

# Duncan Taylor

## List of Publications by Year in descending order

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Version: 2024-02-01

123  
papers

3,094  
citations

168829

31  
h-index

232693

48  
g-index

126  
all docs

126  
docs citations

126  
times ranked

981  
citing authors

#	ARTICLE	IF	CITATIONS
1	Investigation of X-STR haplotype diversity in the Australian Aboriginal population. Australian Journal of Forensic Sciences, 2023, 55, 547-559.	0.7	0
2	Using a multi-head, convolutional neural network with data augmentation to improve electropherogram classification performance. Forensic Science International: Genetics, 2022, 56, 102605.	1.6	5
3	Using big data from probabilistic genotyping to solve crime. Forensic Science International: Genetics, 2022, 57, 102631.	1.6	4
4	Exploring tapelifts as a method for dual workflow STR amplification. Forensic Science International: Genetics, 2022, 57, 102653.	1.6	1
5	What's on the bag? The DNA composition of evidence bags pre- and post-exhibit examination. Forensic Science International: Genetics, 2022, 57, 102652.	1.6	3
6	Analysis of mixed DNA profiles from the RapidHit <sup>®</sup> , <sup>®</sup> ID platform using probabilistic genotyping software STRmix <sup>®</sup> , <sup>®</sup> . Forensic Science International: Genetics, 2022, 58, 102664.	1.6	7
7	The potential for investigator-mediated contamination to occur during routine search activities. Forensic Science, Medicine, and Pathology, 2022, , 1.	0.6	0
8	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
9	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
10	When evaluating DNA evidence within a likelihood ratio framework, should the propositions be exhaustive?. Forensic Science International: Genetics, 2021, 50, 102406.	1.6	13
11	Evaluation of a fluorescent dye to visualize touch DNA on various substrates. Journal of Forensic Sciences, 2021, 66, 1435-1442.	0.9	8
12	How many cells are required for successful DNA profiling?. Forensic Science International: Genetics, 2021, 51, 102453.	1.6	31
13	Probabilistic interpretation of the Amelogenin locus. Forensic Science International: Genetics, 2021, 52, 102462.	1.6	0
14	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
15	Comparing multiple POI to DNA mixtures. Forensic Science International: Genetics, 2021, 52, 102481.	1.6	12
16	The importance of considering common sources of unknown DNA when evaluating findings given activity level propositions. Forensic Science International: Genetics, 2021, 53, 102518.	1.6	5
17	Can a reference "match" an evidence profile if these have no loci in common?. Forensic Science International: Genetics, 2021, 53, 102520.	1.6	1
18	The level of DNA an individual transfers to untouched items in their immediate surroundings. Forensic Science International: Genetics, 2021, 54, 102561.	1.6	10

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19	A comparison of likelihood ratios obtained from EuroForMix and STRmix <sup>®</sup> . Journal of Forensic Sciences, 2021, 66, 2138-2155.	0.9	14
20	Evaluating DNA evidence possibly involving multiple (mixed) samples, common donors and related contributors. Forensic Science International: Genetics, 2021, 54, 102532.	1.6	13
21	A Review of Probabilistic Genotyping Systems: EuroForMix, DNASTatistX and STRmix <sup>®</sup> . Genes, 2021, 12, 1559.	1.0	25
22	Validation of a neural network approach for STR typing to replace human reading. Forensic Science International: Genetics, 2021, 55, 102591.	1.6	5
23	Comparison of six commercially available STR kits for their application to touch DNA using direct PCR. Forensic Science International: Reports, 2021, 4, 100243.	0.4	2
24	DNA commission of the International society for forensic genetics: Assessing the value of forensic biological evidence - Guidelines highlighting the importance of propositions. Part II: Evaluation of biological traces considering activity level propositions. Forensic Science International: Genetics, 2020, 44, 102186.	1.6	59
25	Response to: Commentary on: Bright et al. (2018) Internal validation of STRmix <sup>®</sup> . "A multi laboratory response to PCAST, Forensic Science International: Genetics, 34: 11-24. Forensic Science International: Genetics, 2020, 44, 102198.	1.6	2
26	Structuring cases into propositions, assumptions, and undisputed case information. Forensic Science International: Genetics, 2020, 44, 102199.	1.6	8
27	The interpretation of forensic DNA profiles: an historical perspective. Journal of the Royal Society of New Zealand, 2020, 50, 211-225.	1.0	2
28	Combining evidence across multiple mixed DNA profiles for improved resolution of a donor when a common contributor can be assumed. Forensic Science International: Genetics, 2020, 49, 102375.	1.6	16
29	Are low LR's reliable?. Forensic Science International: Genetics, 2020, 49, 102350.	1.6	10
30	How can courts take into account the uncertainty in a likelihood ratio?. Forensic Science International: Genetics, 2020, 48, 102361.	1.6	5
31	The use of Bayesian Networks and simulation methods to identify the variables impacting the value of evidence assessed under activity level propositions in stabbing cases. Forensic Science International: Genetics, 2020, 48, 102334.	1.6	9
32	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
33	DNA commission of the International Society of Forensic Genetics (ISFG): Recommendations on the interpretation of Y-STR results in forensic analysis. Forensic Science International: Genetics, 2020, 48, 102308.	1.6	42
34	Investigating the position and level of DNA transfer to undergarments during digital sexual assault. Forensic Science International: Genetics, 2020, 47, 102316.	1.6	6
35	Successful STR amplification of post-blast IED samples by fluorescent visualisation and direct PCR. Forensic Science International: Genetics, 2020, 46, 102256.	1.6	9
36	Examining the additivity of peak heights in forensic DNA profiles. Australian Journal of Forensic Sciences, 2020, , 1-15.	0.7	4

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37	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
38	The Probabilistic Genotyping Software <scp>STR</scp>mix: Utility and Evidence for its Validity. Journal of Forensic Sciences, 2019, 64, 393-405.	0.9	33
39	Testing whether stutter and low-level DNA peaks are additive. Forensic Science International: Genetics, 2019, 43, 102166.	1.6	7
40	A guide to results and diagnostics within a STRmix <sup>®</sup> report. Wiley Interdisciplinary Reviews Forensic Science, 2019, 1, .	1.2	18
41	Using Bayesian networks to track DNA movement through complex transfer scenarios. Forensic Science International: Genetics, 2019, 42, 69-80.	1.6	13
42	The first Australian conviction resulting from a familial search. Australian Journal of Forensic Sciences, 2019, 51, S56-S59.	0.7	7
43	An introductory guide to evaluative reporting in forensic science. Australian Journal of Forensic Sciences, 2019, 51, S247-S251.	0.7	14
44	Analysis of the South Australian Aboriginal population using the Global AIMs Nano ancestry test. Forensic Science International: Genetics, 2019, 41, 34-41.	1.6	2
45	Comment on "DNA mixtures interpretation" A proof-of-concept multi-software comparison highlighting different probabilistic methods' performances on challenging samples by Alladio et al.. Forensic Science International: Genetics, 2019, 40, e248-e251.	1.6	6
46	The efficacy of DNA mixture to mixture matching. Forensic Science International: Genetics, 2019, 41, 64-71.	1.6	17
47	Population genetic analysis of Yfiler <sup>®</sup> Plus haplotype data for three South Australian populations. Forensic Science International: Genetics, 2019, 41, e23-e25.	1.6	11
48	Inter-sample contamination detection using mixture deconvolution comparison. Forensic Science International: Genetics, 2019, 40, 160-167.	1.6	7
49	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
50	STRmix <sup>®</sup> collaborative exercise on DNA mixture interpretation. Forensic Science International: Genetics, 2019, 40, 1-8.	1.6	39
51	The generalisability of artificial neural networks used to classify electrophoretic data produced under different conditions. Forensic Science International: Genetics, 2019, 38, 181-184.	1.6	9
52	Likelihood ratio development for mixed Y-STR profiles. Forensic Science International: Genetics, 2018, 35, 82-96.	1.6	22
53	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
54	A template for constructing Bayesian networks in forensic biology cases when considering activity level propositions. Forensic Science International: Genetics, 2018, 33, 136-146.	1.6	41

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55	Internal validation of STRmix <sup>®</sup> , <sup>®</sup> “ A multi laboratory response to PCAST. Forensic Science International: Genetics, 2018, 34, 11-24.	1.6	72
56	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
57	DNA commission of the International society for forensic genetics: Assessing the value of forensic biological evidence - Guidelines highlighting the importance of propositions. Forensic Science International: Genetics, 2018, 36, 189-202.	1.6	83
58	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
59	Modelling the dependence structure of Y-STR haplotypes using graphical models. Forensic Science International: Genetics, 2018, 37, 29-36.	1.6	11
60	A sensitivity analysis to determine the robustness of STRmix <sup>®</sup> , <sup>®</sup> with respect to laboratory calibration. Forensic Science International: Genetics, 2018, 35, 113-122.	1.6	25
61	Evaluation of forensic genetics findings given activity level propositions: A review. Forensic Science International: Genetics, 2018, 36, 34-49.	1.6	88
62	DNA profiles generated from a range of touched sample types. Forensic Science International: Genetics, 2018, 36, 13-19.	1.6	45
63	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
64	Helping to distinguish primary from secondary transfer events for trace DNA. Forensic Science International: Genetics, 2017, 28, 155-177.	1.6	55
65	Typing DNA profiles from previously enhanced fingerprints using direct PCR. Forensic Science International: Genetics, 2017, 29, 276-282.	1.6	18
66	Allele frequency database for GlobalFiler <sup>®</sup> , <sup>®</sup> STR loci in Australian and New Zealand populations. Forensic Science International: Genetics, 2017, 28, e38-e40.	1.6	25
67	Internal validation of STRmix <sup>®</sup> , <sup>®</sup> for the interpretation of single source and mixed DNA profiles. Forensic Science International: Genetics, 2017, 29, 126-144.	1.6	74
68	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
69	Importance sampling allows Hd true tests of highly discriminating DNA profiles. Forensic Science International: Genetics, 2017, 27, 74-81.	1.6	14
70	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
71	The paradigm shift in DNA profile interpretation. Forensic Science International: Genetics, 2017, 31, e24-e32.	1.6	15
72	An artificial neural network system to identify alleles in reference electropherograms. Forensic Science International: Genetics, 2017, 30, 114-126.	1.6	13

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73	A comment on the PCAST report: Skip the "match"/"non-match" stage. <i>Forensic Science International</i> , 2017, 272, e7-e9.	1.3	25
74	Commentary: A "Source" of Error: Computer Code, Criminal Defendants, and the Constitution. <i>Frontiers in Genetics</i> , 2017, 8, 33.	1.1	13
75	Evaluation of Forensic DNA Traces When Propositions of Interest Relate to Activities: Analysis and Discussion of Recurrent Concerns. <i>Frontiers in Genetics</i> , 2016, 7, 215.	1.1	35
76	Antiquity and diversity of aboriginal Australian Y-chromosomes. <i>American Journal of Physical Anthropology</i> , 2016, 159, 367-381.	2.1	26
77	A Practical Guide for the Formulation of Propositions in the Bayesian Approach to DNA Evidence Interpretation in an Adversarial Environment. <i>Journal of Forensic Sciences</i> , 2016, 61, 186-195.	0.9	37
78	Sampling Effects. , 2016, , 181-202.		0
79	Developmental validation of STRmix <sup>®</sup> , expert software for the interpretation of forensic DNA profiles. <i>Forensic Science International: Genetics</i> , 2016, 23, 226-239.	1.6	110
80	Using sensitivity analyses in Bayesian Networks to highlight the impact of data paucity and direct future analyses: a contribution to the debate on measuring and reporting the precision of likelihood ratios. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2016, 56, 402-410.	1.3	38
81	Teaching artificial intelligence to read electropherograms. <i>Forensic Science International: Genetics</i> , 2016, 25, 10-18.	1.6	21
82	Is technology the death of expertise?. <i>Forensic Science International: Genetics</i> , 2016, 24, e1-e3.	1.6	1
83	DNA profiles from clothing fibers using direct PCR. <i>Forensic Science, Medicine, and Pathology</i> , 2016, 12, 331-335.	0.6	23
84	The evaluation of exclusionary DNA results: a discussion of issues in <i>R. v. Drummond</i> . <i>Law, Probability and Risk</i> , 2016, 15, 175-197.	1.2	10
85	Probabilistically determining the cellular source of DNA derived from differential extractions in sexual assault scenarios. <i>Forensic Science International: Genetics</i> , 2016, 24, 124-135.	1.6	10
86	Using probabilistic theory to develop interpretation guidelines for Y-STR profiles. <i>Forensic Science International: Genetics</i> , 2016, 21, 22-34.	1.6	9
87	Population-specific F values for forensic STR markers: A worldwide survey. <i>Forensic Science International: Genetics</i> , 2016, 23, 91-100.	1.6	73
88	Evaluating forensic biology results given source level propositions. <i>Forensic Science International: Genetics</i> , 2016, 21, 54-67.	1.6	32
89	Observations of DNA transfer within an operational Forensic Biology Laboratory. <i>Forensic Science International: Genetics</i> , 2016, 23, 33-49.	1.6	32
90	Factors affecting peak height variability for short tandem repeat data. <i>Forensic Science International: Genetics</i> , 2016, 21, 126-133.	1.6	25

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91	Validating multiplexes for use in conjunction with modern interpretation strategies. <i>Forensic Science International: Genetics</i> , 2016, 20, 6-19.	1.6	50
92	Successful direct amplification of nuclear markers from single dog hairs using DogFiler multiplex. <i>Electrophoresis</i> , 2015, 36, 2082-2085.	1.3	4
93	Direct PCR Improves the Recovery of DNA from Various Substrates. <i>Journal of Forensic Sciences</i> , 2015, 60, 1558-1562.	0.9	48
94	Testing likelihood ratios produced from complex DNA profiles. <i>Forensic Science International: Genetics</i> , 2015, 16, 165-171.	1.6	39
95	Investigating a common approach to DNA profile interpretation using probabilistic software. <i>Forensic Science International: Genetics</i> , 2015, 16, 121-131.	1.6	24
96	DNA profiles from fingernails using direct PCR. <i>Forensic Science, Medicine, and Pathology</i> , 2015, 11, 99-103.	0.6	30
97	DNA profiles from fingermarks: A mock case study. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e154-e155.	0.1	11
98	Do low template DNA profiles have useful quantitative data?. <i>Forensic Science International: Genetics</i> , 2015, 16, 13-16.	1.6	26
99	A series of recommended tests when validating probabilistic DNA profile interpretation software. <i>Forensic Science International: Genetics</i> , 2015, 14, 125-131.	1.6	36
100	Australian population data for the twenty Promega PowerPlex 21 short tandem repeat loci. <i>Australian Journal of Forensic Sciences</i> , 2014, 46, 442-446.	0.7	7
101	Interpreting forensic DNA profiling evidence without specifying the number of contributors. <i>Forensic Science International: Genetics</i> , 2014, 13, 269-280.	1.6	40
102	The "factor of two" issue in mixed DNA profiles. <i>Journal of Theoretical Biology</i> , 2014, 363, 300-306.	0.8	36
103	Considering relatives when assessing the evidential strength of mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2014, 13, 259-263.	1.6	30
104	Searching mixed DNA profiles directly against profile databases. <i>Forensic Science International: Genetics</i> , 2014, 9, 102-110.	1.6	62
105	An illustration of the effect of various sources of uncertainty on DNA likelihood ratio calculations. <i>Forensic Science International: Genetics</i> , 2014, 11, 56-63.	1.6	34
106	Characterisation of novel and rare Y-chromosome short tandem repeat alleles in self-declared South Australian Aboriginal database. <i>International Journal of Legal Medicine</i> , 2014, 128, 27-31.	1.2	3
107	Helping formulate propositions in forensic DNA analysis. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2014, 54, 258-261.	1.3	27
108	Using continuous DNA interpretation methods to revisit likelihood ratio behaviour. <i>Forensic Science International: Genetics</i> , 2014, 11, 144-153.	1.6	59

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109	Utilising allelic dropout probabilities estimated by logistic regression in casework. <i>Forensic Science International: Genetics</i> , 2014, 9, 9-11.	1.6	23
110	Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. <i>Human Mutation</i> , 2014, 35, 1021-1032.	1.1	151
111	Modeling forward stutter: Toward increased objectivity in forensic <scp>DNA</scp> interpretation. <i>Electrophoresis</i> , 2014, 35, 3152-3157.	1.3	22
112	Successful direct amplification of nuclear markers from a single hair follicle. <i>Forensic Science, Medicine, and Pathology</i> , 2013, 9, 238-243.	0.6	40
113	Application of direct PCR in forensic casework. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e47-e48.	0.1	31
114	Developing allelic and stutter peak height models for a continuous method of DNA interpretation. <i>Forensic Science International: Genetics</i> , 2013, 7, 296-304.	1.6	130
115	Optimising direct PCR from anagen hair samples. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e109-e110.	0.1	17
116	Genetic profiling from challenging samples: Direct PCR of touch DNA. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e224-e225.	0.1	34
117	The interpretation of single source and mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2013, 7, 516-528.	1.6	237
118	Degradation of forensic DNA profiles. <i>Australian Journal of Forensic Sciences</i> , 2013, 45, 445-449.	0.7	56
119	Haplotype data for 16 Y-chromosome STR loci in Aboriginal and Caucasian populations in South Australia. <i>Forensic Science International: Genetics</i> , 2012, 6, e187-e188.	1.6	12
120	An investigation of admixture in an Australian Aboriginal Y-chromosome STR database. <i>Forensic Science International: Genetics</i> , 2012, 6, 532-538.	1.6	21
121	Knowing your DNA database: Issues with determining ancestral Y haplotypes in a Y-File database. <i>Forensic Science International: Genetics Supplement Series</i> , 2009, 2, 411-412.	0.1	2
122	South Australian Aboriginal sub-population data for the nine AMPFISTRÂ® Profiler Plusâ„¢ short tandem repeat (STR) loci. <i>Forensic Science International: Genetics</i> , 2008, 2, e27-e30.	1.6	2
123	The effect of a user selected number of contributors within the LR assignment. <i>Australian Journal of Forensic Sciences</i> , 0, , 1-14.	0.7	1