

# Michael D Coble

## List of Publications by Year in descending order

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Version: 2024-02-01

88  
papers

3,712  
citations

182225

30  
h-index

150775

59  
g-index

92  
all docs

92  
docs citations

92  
times ranked

2716  
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring likelihood ratios assigned for siblings of the true mixture contributor as an alternate contributor. <i>Journal of Forensic Sciences</i> , 2022, 67, 1167-1175.	0.9	6
2	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, 59, 102709.	1.6	7
3	A new implementation of a semi-continuous method for DNA mixture interpretation. <i>Forensic Science International: Reports</i> , 2022, 6, 100281.	0.4	0
4	A description of the likelihood ratios in the probabilistic genotyping software STRmix <sup>®</sup> . <i>Wiley Interdisciplinary Reviews Forensic Science</i> , 2020, 2, .	1.2	8
5	Mitochondrial DNA control region variation in Lebanon, Jordan, and Bahrain. <i>Forensic Science International: Genetics</i> , 2019, 42, 99-102.	1.6	6
6	Probabilistic genotyping software: An overview. <i>Forensic Science International: Genetics</i> , 2019, 38, 219-224.	1.6	116
7	STRmix <sup>®</sup> collaborative exercise on DNA mixture interpretation. <i>Forensic Science International: Genetics</i> , 2019, 40, 1-8.	1.6	39
8	Expanding beyond the current core STR loci: An exploration of 73 STR markers with increased diversity for enhanced DNA mixture deconvolution. <i>Forensic Science International: Genetics</i> , 2019, 38, 121-129.	1.6	23
9	NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis. <i>Forensic Science International: Genetics</i> , 2018, 37, 172-179.	1.6	35
10	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.	1.3	12
11	The peopling of South America and the trans-Andean gene flow of the first settlers. <i>Genome Research</i> , 2018, 28, 767-779.	2.4	59
12	NIST interlaboratory studies involving DNA mixtures (MIX05 and MIX13): Variation observed and lessons learned. <i>Forensic Science International: Genetics</i> , 2018, 37, 81-94.	1.6	64
13	Initial assessment of the Precision ID Globalfiler Mixture ID panel on the Ion Torrent S5XL DNA sequencer and Converge v2.0 software. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e94-e95.	0.1	1
14	A collaborative EDNAP exercise on SNaPshot <sup>®</sup> -based mtDNA control region typing. <i>Forensic Science International: Genetics</i> , 2017, 26, 77-84.	1.6	5
15	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	D5S2500 is an ambiguously characterized STR: Identification and description of forensic microsatellites in the genomics age.. <i>Forensic Science International: Genetics</i> , 2016, 23, 19-24.	1.6	21
17	Expected net gain data of low-template DNA analyses. <i>Data in Brief</i> , 2016, 8, 375-386.	0.5	5
18	DNA Commission of the International Society for Forensic Genetics: Recommendations on the validation of software programs performing biostatistical calculations for forensic genetics applications. <i>Forensic Science International: Genetics</i> , 2016, 25, 191-197.	1.6	72

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19	Genetic mapping of 15 human X chromosomal forensic short tandem repeat (STR) loci by means of multi-core parallelization. <i>Forensic Science International: Genetics</i> , 2016, 25, 39-44.	1.6	21
20	Low-template DNA: A single DNA analysis or two replicates?. <i>Forensic Science International</i> , 2016, 264, 139-145.	1.3	16
21	The mitochondrial landscape of African Americans: An examination of more than 2500 control region haplotypes from 22 U.S. locations. <i>Forensic Science International: Genetics</i> , 2016, 22, 139-148.	1.6	10
22	Sequence-based analysis of stutter at STR loci: Characterization and utility. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e456-e458.	0.1	17
23	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
24	The mitochondrial DNA history of a former native American village in northern Uruguay. <i>American Journal of Human Biology</i> , 2015, 27, 407-416.	0.8	8
25	Demographic History of Indigenous Populations in Mesoamerica Based on mtDNA Sequence Data. <i>PLoS ONE</i> , 2015, 10, e0131791.	1.1	29
26	Comparison of the performance of different models for the interpretation of low level mixed DNA profiles. <i>Electrophoresis</i> , 2014, 35, 3125-3133.	1.3	36
27	Population genetic data for 15 X chromosomal short tandem repeat markers in three U.S. populations. <i>Forensic Science International: Genetics</i> , 2014, 8, 64-67.	1.6	10
28	Mitochondrial control region variation in a Korean population sample. <i>International Journal of Legal Medicine</i> , 2014, 128, 745-746.	1.2	3
29	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. <i>Forensic Science International: Genetics</i> , 2014, 12, 12-23.	1.6	214
30	Comparison of base composition analysis and Sanger sequencing of mitochondrial DNA for four U.S. population groups. <i>Forensic Science International: Genetics</i> , 2014, 8, 226-232.	1.6	4
31	Mutation rates of 15 X chromosomal short tandem repeat markers. <i>International Journal of Legal Medicine</i> , 2014, 128, 579-587.	1.2	16
32	Characterising the STR locus D6S1043 and examination of its effect on stutter rates. <i>Forensic Science International: Genetics</i> , 2014, 8, 20-23.	1.6	21
33	Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. <i>Human Mutation</i> , 2014, 35, 1021-1032.	1.1	151
34	Nomenclature update and allele repeat structure for the markers DYS518 and DYS449. <i>Forensic Science International: Genetics</i> , 2014, 13, e3.	1.6	5
35	Additional sequence characterization of NIST SRM 2391c: PCR-Based DNA Profiling Standard. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e133-e134.	0.1	0
36	A gonosomal marker multiplex to aid in mixture interpretation. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e184-e185.	0.1	1

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37	Demographic expansions in South America: Enlightening a complex scenario with genetic and linguistic data. <i>American Journal of Physical Anthropology</i> , 2013, 150, 453-463.	2.1	31
38	Developmental validation of 15 X chromosomal short tandem repeat markers. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e142-e143.	0.1	1
39	U.S. population data for 29 autosomal STR loci. <i>Forensic Science International: Genetics</i> , 2013, 7, e82-e83.	1.6	135
40	Haplotype data for 23 Y-chromosome markers in four U.S. population groups. <i>Forensic Science International: Genetics</i> , 2013, 7, e66-e68.	1.6	51
41	A cautionary note on switching mitochondrial DNA reference sequences in forensic genetics. <i>Forensic Science International: Genetics</i> , 2012, 6, e182-e184.	1.6	24
42	Assessing a novel room temperature DNA storage medium for forensic biological samples. <i>Forensic Science International: Genetics</i> , 2012, 6, 31-40.	1.6	45
43	An optimized protocol for forensic application of the PreCRâ„¢ Repair Mix to multiplex STR amplification of UV-damaged DNA. <i>Forensic Science International: Genetics</i> , 2012, 6, 498-503.	1.6	41
44	Sequence variation of mitochondrial DNA control region in North Central Venezuela. <i>Forensic Science International: Genetics</i> , 2012, 6, e131-e133.	1.6	12
45	Capillary Electrophoresis of MiniSTR Markers to Genotype Highly Degraded DNA Samples. <i>Methods in Molecular Biology</i> , 2012, 830, 31-42.	0.4	4
46	Allele frequency distribution of twelve X-chromosomal short tandem repeat markers in four U.S. population groups. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e481-e483.	0.1	12
47	The new Standard Reference Material® 2391c: PCR-based DNA profiling standard. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e355-e356.	0.1	11
48	Development and characterization of two mini-X chromosomal short tandem repeat multiplexes. <i>Forensic Science International: Genetics</i> , 2011, 5, 415-421.	1.6	29
49	Population study of fourteen X chromosomal short tandem repeat loci in a population from Bosnia and Herzegovina. <i>Forensic Science International: Genetics</i> , 2011, 5, 350-351.	1.6	10
50	Titanic's unknown child: The critical role of the mitochondrial DNA coding region in a re-identification effort. <i>Forensic Science International: Genetics</i> , 2011, 5, 231-235.	1.6	17
51	mtGenome reference population databases and the future of forensic mtDNA analysis. <i>Forensic Science International: Genetics</i> , 2011, 5, 222-225.	1.6	33
52	Autosomal SNP typing of forensic samples with the GenPlexâ„¢ HID System: Results of a collaborative study. <i>Forensic Science International: Genetics</i> , 2011, 5, 369-375.	1.6	17
53	Inspecting close maternal relatedness: Towards better mtDNA population samples in forensic databases. <i>Forensic Science International: Genetics</i> , 2011, 5, 138-141.	1.6	20
54	Mitochondrial DNA control region variation in a Kuwaiti population sample. <i>Forensic Science International: Genetics</i> , 2011, 5, e112-e113.	1.6	18

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55	Metrology needs and NIST resources for the forensic DNA community. Accreditation and Quality Assurance, 2011, 16, 293-297.	0.4	2
56	The identification of the Romanovs: Can we (finally) put the controversies to rest?. Investigative Genetics, 2011, 2, 20.	3.3	8
57	Homogeneity in mitochondrial DNA control region sequences in Swedish subpopulations. International Journal of Legal Medicine, 2010, 124, 91-98.	1.2	17
58	Evaluating self-declared ancestry of U.S. Americans with autosomal, Y-chromosomal and mitochondrial DNA. Human Mutation, 2010, 31, E1875-E1893.	1.1	86
59	Population genetic data for 17 STR markers from Lebanon. Legal Medicine, 2010, 12, 324-326.	0.6	14
60	Mystery Solved: The Identification of the Two Missing Romanov Children Using DNA Analysis. PLoS ONE, 2009, 4, e4838.	1.1	135
61	Evaluation of Modified Yfiler <sup>®</sup> , <sup>®</sup> Amplification Strategy for Compromised Samples. Croatian Medical Journal, 2009, 50, 228-238.	0.2	16
62	SNP typing of forensic samples with the GenPlex <sup>®</sup> , <sup>®</sup> HID system: A collaborative study. Forensic Science International: Genetics Supplement Series, 2009, 2, 508-509.	0.1	1
63	Uses of the NIST 26plex STR assay for human identity testing. Forensic Science International: Genetics Supplement Series, 2009, 2, 29-30.	0.1	0
64	The genetic composition of Argentina prior to the massive immigration era: Insights from matrilineages of extant criollos in central-western Argentina. Forensic Science International: Genetics Supplement Series, 2009, 2, 342-343.	0.1	2
65	Characterization of 26 MiniSTR Loci for Improved Analysis of Degraded DNA Samples. Journal of Forensic Sciences, 2008, 53, 73-80.	0.9	122
66	Identification of West Eurasian mitochondrial haplogroups by mtDNA SNP screening: Results of the 2006-2007 EDNAP collaborative exercise. Forensic Science International: Genetics, 2008, 2, 61-68.	1.6	13
67	The application of mtDNA SNPs to a forensic case. Forensic Science International: Genetics Supplement Series, 2008, 1, 295-297.	0.1	4
68	The Phylogeny of the Four Pan-American MtDNA Haplogroups: Implications for Evolutionary and Disease Studies. PLoS ONE, 2008, 3, e1764.	1.1	227
69	Forensic application of the affymetrix human mitochondrial resequencing array. Forensic Science International: Genetics, 2007, 1, 196-198.	1.6	15
70	Development and expansion of high-quality control region databases to improve forensic mtDNA evidence interpretation. Forensic Science International: Genetics, 2007, 1, 154-157.	1.6	49
71	Application of novel "mini-amplicon" STR multiplexes to high volume casework on degraded skeletal remains. Forensic Science International: Genetics, 2007, 1, 175-179.	1.6	83
72	High efficiency DNA extraction from bone by total demineralization. Forensic Science International: Genetics, 2007, 1, 191-195.	1.6	250

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73	STRs vs. SNPs: thoughts on the future of forensic DNA testing. <i>Forensic Science, Medicine, and Pathology</i> , 2007, 3, 200-205.	0.6	140
74	Characterization of mtDNA SNP typing using quantitative real-time PCR with special emphasis on heteroplasmy detection and mixture ratio assessment. <i>International Congress Series</i> , 2006, 1288, 1-3.	0.2	1
75	Characterization and performance of new MiniSTR loci for typing degraded samples. <i>International Congress Series</i> , 2006, 1288, 504-506.	0.2	3
76	Setting standards and developing technology to aid the human identity testing community. <i>International Congress Series</i> , 2006, 1288, 628-635.	0.2	2
77	The evaluation of an autosomal SNP 12-plex assay. <i>International Congress Series</i> , 2006, 1288, 61-63.	0.2	1
78	Characterization of mtDNA SNP typing and mixture ratio assessment with simultaneous real-time PCR quantification of both allelic states. <i>International Journal of Legal Medicine</i> , 2006, 120, 18-23.	1.2	11
79	Effective strategies for forensic analysis in the mitochondrial DNA coding region. <i>International Journal of Legal Medicine</i> , 2006, 120, 27-32.	1.2	34
80	Mitochondrial DNA as a Cancer Biomarker. <i>Journal of Molecular Diagnostics</i> , 2005, 7, 258-267.	1.2	77
81	Characterization of New MiniSTR Loci to Aid Analysis of Degraded DNA. <i>Journal of Forensic Sciences</i> , 2005, 50, 1-11.	0.9	254
82	Characterization of new miniSTR loci to aid analysis of degraded DNA. <i>Journal of Forensic Sciences</i> , 2005, 50, 43-53.	0.9	42
83	Single nucleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians. <i>International Journal of Legal Medicine</i> , 2004, 118, 137-146.	1.2	195
84	A multiplex allele-specific primer extension assay for forensically informative SNPs distributed throughout the mitochondrial genome. <i>International Journal of Legal Medicine</i> , 2004, 118, 147-157.	1.2	125
85	Toward increased utility of mtDNA in forensic identifications. <i>Forensic Science International</i> , 2004, 146, S147-S149.	1.3	29
86	Comparison of the complete mtDNA genome sequences of human cell lines "HL-60 and GM10742A" from individuals with pro-myelocytic leukemia and leber hereditary optic neuropathy, respectively, and the inclusion of HL-60 in the NIST human mitochondrial DNA standard reference material "SRM 2392-I. <i>Mitochondrion</i> , 2003, 2, 387-400.	1.6	24
87	Exploring the advantages of amplifying the entire extract versus splitting the extract and interpreting replicates using a continuous model of interpretation. <i>Australian Journal of Forensic Sciences</i> , 0, , 1-12.	0.7	0
88	Forensic DNA Profiling. , 0, , .		5