# Peter Gill

## List of Publications by Year
in descending order

| 60 papers | 6,078 citations | 126858 33 h-index | 138417 58 g-index |
|-----------|-----------------|--------------------|--------------------|
| 62 all docs | 62 docs citations | 62 times ranked | 2652 citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Forensic application of DNA â€˜fingerprintsâ€™. Nature, 1985, 318, 577-579. | 13.7 | 1,010 |
| 2 | Identification of the remains of the Romanov family by DNA analysis. Nature Genetics, 1994, 6, 130-135. | 9.4 | 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. | 1.3 | 510 |
| 4 | Encoded evidence: DNA in forensic analysis. Nature Reviews Genetics, 2004, 5, 739-751. | 7.7 | 457 |
| 5 | A high observed substitution rate in the human mitochondrial DNA control region. Nature Genetics, 1997, 15, 363-368. | 9.4 | 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. | 1.2 | 204 |
| 7 | An assessment of the utility of single nucleotide polymorphisms (SNPs) for forensic purposes. International Journal of Legal Medicine, 2001, 114, 204-210. | 1.2 | 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. | 1.6 | 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. | 1.6 | 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. | 1.2 | 167 |
| 11 | Mystery Solved: The Identification of the Two Missing Romanov Children Using DNA Analysis. PLoS ONE, 2009, 4, e4838. | 1.1 | 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. | 1.6 | 130 |
| 13 | 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. | 1.6 | 116 |
| 14 | Role of Short Tandem Repeat DNA in Forensic Casework in the UKâ€"Past, Present, and Future Perspectives. BioTechniques, 2002, 32, 366-385. | 0.8 | 112 |
| 15 | Validation of highly discriminating multiplex short tandem repeat amplification systems for individual identification. Electrophoresis, 1996, 17, 1283-1293. | 1.3 | 109 |
| 16 | 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. | 1.3 | 95 |
| 17 | An evaluation of DNA fingerprinting for forensic purposes. Electrophoresis, 1987, 8, 38-44. | 1.3 | 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. | 1.6 | 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. | 1.6 | 80 |
| 20 | Secondary and subsequent DNA transfer during criminal investigation. Forensic Science International: Genetics, 2015, 17, 155-162. | 1.6 | 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. | 1.6 | 73 |
| 22 | Individual specific DNA fingerprints from a hypervariable region probe: alpha-globin 3?HVR. Human Genetics, 1988, 79, 142-146. | 1.8 | 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. | 1.8 | 71 |
| 24 | Automated amplification and sequencing of human mitochondrial DNA. Electrophoresis, 1991, 12, 17-21. | 1.3 | 63 |
| 25 | Automated short tandem repeat (STR) analysis in forensic casework â€" a strategy for the future. Electrophoresis, 1995, 16, 1543-1552. | 1.3 | 61 |
| 26 | Body fluid prediction from microbial patterns for forensic application. Forensic Science International: Genetics, 2017, 30, 10-17. | 1.6 | 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. | 1.6 | 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. | 1.6 | 59 |
| 29 | Exclusion of a man charged with murder by DNA fingerprinting. Forensic Science International, 1987, 35, 145-148. | 1.3 | 53 |
| 30 | Analysis and implications of the miscarriages of justice of Amanda Knox and Raffaele Sollecito. Forensic Science International: Genetics, 2016, 23, 9-18. | 1.6 | 46 |
| 31 | Population genetics of short tandem repeat (STR) loci. Genetica, 1995, 96, 69-87. | 0.5 | 44 |
| 32 | Establishing the identity of Anna Anderson Manahan. Nature Genetics, 1995, 9, 9-10. | 9.4 | 38 |
| 33 | Contamination during criminal investigation: Detecting police contamination and secondary DNA transfer from evidence bags. Forensic Science International: Genetics, 2016, 23, 121-129. | 1.6 | 37 |
| 34 | Open source software EuroForMix can be used to analyse complex SNP mixtures. Forensic Science International: Genetics, 2017, 31, 105-110. | 1.6 | 37 |
| 35 | A new method for sex determination of the donor of forensic samples using a recombinant DNA probe. Electrophoresis, 1987, 8, 35-38. | 1.3 | 33 |
| 36 | Exact computation of the distribution of likelihood ratios with forensic applications. Forensic Science International: Genetics, 2014, 9, 93-101. | 1.6 | 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. | 1.2 | 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. | 1.3 | 23 |
| 39 | Optimizing body fluid recognition from microbial taxonomic profiles. Forensic Science International: Genetics, 2018, 37, 13-20. | 1.6 | 23 |
| 40 | Guidelines for Mitochondrial DNA Typing. Vox Sanguinis, 2000, 79, 121-125. | 0.7 | 22 |
| 41 | CaseSolver: An investigative open source expert system based on EuroForMix. Forensic Science International: Genetics, 2019, 41, 83-92. | 1.6 | 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. | 1.6 | 18 |
| 43 | Database extraction strategies for low-template evidence. Forensic Science International: Genetics, 2014, 9, 134-141. | 1.6 | 17 |
| 44 | STR-validator: An open source platform for validation and process control. Forensic Science International: Genetics, 2014, 13, 154-166. | 1.6 | 16 |
| 45 | Degradation in forensic trace DNA samples explored by massively parallel sequencing. Forensic Science International: Genetics, 2017, 27, 160-166. | 1.6 | 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. | 0.9 | 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. | 1.6 | 10 |
| 48 | Are low LRs reliable?. Forensic Science International: Genetics, 2020, 49, 102350. | 1.6 | 10 |
| 49 | An examination of STR nomenclatures, filters and models for MPS mixture interpretation. Forensic Science International: Genetics, 2020, 48, 102319. | 1.6 | 10 |
| 50 | An $LR$ framework incorporating sensitivity analysis to model multiple direct and secondary transfer events on skin surface. Forensic Science International: Genetics, 2021, 53, 102509. | 1.6 | 10 |
| 51 | LCN DNA: proof beyond reasonable doubt? â€" a response. Nature Reviews Genetics, 2008, 9, 726-726. | 7.7 | 7 |
| 52 | A response to â€œAbout the number of Contributors to a forensic sampleâ€. Forensic Science International: Genetics, 2017, 26, e9-e13. | 1.6 | 7 |
| 53 | Population genetics of short tandem repeat (STR) loci. Contemporary Issues in Genetics and Evolution, 1995, , 69-87. | 0.9 | 7 |
| 54 | $RFU$ derived $LR$s for activity level assignments using Bayesian Networks. Forensic Science International: Genetics, 2022, 56, 102608. | 1.6 | 7 |

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|---|---------|-----|-----------|
| 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. | 1.6 | 7 |
| 56 | Source level interpretation of mixed biological stains using coding region SNPs. Forensic Science International: Genetics, 2022, 59, 102685. | 1.6 | 5 |
| 57 | Non-self DNA on the neck: a 24 hours time-course study. Forensic Science International: Genetics, 2022, 57, 102661. | 1.6 | 4 |
| 58 | Overcoming the undetected inhibition of bone DNA extracts obtained by total demineralization. Forensic Science International: Genetics, 2020, 48, 102363. | 1.6 | 2 |
| 59 | Low-template DNA. , 2020, , 111-128. | | 0 |
| 60 | Estimating wildlife vaccination coverage using genetic methods. Preventive Veterinary Medicine, 2020, 183, 105096. | 0.7 | 0 |