference 'match' an evidence profile if these have no loci in common?. Forensic Science International: Genetics, 2021, 53, 102520.	3.1	1
14	A comparison of likelihood ratios obtained from EuroForMix and STRmix™. Journal of Forensic Sciences, 2021, 66, 2138-2155.	1.6	14
15	A Review of Probabilistic Genotyping Systems: EuroForMix, DNAStatistX and STRmix™. Genes, 2021, 12, 1559.	2.4	25
16	A mixed DNA profile controversy revisited. Journal of Forensic Sciences, 2021, , .	1.6	4
17	The interpretation of mixed DNA profiles from a mother, father, and child trio. Forensic Science International: Genetics, 2020, 44, 102175.	3.1	8
18	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

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19	The interpretation of forensic DNA profiles: an historical perspective. Journal of the Royal Society of New Zealand, 2020, 50, 211-225.	1.9	2
20	Are low LRs reliable?. Forensic Science International: Genetics, 2020, 49, 102350.	3.1	10
21	Variability and additivity of read counts for aSTRs in NGS DNA profiles. Forensic Science International: Genetics, 2020, 48, 102351.	3.1	5
22	Performance of a method for weighting a range in the number of contributors in probabilistic genotyping. Forensic Science International: Genetics, 2020, 48, 102352.	3.1	9
23	Examining the additivity of peak heights in forensic DNA profiles. Australian Journal of Forensic Sciences, 2020, , 1-15.	1.2	4
24	A review of likelihood ratios in forensic science based on a critique of Stiffelman â€œNo longer the Gold standard: Probabilistic genotyping is changing the nature of DNA evidence in criminal trialsâ€. Forensic Science International, 2020, 310, 110251.	2.2	11
25	The Probabilistic Genotyping Software <scp>STR</scp>mix: Utility and Evidence for its Validity. Journal of Forensic Sciences, 2019, 64, 393-405.	1.6	33
26	Testing whether stutter and low-level DNA peaks are additive. Forensic Science International: Genetics, 2019, 43, 102166.	3.1	7
27	A guide to results and diagnostics within a STRmixâ„¢ report. Wiley Interdisciplinary Reviews Forensic Science, 2019, 1, .	2.1	18
28	Exploring the probative value of mixed DNA profiles. Forensic Science International: Genetics, 2019, 41, 1-10.	3.1	14
29	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.	3.1	6
30	The efficacy of DNA mixture to mixture matching. Forensic Science International: Genetics, 2019, 41, 64-71.	3.1	17
31	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
32	Inter-sample contamination detection using mixture deconvolution comparison. Forensic Science International: Genetics, 2019, 40, 160-167.	3.1	7
33	The effect of varying the number of contributors in the prosecution and alternate propositions. Forensic Science International: Genetics, 2019, 38, 225-231.	3.1	21
34	STRmixâ„¢ collaborative exercise on DNA mixture interpretation. Forensic Science International: Genetics, 2019, 40, 1-8.	3.1	39
35	Likelihood ratio development for mixed Y-STR profiles. Forensic Science International: Genetics, 2018, 35, 82-96.	3.1	22
36	Implementation and validation of an improved allele specific stutter filtering method for electropherogram interpretation. Forensic Science International: Genetics, 2018, 35, 50-56.	3.1	16

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37	Internal validation of STRmix™ – A multi laboratory response to PCAST. Forensic Science International: Genetics, 2018, 34, 11-24.	3.1	72
38	Combating transnational organized crime by linking multiple large ivory seizures to the same dealer. Science Advances, 2018, 4, eaat0625.	10.3	31
39	NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis. Forensic Science International: Genetics, 2018, 37, 172-179.	3.1	35
40	A response to "Likelihood ratio as weight of evidence: A closer look" by Lund and Iyer. Forensic Science International, 2018, 288, e15-e19.	2.2	12
41	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
42	Modelling the dependence structure of Y-STR haplotypes using graphical models. Forensic Science International: Genetics, 2018, 37, 29-36.	3.1	11
43	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
44	Does the use of probabilistic genotyping change the way we should view sub-threshold data?. Australian Journal of Forensic Sciences, 2017, 49, 78-92.	1.2	11
45	The factor of 10 in forensic DNA match probabilities. Forensic Science International: Genetics, 2017, 28, 178-187.	3.1	5
46	Internal validation of STRmix™ for the interpretation of single source and mixed DNA profiles. Forensic Science International: Genetics, 2017, 29, 126-144.	3.1	74
47	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
48	Importance sampling allows Hd true tests of highly discriminating DNA profiles. Forensic Science International: Genetics, 2017, 27, 74-81.	3.1	14
49	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.	3.1	13
50	The paradigm shift in DNA profile interpretation. Forensic Science International: Genetics, 2017, 31, e24-e32.	3.1	15
51	Commentary: A "Source" of Error: Computer Code, Criminal Defendants, and the Constitution. Frontiers in Genetics, 2017, 8, 33.	2.3	13
52	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
53	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.	1.6	37
54	Developmental validation of STRmix™, expert software for the interpretation of forensic DNA profiles. Forensic Science International: Genetics, 2016, 23, 226-239.	3.1	110

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55	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.	3.1	78
56	Using probabilistic theory to develop interpretation guidelines for Y-STR profiles. Forensic Science International: Genetics, 2016, 21, 22-34.	3.1	9
57	Population-specific F values for forensic STR markers: A worldwide survey. Forensic Science International: Genetics, 2016, 23, 91-100.	3.1	73
58	Factors affecting peak height variability for short tandem repeat data. Forensic Science International: Genetics, 2016, 21, 126-133.	3.1	25
59	Validating multiplexes for use in conjunction with modern interpretation strategies. Forensic Science International: Genetics, 2016, 20, 6-19.	3.1	50
60	Authors' Response. Journal of Forensic Sciences, 2015, 60, 1669-1670.	1.6	0
61	Testing likelihood ratios produced from complex DNA profiles. Forensic Science International: Genetics, 2015, 16, 165-171.	3.1	39
62	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
63	Investigating a common approach to DNA profile interpretation using probabilistic software. Forensic Science International: Genetics, 2015, 16, 121-131.	3.1	24
64	Uncertainty in the number of contributors in the proposed new CODIS set. Forensic Science International: Genetics, 2015, 19, 207-211.	3.1	33
65	Do low template DNA profiles have useful quantitative data?. Forensic Science International: Genetics, 2015, 16, 13-16.	3.1	26
66	The variability in likelihood ratios due to different mechanisms. Forensic Science International: Genetics, 2015, 14, 187-190.	3.1	27
67	A more straightforward derivation of the LR for a database search. Forensic Science International: Genetics, 2015, 14, 156-160.	3.1	10
68	A series of recommended tests when validating probabilistic DNA profile interpretation software. Forensic Science International: Genetics, 2015, 14, 125-131.	3.1	36
69	Identifying and modelling the drivers of stutter in forensic DNA profiles. Australian Journal of Forensic Sciences, 2014, 46, 194-203.	1.2	10
70	Comparison of the performance of different models for the interpretation of low level mixed DNA profiles. Electrophoresis, 2014, 35, 3125-3133.	2.4	36
71	Interpreting forensic DNA profiling evidence without specifying the number of contributors. Forensic Science International: Genetics, 2014, 13, 269-280.	3.1	40
72	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.	3.1	44

#	ARTICLE	IF	CITATIONS
73	Investigation into stutter ratio variance. Australian Journal of Forensic Sciences, 2014, 46, 313-316.	1.2	0
74	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
75	The â€˜factor of twoâ€™ issue in mixed DNA profiles. Journal of Theoretical Biology, 2014, 363, 300-306.	1.7	36
76	Considering relatives when assessing the evidential strength of mixed DNA profiles. Forensic Science International: Genetics, 2014, 13, 259-263.	3.1	30
77	Searching mixed DNA profiles directly against profile databases. Forensic Science International: Genetics, 2014, 9, 102-110.	3.1	62
78	Variability of mixed DNA profiles separated on a 3130 and 3500 capillary electrophoresis instrument. Australian Journal of Forensic Sciences, 2014, 46, 304-312.	1.2	19
79	Combining autosomal and Y chromosome match probabilities using coalescent theory. Forensic Science International: Genetics, 2014, 11, 52-55.	3.1	6
80	Geographical variation of shoeprint comparison class correspondences. Science and Justice - Journal of the Forensic Science Society, 2014, 54, 335-337.	2.1	1
81	Helping formulate propositions in forensic DNA analysis. Science and Justice - Journal of the Forensic Science Society, 2014, 54, 258-261.	2.1	27
82	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.	2.1	54
83	Modelling PowerPlexÂ® Y stutter and artefacts. Forensic Science International: Genetics, 2014, 11, 126-136.	3.1	9
84	Utilising allelic dropout probabilities estimated by logistic regression in casework. Forensic Science International: Genetics, 2014, 9, 9-11.	3.1	23
85	Characterising the STR locus D6S1043 and examination of its effect on stutter rates. Forensic Science International: Genetics, 2014, 8, 20-23.	3.1	21
86	Uncertainty in the number of contributors for the European Standard Set of loci. Forensic Science International: Genetics, 2014, 11, 205-206.	3.1	14
87	Modeling forward stutter: Toward increased objectivity in forensic <scp>DNA</scp> interpretation. Electrophoresis, 2014, 35, 3152-3157.	2.4	22
88	Decision-making in familial database searching: KI alone or not alone?. Forensic Science International: Genetics, 2013, 7, 52-54.	3.1	24
89	Developing allelic and stutter peak height models for a continuous method of DNA interpretation. Forensic Science International: Genetics, 2013, 7, 296-304.	3.1	130
90	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

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91	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
92	Investigation into the performance of different models for predicting stutter. Forensic Science International: Genetics, 2013, 7, 422-427.	3.1	27
93	The interpretation of single source and mixed DNA profiles. Forensic Science International: Genetics, 2013, 7, 516-528.	3.1	237
94	Degradation of forensic DNA profiles. Australian Journal of Forensic Sciences, 2013, 45, 445-449.	1.2	56
95	Relatedness calculations for linked loci incorporating subpopulation effects. Forensic Science International: Genetics, 2013, 7, 380-383.	3.1	26
96	Application of Random Match Probability Calculations to Mixed <scp>STR</scp> Profiles. Journal of Forensic Sciences, 2013, 58, 474-485.	1.6	30
97	Characterising stutter in forensic STR multiplexes. Forensic Science International: Genetics, 2012, 6, 58-63.	3.1	121
98	A comparison of stochastic variation in mixed and unmixed casework and synthetic samples. Forensic Science International: Genetics, 2012, 6, 180-184.	3.1	35
99	The interpretation of low level DNA mixtures. Forensic Science International: Genetics, 2012, 6, 191-197.	3.1	30
100	Interpreting lineage markers in view of subpopulation effects. Forensic Science International: Genetics, 2012, 6, 393-397.	3.1	5
101	Composite profiles in DNA analysis. Forensic Science International: Genetics, 2012, 6, 317-321.	3.1	34
102	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.	3.1	59
103	Modelling heterozygote balance in forensic DNA profiles. Forensic Science International: Genetics, 2012, 6, 729-734.	3.1	33
104	The interpretation of shoeprint comparison class correspondences. Science and Justice - Journal of the Forensic Science Society, 2012, 52, 243-248.	2.1	11
105	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.	3.1	11
106	Determination of the variables affecting mixed MiniFiler™ DNA profiles. Forensic Science International: Genetics, 2011, 5, 381-385.	3.1	29
107	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.	3.1	15
108	Re: Comments on ''Interpreting Y chromosome STR haplotype mixture" Legal Medicine, 2011, 13, 52-53.	1.3	4

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109	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.	2.1	87
110	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.	1.6	17
111	Modeling Forensic DNA Database Performance*. Journal of Forensic Sciences, 2010, 55, 1174-1183.	1.6	13
112	Inclusion Probabilities and Dropout. Journal of Forensic Sciences, 2010, 55, 1171-1173.	1.6	29
113	Allele frequencies for the four major sub-populations of New Zealand for the 15 Identifiler loci. Forensic Science International: Genetics, 2010, 4, e65-e66.	3.1	11
114	Re: Sign mistake in allele sharing probability formulae of Curran, et al.. Forensic Science International: Genetics, 2010, 4, 215-217.	3.1	0
115	Examination of the variability in mixed DNA profile parameters for the Identifilerâ„¢ multiplex. Forensic Science International: Genetics, 2010, 4, 111-114.	3.1	51
116	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.	3.1	76
117	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.	3.1	59
118	Database crime to crime match rate calculation. Forensic Science International: Genetics, 2009, 3, 200-201.	3.1	5
119	Interpreting low template DNA profiles. Forensic Science International: Genetics, 2009, 4, 1-10.	3.1	167
120	Validation issues around DNA typing of low level DNA. Forensic Science International: Genetics, 2009, 3, 255-260.	3.1	34
121	Low copy number typingâ€"Where next?. Forensic Science International: Genetics Supplement Series, 2009, 2, 553-555.	0.3	5
122	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.	2.1	5
123	Effectiveness of familial searches. Science and Justice - Journal of the Forensic Science Society, 2008, 48, 164-167.	2.1	42
124	The Impact of MÄori Cultural Values on Forensic Science Practice in New Zealand. Journal of Forensic Sciences, 2008, 53, 380-383.	1.6	12
125	A discussion of the merits of random man not excluded and likelihood ratios. Forensic Science International: Genetics, 2008, 2, 343-348.	3.1	57
126	Empirical support for the reliability of DNA interpretation in Croatia. Forensic Science International: Genetics, 2008, 3, 50-53.	3.1	8

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127	Comparing the growth and effectiveness of forensic DNA databases. Forensic Science International: Genetics Supplement Series, 2008, 1, 667-668.	0.3	12
128	Empirical support for the reliability of DNA evidence interpretation in Australia and New Zealand. Australian Journal of Forensic Sciences, 2008, 40, 99-108.	1.2	8
129	Towards understanding the effect of uncertainty in the number of contributors to DNA stains. Forensic Science International: Genetics, 2007, 1, 20-28.	3.1	82
130	Use of subpopulation data in Australian forensic DNA casework. Forensic Science International: Genetics, 2007, 1, 238-246.	3.1	13
131	Empirical testing of estimated DNA frequencies. Forensic Science International: Genetics, 2007, 1, 267-272.	3.1	23
132	The appropriate use of subpopulation corrections for differences in endogamous communities. Forensic Science International, 2007, 168, 106-111.	2.2	7
133	A comprehensive analysis of microsatellite diversity in Aboriginal Australians. Journal of Human Genetics, 2007, 52, 712-728.	2.3	19
134	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
135	The effect of linkage on the calculation of DNA match probabilities for siblings and half siblings. Forensic Science International, 2006, 160, 193-199.	2.2	28
136	How reliable is the sub-population model in DNA testimony?. Forensic Science International, 2006, 157, 144-148.	2.2	27
137	Is the 2p rule always conservative?. Forensic Science International, 2006, 159, 206-209.	2.2	45
138	Dealing with allelic dropout when reporting the evidential value in DNA relatedness analysis. Forensic Science International, 2006, 160, 134-139.	2.2	12
139	PENDULUM—a guideline-based approach to the interpretation of STR mixtures. Forensic Science International, 2005, 148, 181-189.	2.2	75
140	Relatedness and DNA: are we taking it seriously enough?. Forensic Science International, 2005, 152, 115-119.	2.2	35
141	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
142	DNA Profiling and Criminal Justice: A Contribution to a Changing Debate. Australian Journal of Forensic Sciences, 2004, 36, 34-43.	1.2	13
143	What is the magnitude of the subpopulation effect?. Forensic Science International, 2003, 135, 1-8.	2.2	43
144	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

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145	Western Australian sub-population data for the thirteen AMPFlSTR Profiler Plus and COfiler STR loci. Journal of Forensic Sciences, 2002, 47, 1149-53.	1.6	2
146	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.	2.2	510
147	Interpreting DNA Mixtures in Structured Populations. Journal of Forensic Sciences, 1999, 44, 987-995.	1.6	82
148	Forensic DNA profiling: The importance of giving accurate answers to the right questions. Criminal Law Forum, 1997, 8, 445-459.	0.4	6
149	The interpretation of elemental composition measurements from forensic glass evidence: II. Science and Justice - Journal of the Forensic Science Society, 1997, 37, 245-249.	2.1	33
150	Synthesis and characterization of masked aminopyrazolecarboxylic acid synthons. Journal of Organic Chemistry, 1989, 54, 428-431.	3.2	51
151	Some aspects of the Bayesian approach to evidence evaluation. Journal - Forensic Science Society, 1989, 29, 317-324.	0.2	45
152	132,173-Cyclopheophorbide enol, the first porphyrin isolated from a sponge. Tetrahedron Letters, 1986, 27, 2177-2178.	1.4	77
153	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
154	The effect of a user selected number of contributors within the LR assignment. Australian Journal of Forensic Sciences, 0, , 1-14.	1.2	1