

Maarten Kruijver

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5693570/publications.pdf>

Version: 2024-02-01

20
papers

275
citations

933447

10
h-index

940533

16
g-index

20
all docs

20
docs citations

20
times ranked

107
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Internal validation of STRmix [®] , [®] A multi laboratory response to PCAST. Forensic Science International: Genetics, 2018, 34, 11-24. | 3.1 | 72 |
| 2 | Efficient computations with the likelihood ratio distribution. Forensic Science International: Genetics, 2015, 14, 116-124. | 3.1 | 29 |
| 3 | A sensitivity analysis to determine the robustness of STRmix [®] , [®] with respect to laboratory calibration. Forensic Science International: Genetics, 2018, 35, 113-122. | 3.1 | 25 |
| 4 | Optimal strategies for familial searching. Forensic Science International: Genetics, 2014, 13, 90-103. | 3.1 | 18 |
| 5 | The efficacy of DNA mixture to mixture matching. Forensic Science International: Genetics, 2019, 41, 64-71. | 3.1 | 17 |
| 6 | Estimating the number of contributors to a DNA profile using decision trees. Forensic Science International: Genetics, 2021, 50, 102407. | 3.1 | 17 |
| 7 | Combining evidence across multiple mixed DNA profiles for improved resolution of a donor when a common contributor can be assumed. Forensic Science International: Genetics, 2020, 49, 102375. | 3.1 | 16 |
| 8 | p-Values should not be used for evaluating the strength of DNA evidence. Forensic Science International: Genetics, 2015, 16, 226-231. | 3.1 | 14 |
| 9 | Exploring the probative value of mixed DNA profiles. Forensic Science International: Genetics, 2019, 41, 1-10. | 3.1 | 14 |
| 10 | Evaluating DNA evidence possibly involving multiple (mixed) samples, common donors and related contributors. Forensic Science International: Genetics, 2021, 54, 102532. | 3.1 | 13 |
| 11 | Are low LR's reliable?. Forensic Science International: Genetics, 2020, 49, 102350. | 3.1 | 10 |
| 12 | Inter-sample contamination detection using mixture deconvolution comparison. Forensic Science International: Genetics, 2019, 40, 160-167. | 3.1 | 7 |
| 13 | 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 |
| 14 | Characterizing the genetic structure of a forensic DNA database using a latent variable approach. Forensic Science International: Genetics, 2016, 23, 130-149. | 3.1 | 4 |
| 15 | Developmental validation of a software implementation of a flexible framework for the assignment of likelihood ratios for forensic investigations. Forensic Science International: Reports, 2021, 4, 100231. | 0.8 | 4 |
| 16 | Exploring the DNA mixture deconvolution through simulation. Australian Journal of Forensic Sciences, 2019, 51, S14-S17. | 1.2 | 3 |
| 17 | A tool for simulating single source and mixed DNA profiles. Forensic Science International: Genetics, 2022, 60, 102746. | 3.1 | 3 |
| 18 | Response to: Commentary on: Bright et al. (2018) Internal validation of STRmix [®] , [®] A multi laboratory response to PCAST, Forensic Science International: Genetics, 34: 11-24. Forensic Science International: Genetics, 2020, 44, 102198. | 3.1 | 2 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | The effect of a user selected number of contributors within the LR assignment. Australian Journal of Forensic Sciences, 0, , 1-14. | 1.2 | 1 |
| 20 | Introducing a latent variable approach for finding populations in a forensic DNA database. Forensic Science International: Genetics Supplement Series, 2015, 5, e289-e290. | 0.3 | 0 |