Peter Gill

List of Publications by Year in descending order

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126907 138484 6,078 60 33 58 citations h-index g-index papers 62 62 62 2652 docs citations citing authors all docs times ranked

#	Article	IF	CITATIONS
1	Forensic application of DNA â€~fingerprints'. Nature, 1985, 318, 577-579.	27.8	1,010
2	Identification of the remains of the Romanov family by DNA analysis. Nature Genetics, 1994, 6, 130-135.	21.4	601
3	An investigation of the rigor of interpretation rules for STRs derived from less than 100 pg of DNA. Forensic Science International, 2000, 112, 17-40.	2.2	510
4	Encoded evidence: DNA in forensic analysis. Nature Reviews Genetics, 2004, 5, 739-751.	16.3	457
5	A high observed substitution rate in the human mitochondrial DNA control region. Nature Genetics, 1997, 15, 363-368.	21.4	409
6	Forensic application of a rapid and quantitative DNA sex test by amplification of the X-Y homologous gene amelogenin. International Journal of Legal Medicine, 1994, 106, 190-193.	2.2	204
7	An assessment of the utility of single nucleotide polymorphisms (SNPs) for forensic purposes. International Journal of Legal Medicine, 2001, 114, 204-210.	2.2	199
8	EuroForMix: An open source software based on a continuous model to evaluate STR DNA profiles from a mixture of contributors with artefacts. Forensic Science International: Genetics, 2016, 21, 35-44.	3.1	190
9	Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements. Forensic Science International: Genetics, 2016, 22, 54-63.	3.1	190
10	Evaluation of an automated DNA profiling system employing multiplex amplification of four tetrameric STR loci. International Journal of Legal Medicine, 1994, 106, 302-311.	2.2	167
11	Mystery Solved: The Identification of the Two Missing Romanov Children Using DNA Analysis. PLoS ONE, 2009, 4, e4838.	2.5	135
12	Recommendations of the DNA Commission of the International Society for Forensic Genetics (ISFG) on quality control of autosomal Short Tandem Repeat allele frequency databasing (STRidER). Forensic Science International: Genetics, 2016, 24, 97-102.	3.1	130
13	Genotyping and interpretation of STR-DNA: Low-template, mixtures and database matches—Twenty years of research and development. Forensic Science International: Genetics, 2015, 18, 100-117.	3.1	116
14	Role of Short Tandem Repeat DNA in Forensic Casework in the UKâ€"Past, Present, and Future Perspectives. BioTechniques, 2002, 32, 366-385.	1.8	112
15	Validation of highly discriminating multiplex short tandem repeat amplification systems for individual identification. Electrophoresis, 1996, 17, 1283-1293.	2.4	109
16	An assessment of whether SNPs will replace STRs in national DNA databasesjoint considerations of the DNA working group of the European Network of Forensic Science Institutes (ENFSI) and the Scientific Working Group on DNA Analysis Methods (SWGDAM). Science and Justice - Journal of the Forensic Science Society, 2004, 44, 51-53.	2.1	95
17	An evaluation of DNA fingerprinting for forensic purposes. Electrophoresis, 1987, 8, 38-44.	2.4	90
18	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.	3.1	83

#	Article	IF	CITATIONS
19	The implications of shedder status and background DNA on direct and secondary transfer in an attack scenario. Forensic Science International: Genetics, 2017, 29, 48-60.	3.1	80
20	Secondary and subsequent DNA transfer during criminal investigation. Forensic Science International: Genetics, 2015, 17, 155-162.	3.1	75
21	A comparative study of qualitative and quantitative models used to interpret complex STR DNA profiles. Forensic Science International: Genetics, 2016, 25, 85-96.	3.1	73
22	Individual specific DNA fingerprints from a hypervariable region probe: alpha-globin 3?HVR. Human Genetics, 1988, 79, 142-146.	3.8	71
23	The analysis of hypervariable DNA profiles: problems associated with the objective determination of the probability of a match. Human Genetics, 1990, 85, 75-9.	3.8	71
24	Automated amplification and sequencing of human mitochondrial DNA. Electrophoresis, 1991, 12, 17-21.	2.4	63
25	Automated short tandem repeat (STR) analysis in forensic casework — a strategy for the future. Electrophoresis, 1995, 16, 1543-1552.	2.4	61
26	Body fluid prediction from microbial patterns for forensic application. Forensic Science International: Genetics, 2017, 30, 10-17.	3.1	61
27	An evaluation of potential allelic association between the STRs vWA and D12S391: Implications in criminal casework and applications to short pedigrees. Forensic Science International: Genetics, 2012, 6, 477-486.	3.1	59
28	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.	3.1	59
29	Exclusion of a man charged with murder by DNA fingerprinting. Forensic Science International, 1987, 35, 145-148.	2.2	53
30	Analysis and implications of the miscarriages of justice of Amanda Knox and Raffaele Sollecito. Forensic Science International: Genetics, 2016, 23, 9-18.	3.1	46
31	Population genetics of short tandem repeat (STR) loci. Genetica, 1995, 96, 69-87.	1.1	44
32	Establishing the identity of Anna Anderson Manahan. Nature Genetics, 1995, 9, 9-10.	21.4	38
33	Contamination during criminal investigation: Detecting police contamination and secondary DNA transfer from evidence bags. Forensic Science International: Genetics, 2016, 23, 121-129.	3.1	37
34	Open source software EuroForMix can be used to analyse complex SNP mixtures. Forensic Science International: Genetics, 2017, 31, 105-110.	3.1	37
35	A new method for sex determination of the donor of forensic samples using a recombinant DNA probe. Electrophoresis, 1987, 8, 35-38.	2.4	33
36	Exact computation of the distribution of likelihood ratios with forensic applications. Forensic Science International: Genetics, 2014, 9, 93-101.	3.1	31

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37	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
38	Validation of probabilistic genotyping software for use in forensic DNA casework: Definitions and illustrations. Science and Justice - Journal of the Forensic Science Society, 2016, 56, 104-108.	2.1	23
39	Optimizing body fluid recognition from microbial taxonomic profiles. Forensic Science International: Genetics, 2018, 37, 13-20.	3.1	23
40	Guidelines for Mitochondrial DNA Typing. Vox Sanguinis, 2000, 79, 121-125.	1.5	22
41	CaseSolver: An investigative open source expert system based on EuroForMix. Forensic Science International: Genetics, 2019, 41, 83-92.	3.1	19
42	Determination of shedder status: A comparison of two methods involving cell counting in fingerprints and the DNA analysis of handheld tubes. Forensic Science International: Genetics, 2021, 53, 102541.	3.1	18
43	Database extraction strategies for low-template evidence. Forensic Science International: Genetics, 2014, 9, 134-141.	3.1	17
44	STR-validator: An open source platform for validation and process control. Forensic Science International: Genetics, 2014, 13, 154-166.	3.1	16
45	Degradation in forensic trace DNA samples explored by massively parallel sequencing. Forensic Science International: Genetics, 2017, 27, 160-166.	3.1	16
46	Development of a simulation model to assess the impact of contamination in casework using STRs. Journal of Forensic Sciences, 2004, 49, 485-91.	1.6	11
47	A retrospective study on the transfer, persistence and recovery of sperm and epithelial cells in samples collected in sexual assault casework. Forensic Science International: Genetics, 2019, 43, 102153.	3.1	10
48	Are low LRs reliable?. Forensic Science International: Genetics, 2020, 49, 102350.	3.1	10
49	An examination of STR nomenclatures, filters and models for MPS mixture interpretation. Forensic Science International: Genetics, 2020, 48, 102319.	3.1	10
50	An <mml:math altimg="si2.svg" display="inline" id="d1e2787" xmlns:mml="http://www.w3.org/1998/Math/MathML"><mml:mrow><mml:mi>L</mml:mi><mml:mi>R</mml:mi></mml:mrow></mml:math> framework incorporating sensitivity analysis to model multiple direct and secondary transfer events on skin surface. Forensic Science International: Genetics, 2021, 53, 102509.	3.1	10
51	LCN DNA: proof beyond reasonable doubt? — a response. Nature Reviews Genetics, 2008, 9, 726-726.	16.3	7
52	A response to $\hat{a} \in \infty$ About the number of Contributors to a forensic sample $\hat{a} \in \infty$ Forensic Science International: Genetics, 2017, 26, e9-e13.	3.1	7
53	Population genetics of short tandem repeat (STR) loci. Contemporary Issues in Genetics and Evolution, 1995, , 69-87. <mml:math <="" display="inline" id="d1e963" td="" xmlns:mml="http://www.w3.org/1998/Math/MathML"><td>0.9</td><td>7</td></mml:math>	0.9	7
54	altimg="si5.svg"> <mml:mrow><mml:mi>R</mml:mi><mml:mi><mml:mi><mml:mi><mml:mi></mml:mi></mml:mi></mml:mi></mml:mi><td>mml:math 3.1</td><td>1> 7</td></mml:mrow>	mml:math 3.1	1> 7

#	Article	lF	CITATIONS
55	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
56	Source level interpretation of mixed biological stains using coding region SNPs. Forensic Science International: Genetics, 2022, 59, 102685.	3.1	5
57	Non-self DNA on the neck: a 24 hours time-course study. Forensic Science International: Genetics, 2022, 57, 102661.	3.1	4
58	Overcoming the undetected inhibition of bone DNA extracts obtained by total demineralization. Forensic Science International: Genetics, 2020, 48, 102363.	3.1	2
59	Low-template DNA. , 2020, , 111-128.		0
60	Estimating wildlife vaccination coverage using genetic methods. Preventive Veterinary Medicine, 2020, 183, 105096.	1.9	0