

Maarten Kruijver

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

275
citations

1051969

10
h-index

1051228

16
g-index

20
all docs

20
docs citations

20
times ranked

118
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring likelihood ratios assigned for siblings of the true mixture contributor as an alternate contributor. <i>Journal of Forensic Sciences</i> , 2022, 67, 1167-1175.	0.9	6
2	A tool for simulating single source and mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2022, 60, 102746.	1.6	3
3	Estimating the number of contributors to a DNA profile using decision trees. <i>Forensic Science International: Genetics</i> , 2021, 50, 102407.	1.6	17
4	Evaluating DNA evidence possibly involving multiple (mixed) samples, common donors and related contributors. <i>Forensic Science International: Genetics</i> , 2021, 54, 102532.	1.6	13
5	Developmental validation of a software implementation of a flexible framework for the assignment of likelihood ratios for forensic investigations. <i>Forensic Science International: Reports</i> , 2021, 4, 100231.	0.4	4
6	Response to: Commentary on: Bright et al. (2018) Internal validation of STRmix [®] , “ A multi laboratory response to PCAST, <i>Forensic Science International: Genetics</i> , 34: 11-24. <i>Forensic Science International: Genetics</i> , 2020, 44, 102198.	1.6	2
7	Combining evidence across multiple mixed DNA profiles for improved resolution of a donor when a common contributor can be assumed. <i>Forensic Science International: Genetics</i> , 2020, 49, 102375.	1.6	16
8	Are low LRs reliable?. <i>Forensic Science International: Genetics</i> , 2020, 49, 102350.	1.6	10
9	Exploring the DNA mixture deconvolution through simulation. <i>Australian Journal of Forensic Sciences</i> , 2019, 51, S14-S17.	0.7	3
10	Exploring the probative value of mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2019, 41, 1-10.	1.6	14
11	The efficacy of DNA mixture to mixture matching. <i>Forensic Science International: Genetics</i> , 2019, 41, 64-71.	1.6	17
12	Inter-sample contamination detection using mixture deconvolution comparison. <i>Forensic Science International: Genetics</i> , 2019, 40, 160-167.	1.6	7
13	Internal validation of STRmix [®] , “ A multi laboratory response to PCAST. <i>Forensic Science International: Genetics</i> , 2018, 34, 11-24.	1.6	72
14	A sensitivity analysis to determine the robustness of STRmix [®] , “ with respect to laboratory calibration. <i>Forensic Science International: Genetics</i> , 2018, 35, 113-122.	1.6	25
15	Characterizing the genetic structure of a forensic DNA database using a latent variable approach. <i>Forensic Science International: Genetics</i> , 2016, 23, 130-149.	1.6	4
16	Introducing a latent variable approach for finding populations in a forensic DNA database. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e289-e290.	0.1	0
17	p-Values should not be used for evaluating the strength of DNA evidence. <i>Forensic Science International: Genetics</i> , 2015, 16, 226-231.	1.6	14
18	Efficient computations with the likelihood ratio distribution. <i>Forensic Science International: Genetics</i> , 2015, 14, 116-124.	1.6	29

#	ARTICLE	IF	CITATIONS
19	Optimal strategies for familial searching. Forensic Science International: Genetics, 2014, 13, 90-103.	1.6	18
20	The effect of a user selected number of contributors within the LR assignment. Australian Journal of Forensic Sciences, 0, , 1-14.	0.7	1