Peter Gill

List of Publications by Year
in descending order

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

#	Article	IF	Citations
1	RFU derived LRs for activity level assignments using Bayesian Networks. Forensic Science International: Genetics, 2022, 56, 102608.	3.1	7
2	Non-self DNA on the neck: a 24 hours time-course study. Forensic Science International: Genetics, 2022, 57, 102661.	3.1	4
3	Source level interpretation of mixed biological stains using coding region SNPs. Forensic Science International: Genetics, 2022, 59, 102685.	3.1	5
4	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
5	An LR 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
6	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
7	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
8	Are low LRs reliable?. Forensic Science International: Genetics, 2020, 49, 102350.	3.1	10
9	Overcoming the undetected inhibition of bone DNA extracts obtained by total demineralization. Forensic Science International: Genetics, 2020, 48, 102363.	3.1	2
10	Low-template DNA. , 2020, , 111-128.		0
11	Estimating wildlife vaccination coverage using genetic methods. Preventive Veterinary Medicine, 2020, 183, 105096.	1.9	0
12	An examination of STR nomenclatures, filters and models for MPS mixture interpretation. Forensic Science International: Genetics, 2020, 48, 102319.	3.1	10
13	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
14	CaseSolver: An investigative open source expert system based on EuroForMix. Forensic Science International: Genetics, 2019, 41, 83-92.	3.1	19
15	Optimizing body fluid recognition from microbial taxonomic profiles. Forensic Science International: Genetics, 2018, 37, 13-20.	3.1	23
16	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
17	Degradation in forensic trace DNA samples explored by massively parallel sequencing. Forensic Science International: Genetics, 2017, 27, 160-166.	3.1	16
18	Body fluid prediction from microbial patterns for forensic application. Forensic Science International: Genetics, 2017, 30, 10-17.	3.1	61

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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	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
21	Open source software EuroForMix can be used to analyse complex SNP mixtures. Forensic Science International: Genetics, 2017, 31, 105-110.	3.1	37
22	A response to â€œAbout the number of Contributors to a forensic sampleâ€• Forensic Science International: Genetics, 2017, 26, e9-e13.	3.1	7
23	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
24	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
25	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
26	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
27	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
28	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
29	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
30	Secondary and subsequent DNA transfer during criminal investigation. Forensic Science International: Genetics, 2015, 17, 155-162.	3.1	75
31	Genotyping and interpretation of STR-DNA: Low-template, mixtures and database matchesâ€"Twenty years of research and development. Forensic Science International: Genetics, 2015, 18, 100-117.	3.1	116
32	STR-validator: An open source platform for validation and process control. Forensic Science International: Genetics, 2014, 13, 154-166.	3.1	16
33	Database extraction strategies for low-template evidence. Forensic Science International: Genetics, 2014, 9, 134-141.	3.1	17
34	Exact computation of the distribution of likelihood ratios with forensic applications. Forensic Science International: Genetics, 2014, 9, 93-101.	3.1	31
35	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
36	Mystery Solved: The Identification of the Two Missing Romanov Children Using DNA Analysis. PLoS ONE, 2009, 4, e4838.	2.5	135

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37	LCN DNA: proof beyond reasonable doubt? â€" a response. Nature Reviews Genetics, 2008, 9, 726-726.	16.3	7
38	Encoded evidence: DNA in forensic analysis. Nature Reviews Genetics, 2004, 5, 739-751.	16.3	457
39	An assessment of whether SNPs will replace STRs in national DNA databases--joint 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
40	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
41	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
42	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
43	Guidelines for Mitochondrial DNA Typing. Vox Sanguinis, 2000, 79, 121-125.	1.5	22
44	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
45	A high observed substitution rate in the human mitochondrial DNA control region. Nature Genetics, 1997, 15, 363-368.	21.4	409
46	Validation of highly discriminating multiplex short tandem repeat amplification systems for individual identification. Electrophoresis, 1996, 17, 1283-1293.	2.4	109
47	Automated short tandem repeat (STR) analysis in forensic casework â€" a strategy for the future. Electrophoresis, 1995, 16, 1543-1552.	2.4	61
48	Population genetics of short tandem repeat (STR) loci. Genetica, 1995, 96, 69-87.	1.1	44
49	Establishing the identity of Anna Anderson Manahan. Nature Genetics, 1995, 9, 9-10.	21.4	38
50	Population genetics of short tandem repeat (STR) loci. Contemporary Issues in Genetics and Evolution, 1995, , 69-87.	0.9	7
51	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
52	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
53	Identification of the remains of the Romanov family by DNA analysis. Nature Genetics, 1994, 6, 130-135.	21.4	601
54	Automated amplification and sequencing of human mitochondrial DNA. Electrophoresis, 1991, 12, 17-21.	2.4	63

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55	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
56	Individual specific DNA fingerprints from a hypervariable region probe: alpha-globin 3?HVR. Human Genetics, 1988, 79, 142-146.	3.8	71
57	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
58	An evaluation of DNA fingerprinting for forensic purposes. Electrophoresis, 1987, 8, 38-44.	2.4	90
59	Exclusion of a man charged with murder by DNA fingerprinting. Forensic Science International, 1987, 35, 145-148.	2.2	53
60	Forensic application of DNA â€˜fingerprintsâ€™. Nature, 1985, 318, 577-579.	27.8	1,010