Michael D Coble

List of Publications by Year
in descending order

88 papers	3,712 citations	159585 30 h-index	133252 59 g-index
92 all docs	92 docs citations	92 times ranked	2490 citing authors

#	Article	IF	Citations
1	Characterization of New MiniSTR Loci to Aid Analysis of Degraded DNA. Journal of Forensic Sciences, 2005, 50, 1-11.	1.6	254
2	High efficiency DNA extraction from bone by total demineralization. Forensic Science International: Genetics, 2007, 1, 191-195.	3.1	250
3	The Phylogeny of the Four Pan-American MtDNA Haplogroups: Implications for Evolutionary and Disease Studies. PLoS ONE, 2008, 3, e1764.	2.5	227
4	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. Forensic Science International: Genetics, 2014, 12, 12-23.	3.1	214
5	Single nucleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians. International Journal of Legal Medicine, 2004, 118, 137-146.	2.2	195
6	Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. Human Mutation, 2014, 35, 1021-1032.	2.5	151
7	STRs vs. SNPs: thoughts on the future of forensic DNA testing. Forensic Science, Medicine, and Pathology, 2007, 3, 200-205.	1.4	140
8	Mystery Solved: The Identification of the Two Missing Romanov Children Using DNA Analysis. PLoS ONE, 2009, 4, e4838.	2.5	135
9	U.S. population data for 29 autosomal STR loci. Forensic Science International: Genetics, 2013, 7, e82-e83.	3.1	135
10	A multiplex allele-specific primer extension assay for forensically informative SNPs distributed throughout the mitochondrial genome. International Journal of Legal Medicine, 2004, 118, 147-157.	2.2	125
11	Characterization of 26 MiniSTR Loci for Improved Analysis of Degraded DNA Samples. Journal of Forensic Sciences, 2008, 53, 73-80.	1.6	122
12	Probabilistic genotyping software: An overview. Forensic Science International: Genetics, 2019, 38, 219-224.	3.1	116
13	Evaluating self-declared ancestry of U.S. Americans with autosomal, Y-chromosomal and mitochondrial DNA. Human Mutation, 2010, 31, E1875-E1893.	2.5	86
14	Application of novel "mini-amplicon" STR multiplexes to high volume casework on degraded skeletal remains. Forensic Science International: Genetics, 2007, 1, 175-179.	3.1	83
15	Mitochondrial DNA as a Cancer Biomarker. Journal of Molecular Diagnostics, 2005, 7, 258-267.	2.8	77
16	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
17	DNA Commission of the International Society for Forensic Genetics: Recommendations on the validation of software programs performing biostatistical calculations for forensic genetics applications. Forensic Science International: Genetics, 2016, 25, 191-197.	3.1	72
18	NIST interlaboratory studies involving DNA mixtures (MIX05 and MIX13): Variation observed and lessons learned. Forensic Science International: Genetics, 2018, 37, 81-94.	3.1	64

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19	The peopling of South America and the trans-Andean gene flow of the first settlers. Genome Research, 2018, 28, 767-779.	5.5	59
20	Haplotype data for 23 Y-chromosome markers in four U.S. population groups. Forensic Science International: Genetics, 2013, 7, e66-e68.	3.1	51
21	Development and expansion of high-quality control region databases to improve forensic mtDNA evidence interpretation. Forensic Science International: Genetics, 2007, 1, 154-157.	3.1	49
22	Assessing a novel room temperature DNA storage medium for forensic biological samples. Forensic Science International: Genetics, 2012, 6, 31-40.	3.1	45
23	Characterization of new miniSTR loci to aid analysis of degraded DNA. Journal of Forensic Sciences, 2005, 50, 43-53.	1.6	42
24	An optimized protocol for forensic application of the PreCRâ„¢ Repair Mix to multiplex STR amplification of UV-damaged DNA. Forensic Science International: Genetics, 2012, 6, 498-503.	3.1	41
25	STRmixâ„¢ collaborative exercise on DNA mixture interpretation. Forensic Science International: Genetics, 2019, 40, 1-8.	3.1	39
26	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
27	NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis. Forensic Science International: Genetics, 2018, 37, 172-179.	3.1	35
28	Effective strategies for forensic analysis in the mitochondrial DNA coding region. International Journal of Legal Medicine, 2006, 120, 27-32.	2.2	34
29	mtGenome reference population databases and the future of forensic mtDNA analysis. Forensic Science International: Genetics, 2011, 5, 222-225.	3.1	33
30	Uncertainty in the number of contributors in the proposed new CODIS set. Forensic Science International: Genetics, 2015, 19, 207-211.	3.1	33
31	Demographic expansions in South America: Enlightening a complex scenario with genetic and linguistic data. American Journal of Physical Anthropology, 2013, 150, 453-463.	2.1	31
32	Toward increased utility of mtDNA in forensic identifications. Forensic Science International, 2004, 146, S147-S149.	2.2	29
33	Development and characterization of two mini-X chromosomal short tandem repeat multiplexes. Forensic Science International: Genetics, 2011, 5, 415-421.	3.1	29
34	Demographic History of Indigenous Populations in Mesoamerica Based on mtDNA Sequence Data. PLoS ONE, 2015, 10, e0131791.	2.5	29
35	Comparison of the complete mtDNA genome sequences of human cell lines â€" HL-60 and GM10742A â€" 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 â€" SRM 2392-I. Mitochondrion, 2003, 2, 387-400.	3.4	24
36	A cautionary note on switching mitochondrial DNA reference sequences in forensic genetics. Forensic Science International: Genetics, 2012, 6, e182-e184.	3.1	24

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37	Expanding beyond the current core STR loci: An exploration of 73 STR markers with increased diversity for enhanced DNA mixture deconvolution. Forensic Science International: Genetics, 2019, 38, 121-129.	3.1	23
38	Characterising the STR locus D6S1043 and examination of its effect on stutter rates. Forensic Science International: Genetics, 2014, 8, 20-23.	3.1	21
39	D5S2500 is an ambiguously characterized STR: Identification and description of forensic microsatellites in the genomics age.. Forensic Science International: Genetics, 2016, 23, 19-24.	3.1	21
40	Genetic mapping of 15 human X chromosomal forensic short tandem repeat (STR) loci by means of multi-core parallelization. Forensic Science International: Genetics, 2016, 25, 39-44.	3.1	21
41	Inspecting close maternal relatedness: Towards better mtDNA population samples in forensic databases. Forensic Science International: Genetics, 2011, 5, 138-141.	3.1	20
42	Mitochondrial DNA control region variation in a Kuwaiti population sample. Forensic Science International: Genetics, 2011, 5, e112-e113.	3.1	18
43	Homogeneity in mitochondrial DNA control region sequences in Swedish subpopulations. International Journal of Legal Medicine, 2010, 124, 91-98.	2.2	17
44	Titanic's unknown child: The critical role of the mitochondrial DNA coding region in a re-identification effort. Forensic Science International: Genetics, 2011, 5, 231-235.	3.1	17
45	Autosomal SNP typing of forensic samples with the GenPlexâ„¢ HID System: Results of a collaborative study. Forensic Science International: Genetics, 2011, 5, 369-375.	3.1	17
46	Sequence-based analysis of stutter at STR loci: Characterization and utility. Forensic Science International: Genetics Supplement Series, 2015, 5, e456-e458.	0.3	17
47	Evaluation of Modified Yfilerâ„¢ Amplification Strategy for Compromised Samples. Croatian Medical Journal, 2009, 50, 228-238.	0.7	16
48	Mutation rates of 15 X chromosomal short tandem repeat markers. International Journal of Legal Medicine, 2014, 128, 579-587.	2.2	16
49	Low-template DNA: A single DNA analysis or two replicates?. Forensic Science International, 2016, 264, 139-145.	2.2	16
50	Forensic application of the affymetrix human mitochondrial resequencing array. Forensic Science International: Genetics, 2007, 1, 196-198.	3.1	15
51	Population genetic data for 17 STR markers from Lebanon. Legal Medicine, 2010, 12, 324-326.	1.3	14
52	Identification of West Eurasian mitochondrial haplogroups by mtDNA SNP screening: Results of the 2006â€"2007 EDNAP collaborative exercise. Forensic Science International: Genetics, 2008, 2, 61-68.	3.1	13
53	Allele frequency distribution of twelve X-chromosomal short tandem repeat markers in four U.S. population groups. Forensic Science International: Genetics Supplement Series, 2011, 3, e481-e483.	0.3	12
54	Sequence variation of mitochondrial DNA control region in North Central Venezuela. Forensic Science International: Genetics, 2012, 6, e131-e133.	3.1	12

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55	A response to "Likelihood ratio as weight of evidence: A closer look" by Lund and Iyer. Forensic Science International, 2018, 288, e15-e19.	2.2	12
56	Characterization of mtDNA SNP typing and mixture ratio assessment with simultaneous real-time PCR quantification of both allelic states. International Journal of Legal Medicine, 2006, 120, 18-23.	2.2	11
57	The new Standard Reference Material® 2391c: PCR-based DNA profiling standard. Forensic Science International: Genetics Supplement Series, 2011, 3, e355-e356.	0.3	11
58	Population study of fourteen X chromosomal short tandem repeat loci in a population from Bosnia and Herzegovina. Forensic Science International: Genetics, 2011, 5, 350-351.	3.1	10
59	Population genetic data for 15 X chromosomal short tandem repeat markers in three U.S. populations. Forensic Science International: Genetics, 2014, 8, 64-67.	3.1	10
60	The mitochondrial landscape of African Americans: An examination of more than 2500 control region haplotypes from 22 U.S. locations. Forensic Science International: Genetics, 2016, 22, 139-148.	3.1	10
61	The identification of the Romanovs: Can we (finally) put the controversies to rest?. Investigative Genetics, 2011, 2, 20.	3.3	8
62	The mitochondrial <scp>DNA</scp> history of a former native <scp>A</scp>merican village in northern <scp>U</scp>ruguay. American Journal of Human Biology, 2015, 27, 407-416.	1.6	8
63	A description of the likelihood ratios in the probabilistic genotyping softwareSTRmix™. Wiley Interdisciplinary Reviews Forensic Science, 2020, 2, .	2.1	8
64	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.	3.1	7
65	Mitochondrial DNA control region variation in Lebanon, Jordan, and Bahrain. Forensic Science International: Genetics, 2019, 42, 99-102.	3.1	6
66	Exploring likelihood ratios assigned for siblings of the true mixture contributor as an alternate contributor. Journal of Forensic Sciences, 2022, 67, 1167-1175.	1.6	6
67	Nomenclature update and allele repeat structure for the markers DYS518 and DYS449. Forensic Science International: Genetics, 2014, 13, e3.	3.1	5
68	Expected net gain data of low-template DNA analyses. Data in Brief, 2016, 8, 375-386.	1.0	5
69	A collaborative EDNAP exercise on SNaPshot™-based mtDNA control region typing. Forensic Science International: Genetics, 2017, 26, 77-84.	3.1	5
70	Forensic DNA Profiling. , 0, , .		5
71	The application of mtDNA SNPs to a forensic case. Forensic Science International: Genetics Supplement Series, 2008, 1, 295-297.	0.3	4
72	Comparison of base composition analysis and Sanger sequencing of mitochondrial DNA for four U.S. population groups. Forensic Science International: Genetics, 2014, 8, 226-232.	3.1	4

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73	Capillary Electrophoresis of MiniSTR Markers to Genotype Highly Degraded DNA Samples. Methods in Molecular Biology, 2012, 830, 31-42.	0.9	4
74	Characterization and performance of new MiniSTR loci for typing degraded samples. International Congress Series, 2006, 1288, 504-506.	0.2	3
75	Mitochondrial control region variation in a Korean population sample. International Journal of Legal Medicine, 2014, 128, 745-746.	2.2	3
76	Setting standards and developing technology to aid the human identity testing community. International Congress Series, 2006, 1288, 628-635.	0.2	2
77	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.	0.3	2
78	Metrology needs and NIST resources for the forensic DNA community. Accreditation and Quality Assurance, 2011, 16, 293-297.	0.8	2
79	Characterization of mtDNA SNP typing using quantitative real-time PCR with special emphasis on heteroplasmy detection and mixture ratio assessment. International Congress Series, 2006, 1288, 1-3.	0.2	1
80	The evaluation of an autosomal SNP 12-plex assay. International Congress Series, 2006, 1288, 61-63.	0.2	1
81	SNP typing of forensic samples with the GenPlexâ„¢ HID system: A collaborative study. Forensic Science International: Genetics Supplement Series, 2009, 2, 508-509.	0.3	1
82	A gonosomal marker multiplex to aid in mixture interpretation. Forensic Science International: Genetics Supplement Series, 2013, 4, e184-e185.	0.3	1
83	Developmental validation of 15 X chromosomal short tandem repeat markers. Forensic Science International: Genetics Supplement Series, 2013, 4, e142-e143.	0.3	1
84	Initial assessment of the Precision ID Globalfiler Mixture ID panel on the Ion Torrent S5XL DNA sequencer and Converge v2.0 software. Forensic Science International: Genetics Supplement Series, 2017, 6, e94-e95.	0.3	1
85	Uses of the NIST 26plex STR assay for human identity testing. Forensic Science International: Genetics Supplement Series, 2009, 2, 29-30.	0.3	0
86	Additional sequence characterization of NIST SRM 2391c: PCR-Based DNA Profiling Standard. Forensic Science International: Genetics Supplement Series, 2013, 4, e133-e134.	0.3	0
87	Exploring the advantages of amplifying the entire extract versus splitting the extract and interpreting replicates using a continuous model of interpretation. Australian Journal of Forensic Sciences, 0, , 1-12.	1.2	0
88	A new implementation of a semi-continuous method for DNA mixture interpretation. Forensic Science International: Reports, 2022, 6, 100281.	0.8	0