

# 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

933264

10  
h-index

940416

16  
g-index

20  
all docs

20  
docs citations

20  
times ranked

107  
citing authors

#	ARTICLE	IF	CITATIONS
1	Internal validation of STRmix <sup>®</sup> , “ A multi laboratory response to PCAST. Forensic Science International: Genetics, 2018, 34, 11-24.	1.6	72
2	Efficient computations with the likelihood ratio distribution. Forensic Science International: Genetics, 2015, 14, 116-124.	1.6	29
3	A sensitivity analysis to determine the robustness of STRmix <sup>®</sup> , <sup>®</sup> with respect to laboratory calibration. Forensic Science International: Genetics, 2018, 35, 113-122.	1.6	25
4	Optimal strategies for familial searching. Forensic Science International: Genetics, 2014, 13, 90-103.	1.6	18
5	The efficacy of DNA mixture to mixture matching. Forensic Science International: Genetics, 2019, 41, 64-71.	1.6	17
6	Estimating the number of contributors to a DNA profile using decision trees. Forensic Science International: Genetics, 2021, 50, 102407.	1.6	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.	1.6	16
8	p-Values should not be used for evaluating the strength of DNA evidence. Forensic Science International: Genetics, 2015, 16, 226-231.	1.6	14
9	Exploring the probative value of mixed DNA profiles. Forensic Science International: Genetics, 2019, 41, 1-10.	1.6	14
10	Evaluating DNA evidence possibly involving multiple (mixed) samples, common donors and related contributors. Forensic Science International: Genetics, 2021, 54, 102532.	1.6	13
11	Are low LRs reliable?. Forensic Science International: Genetics, 2020, 49, 102350.	1.6	10
12	Inter-sample contamination detection using mixture deconvolution comparison. Forensic Science International: Genetics, 2019, 40, 160-167.	1.6	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.	0.9	6
14	Characterizing the genetic structure of a forensic DNA database using a latent variable approach. Forensic Science International: Genetics, 2016, 23, 130-149.	1.6	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.	0.4	4
16	Exploring the DNA mixture deconvolution through simulation. Australian Journal of Forensic Sciences, 2019, 51, S14-S17.	0.7	3
17	A tool for simulating single source and mixed DNA profiles. Forensic Science International: Genetics, 2022, 60, 102746.	1.6	3
18	Response to: Commentary on: Bright et al. (2018) Internal validation of STRmix <sup>®</sup> , <sup>®</sup> “ A multi laboratory response to PCAST, Forensic Science International: Genetics, 34: 11-24. Forensic Science International: Genetics, 2020, 44, 102198.	1.6	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.	0.7	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.	0.1	0