

# Degradation of forensic DNA profiles

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The interpretation of single source and mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2013, 7, 516-528.	1.6	237
2	Statistical Evaluation of Forensic DNA Profile Evidence. <i>Annual Review of Statistics and Its Application</i> , 2014, 1, 361-384.	4.1	65
3	Comparison of the performance of different models for the interpretation of low level mixed <scp>DNA</scp> profiles. <i>Electrophoresis</i> , 2014, 35, 3125-3133.	1.3	36
4	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, 208-214.	1.6	44
5	Investigation into stutter ratio variance. <i>Australian Journal of Forensic Sciences</i> , 2014, 46, 313-316.	0.7	0
6	Searching mixed DNA profiles directly against profile databases. <i>Forensic Science International: Genetics</i> , 2014, 9, 102-110.	1.6	62
7	Using continuous DNA interpretation methods to revisit likelihood ratio behaviour. <i>Forensic Science International: Genetics</i> , 2014, 11, 144-153.	1.6	59
9	Analysis of Forensic DNA Mixtures with Artefacts. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2015, 64, 1-48.	0.5	90
10	Investigating a common approach to DNA profile interpretation using probabilistic software. <i>Forensic Science International: Genetics</i> , 2015, 16, 121-131.	1.6	24
11	Uncertainty in the number of contributors in the proposed new CODIS set. <i>Forensic Science International: Genetics</i> , 2015, 19, 207-211.	1.6	33
12	The variability in likelihood ratios due to different mechanisms. <i>Forensic Science International: Genetics</i> , 2015, 14, 187-190.	1.6	27
13	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
14	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.	2.7	76
16	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
17	Stabbing simulations and DNA transfer. <i>Forensic Science International: Genetics</i> , 2016, 22, 73-80.	1.6	47
18	Factors affecting peak height variability for short tandem repeat data. <i>Forensic Science International: Genetics</i> , 2016, 21, 126-133.	1.6	25
19	Validating multiplexes for use in conjunction with modern interpretation strategies. <i>Forensic Science International: Genetics</i> , 2016, 20, 6-19.	1.6	50
20	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.	0.7	11

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21	Helping to distinguish primary from secondary transfer events for trace DNA. Forensic Science International: Genetics, 2017, 28, 155-177.	1.6	55
22	Characterisation of artefacts and drop-in events using STR-validator and single-cell analysis. Forensic Science International: Genetics, 2017, 30, 57-65.	1.6	24
23	Characterization of degradation and heterozygote balance by simulation of the forensic DNA analysis process. International Journal of Legal Medicine, 2017, 131, 303-317.	1.2	25
24	Importance sampling allows Hd true tests of highly discriminating DNA profiles. Forensic Science International: Genetics, 2017, 27, 74-81.	1.6	14
25	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
26	Development and validation of open-source software for DNA mixture interpretation based on a quantitative continuous model. PLoS ONE, 2017, 12, e0188183.	1.1	42
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28	DNA mixtures interpretation â€œ A proof-of-concept multi-software comparison highlighting different probabilistic methodsâ€™ performances on challenging samples. Forensic Science International: Genetics, 2018, 37, 143-150.	1.6	44
29	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
30	Data on likelihood ratios of two-person DNA mixtures interpreted using semi- and fully continuous systems. Data in Brief, 2019, 26, 104455.	0.5	0
31	A guide to results and diagnostics within a STRmixâ„¢ report. Wiley Interdisciplinary Reviews Forensic Science, 2019, 1, .	1.2	18
32	Probabilistic approaches to interpreting two-person DNA mixtures from post-coital specimens. Forensic Science International, 2019, 300, 157-163.	1.3	4
33	Inter-sample contamination detection using mixture deconvolution comparison. Forensic Science International: Genetics, 2019, 40, 160-167.	1.6	7
34	A comparative study for the isolation of exogenous trace DNA from fingernails. Forensic Science International: Genetics, 2019, 39, 119-128.	1.6	3
35	Systematic evaluation of STRmixâ„¢ performance on degraded DNA profile data. Forensic Science International: Genetics, 2020, 44, 102174.	1.6	8
36	Low-template DNA. , 2020, , 111-128.		0
37	Towards developing forensically relevant single-cell pipelines by incorporating direct-to-PCR extraction: compatibility, signal quality, and allele detection. International Journal of Legal Medicine, 2021, 135, 727-738.	1.2	12
38	Modeling allelic analyte signals for aSTRs in NGS DNA profiles. Journal of Forensic Sciences, 2021, 66, 1234-1245.	0.9	8

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39	DNA degradation in human teeth exposed to thermal stress. <i>Scientific Reports</i> , 2021, 11, 12118.	1.6	7
41	Evaluating DNA evidence possibly involving multiple (mixed) samples, common donors and related contributors. <i>Forensic Science International: Genetics</i> , 2021, 54, 102532.	1.6	13
42	A Review of Probabilistic Genotyping Systems: EuroForMix, DNASTatistX and STRmix <sup>®</sup> . <i>Genes</i> , 2021, 12, 1559.	1.0	25
44	MaSTR <sup>®</sup> : an effective probabilistic genotyping tool for interpretation of STR mixtures associated with differentially degraded DNA. <i>International Journal of Legal Medicine</i> , 2022, 136, 433-446.	1.2	4
45	High-quality data from a forensically relevant single-cell pipeline enabled by low PBS and proteinase K concentrations. <i>Journal of Forensic Sciences</i> , 2022, 67, 697-706.	0.9	5
47	Assessing the utility of quantitative and qualitative metrics in the DNA quantification process of skeletal remains for autosomal and Y-chromosome STR amplification purposes. <i>Forensic Science International: Genetics</i> , 2022, 60, 102751.	1.6	2
48	Developmental Validation of the <i>forensic</i> GEM Universal Kit for the Extraction of Genomic DNA. <i>Forensic Genomics</i> , 2022, 2, 71-80.	0.3	0
49	Limitations of qPCR to estimate DNA quantity: An RFU method to facilitate inter-laboratory comparisons for activity level, and general applicability. <i>Forensic Science International: Genetics</i> , 2022, 61, 102777.	1.6	4
50	Developmental validation of STRmix <sup>®</sup> NGS, a probabilistic genotyping tool for the interpretation of autosomal STRs from forensic profiles generated using NGS. <i>Forensic Science International: Genetics</i> , 2023, 62, 102804.	1.6	1
51	Using unique molecular identifiers to improve allele calling in low-template mixtures. <i>Forensic Science International: Genetics</i> , 2023, 63, 102807.	1.6	3
52	Genotyping and sequencing of DNA recovered from human skeletal remains using capillary electrophoresis (CE). , 2023, , 285-323.		0