

John S Buckleton

List of Publications by Year in Descending Order

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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	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	0
152	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	0
151	A Logical Framework for Forensic DNA Interpretation. <i>Genes</i> , 2022 , 13, 957	4.2	1
150	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
149	A mixed DNA profile controversy revisited. <i>Journal of Forensic Sciences</i> , 2021 ,	1.8	1
148	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
147	Probabilistic interpretation of the Amelogenin locus. <i>Forensic Science International: Genetics</i> , 2021 , 52, 102462	4.3	
146	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
145	Comparing multiple POI to DNA mixtures. <i>Forensic Science International: Genetics</i> , 2021 , 52, 102481	4.3	5
144	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
143	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
142	Estimating the number of contributors to a DNA profile using decision trees. <i>Forensic Science International: Genetics</i> , 2021 , 50, 102407	4.3	9
141	Modeling allelic analyte signals for aSTRs in NGS DNA profiles. <i>Journal of Forensic Sciences</i> , 2021 , 66, 1234-1245	1.8	3
140	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	0
139	A comparison of likelihood ratios obtained from EuroForMix and STRmix. <i>Journal of Forensic Sciences</i> , 2021 , 66, 2138-2155	1.8	5
138	A Review of Probabilistic Genotyping Systems: , and. <i>Genes</i> , 2021 , 12,	4.2	4
137	Examining the additivity of peak heights in forensic DNA profiles. <i>Australian Journal of Forensic Sciences</i> , 2020 , 1-15	1.1	3

136	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
135	Response to: Commentary on: Bright et al. (2018) Internal validation of STRmix: A multi-laboratory response to PCAST, <i>Forensic Science International: Genetics</i> , 2020 , 44, 102198	4.3	2
134	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
133	Are low LR's reliable?. <i>Forensic Science International: Genetics</i> , 2020 , 49, 102350	4.3	5
132	Variability and additivity of read counts for aSTRs in NGS DNA profiles. <i>Forensic Science International: Genetics</i> , 2020 , 48, 102351	4.3	4
131	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
130	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
129	Exploring the probative value of mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2019 , 41, 1-10	4.3	8
128	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
127	The efficacy of DNA mixture to mixture matching. <i>Forensic Science International: Genetics</i> , 2019 , 41, 64-71	4.3	10
126	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
125	The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity. <i>Journal of Forensic Sciences</i> , 2019 , 64, 393-405	1.8	23
124	Testing whether stutter and low-level DNA peaks are additive. <i>Forensic Science International: Genetics</i> , 2019 , 43, 102166	4.3	5
123	A guide to results and diagnostics within a STRmix report. <i>Wiley Interdisciplinary Reviews Forensic Science</i> , 2019 , 1,	2.6	8
122	Inter-sample contamination detection using mixture deconvolution comparison. <i>Forensic Science International: Genetics</i> , 2019 , 40, 160-167	4.3	5
121	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
120	STRmix: collaborative exercise on DNA mixture interpretation. <i>Forensic Science International: Genetics</i> , 2019 , 40, 1-8	4.3	26
119	Likelihood ratio development for mixed Y-STR profiles. <i>Forensic Science International: Genetics</i> , 2018 , 35, 82-96	4.3	13

118	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
117	Internal validation of STRmix™ A multi laboratory response to PCAST. <i>Forensic Science International: Genetics</i> , 2018 , 34, 11-24	4.3	55
116	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	
115	Modelling the dependence structure of Y-STR haplotypes using graphical models. <i>Forensic Science International: Genetics</i> , 2018 , 37, 29-36	4.3	7
114	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
113	Combating transnational organized crime by linking multiple large ivory seizures to the same dealer. <i>Science Advances</i> , 2018 , 4, eaat0625	14.3	21
112	NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis. <i>Forensic Science International: Genetics</i> , 2018 , 37, 172-179	4.3	27
111	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
110	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
109	The factor of 10 in forensic DNA match probabilities. <i>Forensic Science International: Genetics</i> , 2017 , 28, 178-187	4.3	4
108	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
107	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	
106	Importance sampling allows H true tests of highly discriminating DNA profiles. <i>Forensic Science International: Genetics</i> , 2017 , 27, 74-81	4.3	8
105	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
104	The paradigm shift in DNA profile interpretation. <i>Forensic Science International: Genetics</i> , 2017 , 31, e24-e27	4.3	12
103	Commentary: A "Source" of Error: Computer Code, Criminal Defendants, and the Constitution. <i>Frontiers in Genetics</i> , 2017 , 8, 33	4.5	3
102	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
101	Using probabilistic theory to develop interpretation guidelines for Y-STR profiles. <i>Forensic Science International: Genetics</i> , 2016 , 21, 22-34	4.3	5

100	Population-specific FST values for forensic STR markers: A worldwide survey. <i>Forensic Science International: Genetics</i> , 2016 , 23, 91-100	4.3	52
99	Factors affecting peak height variability for short tandem repeat data. <i>Forensic Science International: Genetics</i> , 2016 , 21, 126-33	4.3	13
98	Validating multiplexes for use in conjunction with modern interpretation strategies. <i>Forensic Science International: Genetics</i> , 2016 , 20, 6-19	4.3	39
97	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
96	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
95	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
94	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
93	Do low template DNA profiles have useful quantitative data?. <i>Forensic Science International: Genetics</i> , 2015 , 16, 13-16	4.3	20
92	The variability in likelihood ratios due to different mechanisms. <i>Forensic Science International: Genetics</i> , 2015 , 14, 187-90	4.3	19
91	A more straightforward derivation of the LR for a database search. <i>Forensic Science International: Genetics</i> , 2015 , 14, 156-60	4.3	6
90	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
89	Authors' Response. <i>Journal of Forensic Sciences</i> , 2015 , 60, 1669-70	1.8	
88	Testing likelihood ratios produced from complex DNA profiles. <i>Forensic Science International: Genetics</i> , 2015 , 16, 165-171	4.3	29
87	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	
86	Investigating a common approach to DNA profile interpretation using probabilistic software. <i>Forensic Science International: Genetics</i> , 2015 , 16, 121-131	4.3	21
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	Combining autosomal and Y chromosome match probabilities using coalescent theory. <i>Forensic Science International: Genetics</i> , 2014 , 11, 52-5	4.3	2
83	Geographical variation of shoeprint comparison class correspondences. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2014 , 54, 335-7	2	1

82	Helping formulate propositions in forensic DNA analysis. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2014 , 54, 258-61	2	20
81	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
80	Modelling PowerPlex [®] Y stutter and artefacts. <i>Forensic Science International: Genetics</i> , 2014 , 11, 126-36	4.3	8
79	Utilising allelic dropout probabilities estimated by logistic regression in casework. <i>Forensic Science International: Genetics</i> , 2014 , 9, 9-11	4.3	18
78	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
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	Modeling forward stutter: toward increased objectivity in forensic DNA interpretation. <i>Electrophoresis</i> , 2014 , 35, 3152-7	3.6	17
75	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
74	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
73	Interpreting forensic DNA profiling evidence without specifying the number of contributors. <i>Forensic Science International: Genetics</i> , 2014 , 13, 269-80	4.3	27
72	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
71	Investigation into stutter ratio variance. <i>Australian Journal of Forensic Sciences</i> , 2014 , 46, 313-316	1.1	
70	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
69	The 'factor of two' issue in mixed DNA profiles. <i>Journal of Theoretical Biology</i> , 2014 , 363, 300-6	2.3	24
68	Considering relatives when assessing the evidential strength of mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2014 , 13, 259-63	4.3	19
67	Searching mixed DNA profiles directly against profile databases. <i>Forensic Science International: Genetics</i> , 2014 , 9, 102-10	4.3	51
66	Decision-making in familial database searching: KI alone or not alone?. <i>Forensic Science International: Genetics</i> , 2013 , 7, 52-4	4.3	17
65	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

64	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
63	Investigation into the performance of different models for predicting stutter. <i>Forensic Science International: Genetics</i> , 2013 , 7, 422-7	4.3	24
62	The interpretation of single source and mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2013 , 7, 516-28	4.3	187
61	Degradation of forensic DNA profiles. <i>Australian Journal of Forensic Sciences</i> , 2013 , 45, 445-449	1.1	41
60	Relatedness calculations for linked loci incorporating subpopulation effects. <i>Forensic Science International: Genetics</i> , 2013 , 7, 380-3	4.3	19
59	Application of random match probability calculations to mixed STR profiles. <i>Journal of Forensic Sciences</i> , 2013 , 58, 474-85	1.8	23
58	Characterising stutter in forensic STR multiplexes. <i>Forensic Science International: Genetics</i> , 2012 , 6, 58-63	4.3	103
57	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
56	The interpretation of low level DNA mixtures. <i>Forensic Science International: Genetics</i> , 2012 , 6, 191-7	4.3	22
55	Interpreting lineage markers in view of subpopulation effects. <i>Forensic Science International: Genetics</i> , 2012 , 6, 393-7	4.3	5
54	Composite profiles in DNA analysis. <i>Forensic Science International: Genetics</i> , 2012 , 6, 317-21	4.3	24
53	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
52	Modelling heterozygote balance in forensic DNA profiles. <i>Forensic Science International: Genetics</i> , 2012 , 6, 729-34	4.3	30
51	The interpretation of shoeprint comparison class correspondences. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2012 , 52, 243-8	2	11
50	Further Comment on How copy number typing has yet to achieve general acceptance by Budowle, B., et al, 2009. <i>Forensic Sci. Int. Genetics: Supplement Series 2</i> , 551-52. <i>Forensic Science International: Genetics</i> , 2011 , 5, 7-11	4.3	7
49	Determination of the variables affecting mixed MiniFiler DNA profiles. <i>Forensic Science International: Genetics</i> , 2011 , 5, 381-5	4.3	27
48	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
47	Re: Comments on Interpreting Y chromosome STR haplotype mixture. <i>Legal Medicine</i> , 2011 , 13, 52-53	1.9	3

46	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
45	Commentary on: Budowle B, Onorato AJ, Callaghan TF, Della Manna A, Gross AM, Guerrieri RA, Luttmann 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
44	Modeling forensic DNA database performance. <i>Journal of Forensic Sciences</i> , 2010 , 55, 1174-83	1.8	9
43	Inclusion probabilities and dropout. <i>Journal of Forensic Sciences</i> , 2010 , 55, 1171-3	1.8	25
42	Allele frequencies for the four major sub-populations of New Zealand for the 15 Identifiler loci. <i>Forensic Science International: Genetics</i> , 2010 , 4, e65-6	4.3	9
41	Re: Sign mistake in allele sharing probability formulae of Curran, et al.. <i>Forensic Science International: Genetics</i> , 2010 , 4, 215-217	4.3	
40	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
39	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
38	Validation and development of interpretation guidelines for low copy number (LCN) DNA profiling in New Zealand using the AmpFLSTR SGM Plus multiplex. <i>Forensic Science International: Genetics</i> , 2010 , 4, 305-10	4.3	47
37	Database crime to crime match rate calculation. <i>Forensic Science International: Genetics</i> , 2009 , 3, 200-1	4.3	5
36	Interpreting low template DNA profiles. <i>Forensic Science International: Genetics</i> , 2009 , 4, 1-10	4.3	139
35	Validation issues around DNA typing of low level DNA. <i>Forensic Science International: Genetics</i> , 2009 , 3, 255-60	4.3	29
34	Low copy number typing Where next?. <i>Forensic Science International: Genetics Supplement Series</i> , 2009 , 2, 553-555	0.5	4
33	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
32	Empirical support for the reliability of DNA interpretation in Croatia. <i>Forensic Science International: Genetics</i> , 2008 , 3, 50-3	4.3	5
31	Comparing the growth and effectiveness of forensic DNA databases. <i>Forensic Science International: Genetics Supplement Series</i> , 2008 , 1, 667-668	0.5	10
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	Effectiveness of familial searches. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2008 , 48, 164-7	2	32
27	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
26	The appropriate use of subpopulation corrections for differences in endogamous communities. <i>Forensic Science International</i> , 2007 , 168, 106-11	2.6	7
25	A comprehensive analysis of microsatellite diversity in Aboriginal Australians. <i>Journal of Human Genetics</i> , 2007 , 52, 712-728	4.3	16
24	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
23	Use of subpopulation data in Australian forensic DNA casework. <i>Forensic Science International: Genetics</i> , 2007 , 1, 238-46	4.3	11
22	Empirical testing of estimated DNA frequencies. <i>Forensic Science International: Genetics</i> , 2007 , 1, 267-72	4.3	17
21	How reliable is the sub-population model in DNA testimony?. <i>Forensic Science International</i> , 2006 , 157, 144-8	2.6	20
20	Is the 2p rule always conservative?. <i>Forensic Science International</i> , 2006 , 159, 206-9	2.6	36
19	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
18	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
17	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
16	PENDULUM--a guideline-based approach to the interpretation of STR mixtures. <i>Forensic Science International</i> , 2005 , 148, 181-9	2.6	66
15	Relatedness and DNA: are we taking it seriously enough?. <i>Forensic Science International</i> , 2005 , 152, 115-9	2.6	29
14	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
13	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
12	What is the magnitude of the subpopulation effect?. <i>Forensic Science International</i> , 2003 , 135, 1-8	2.6	32
11	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

10	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
9	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
8	Interpreting DNA Mixtures in Structured Populations. <i>Journal of Forensic Sciences</i> , 1999 , 44, 12028J	1.8	62
7	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
6	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
5	Synthesis and characterization of masked aminopyrazolecarboxylic acid synthons. <i>Journal of Organic Chemistry</i> , 1989 , 54, 428-431	4.2	43
4	Some aspects of the Bayesian approach to evidence evaluation. <i>Journal - Forensic Science Society</i> , 1989 , 29, 317-324		39
3	132,173-Cyclophosphoramide enol, the first porphyrin isolated from a sponge. <i>Tetrahedron Letters</i> , 1986 , 27, 2177-2178	2	74
2	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
1	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