

# Degradation of forensic DNA profiles

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The interpretation of single source and mixed DNA profiles. Forensic Science International: Genetics, 2013, 7, 516-528.	3.1	237
2	Statistical Evaluation of Forensic DNA Profile Evidence. Annual Review of Statistics and Its Application, 2014, 1, 361-384.	7.0	65
3	Comparison of the performance of different models for the interpretation of low level mixed <scp>DNA</scp> profiles. Electrophoresis, 2014, 35, 3125-3133.	2.4	36
4	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
5	Investigation into stutter ratio variance. Australian Journal of Forensic Sciences, 2014, 46, 313-316.	1.2	0
6	Searching mixed DNA profiles directly against profile databases. Forensic Science International: Genetics, 2014, 9, 102-110.	3.1	62
7	Using continuous DNA interpretation methods to revisit likelihood ratio behaviour. Forensic Science International: Genetics, 2014, 11, 144-153.	3.1	59
9	Analysis of Forensic DNA Mixtures with Artefacts. Journal of the Royal Statistical Society Series C: Applied Statistics, 2015, 64, 1-48.	1.0	90
10	Investigating a common approach to DNA profile interpretation using probabilistic software. Forensic Science International: Genetics, 2015, 16, 121-131.	3.1	24
11	Uncertainty in the number of contributors in the proposed new CODIS set. Forensic Science International: Genetics, 2015, 19, 207-211.	3.1	33
12	The variability in likelihood ratios due to different mechanisms. Forensic Science International: Genetics, 2015, 14, 187-190.	3.1	27
13	A series of recommended tests when validating probabilistic DNA profile interpretation software. Forensic Science International: Genetics, 2015, 14, 125-131.	3.1	36
14	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
16	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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19	Validating multiplexes for use in conjunction with modern interpretation strategies. Forensic Science International: Genetics, 2016, 20, 6-19.	3.1	50
20	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

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21	Helping to distinguish primary from secondary transfer events for trace DNA. Forensic Science International: Genetics, 2017, 28, 155-177.	3.1	55
22	Characterisation of artefacts and drop-in events using STR-validator and single-cell analysis. Forensic Science International: Genetics, 2017, 30, 57-65.	3.1	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.	2.2	25
24	Importance sampling allows Hd true tests of highly discriminating DNA profiles. Forensic Science International: Genetics, 2017, 27, 74-81.	3.1	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.	3.1	13
26	Development and validation of open-source software for DNA mixture interpretation based on a quantitative continuous model. PLoS ONE, 2017, 12, e0188183.	2.5	42
27	Statistical Modeling of Short-Tandem Repeat Capillary Electrophoresis Profiles. , 2018, , .		1
28	DNA mixtures interpretation “ A proof-of-concept multi-software comparison highlighting different probabilistic methods”™ performances on challenging samples. Forensic Science International: Genetics, 2018, 37, 143-150.	3.1	44
29	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
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33	Inter-sample contamination detection using mixture deconvolution comparison. Forensic Science International: Genetics, 2019, 40, 160-167.	3.1	7
34	A comparative study for the isolation of exogenous trace DNA from fingernails. Forensic Science International: Genetics, 2019, 39, 119-128.	3.1	3
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38	Modeling allelic analyte signals for aSTRs in NGS DNA profiles. Journal of Forensic Sciences, 2021, 66, 1234-1245.	1.6	8

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41	Evaluating DNA evidence possibly involving multiple (mixed) samples, common donors and related contributors. Forensic Science International: Genetics, 2021, 54, 102532.	3.1	13
42	A Review of Probabilistic Genotyping Systems: EuroForMix, DNASTatistX and STRmix <sup>®</sup> . Genes, 2021, 12, 1559.	2.4	25
44	MaSTR <sup>®</sup> : an effective probabilistic genotyping tool for interpretation of STR mixtures associated with differentially degraded DNA. International Journal of Legal Medicine, 2022, 136, 433-446.	2.2	4
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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. Forensic Science International: Genetics, 2022, 60, 102751.	3.1	2
48	Developmental Validation of the <i>forensic</i> GEM Universal Kit for the Extraction of Genomic DNA. Forensic Genomics, 2022, 2, 71-80.	0.5	0
49	Limitations of qPCR to estimate DNA quantity: An RFU method to facilitate inter-laboratory comparisons for activity level, and general applicability. Forensic Science International: Genetics, 2022, 61, 102777.	3.1	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. Forensic Science International: Genetics, 2023, 62, 102804.	3.1	1
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52	Genotyping and sequencing of DNA recovered from human skeletal remains using capillary electrophoresis (CE). , 2023, , 285-323.		0
53	Validation and expansion of sex determination method through analysis of human hair using electrothermal vaporization coupled to inductively coupled plasma optical emission spectrometry. Journal of Analytical Atomic Spectrometry, 0, , .	3.0	0
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