

# Keiji Tamaki

## List of Publications by Year in descending order

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16  
papers

247  
citations

1163117

8  
h-index

940533

16  
g-index

16  
all docs

16  
docs citations

16  
times ranked

200  
citing authors

#	ARTICLE	IF	CITATIONS
1	Development and validation of Kongoh ver. 3.0.1: Open-source software for DNA mixture interpretation in the GlobalFiler system based on a quantitative continuous model. <i>Legal Medicine</i> , 2022, 54, 101972.	1.3	6
2	Rapid semen identification from mixed body fluids using methylation-sensitive high-resolution melting analysis of the DACT1 gene. <i>Legal Medicine</i> , 2021, 48, 101806.	1.3	4
3	Evaluation of probability distribution models for stutter ratios in the typing system of GlobalFiler and 3500xL Genetic Analyzer. <i>Legal Medicine</i> , 2021, 52, 101906.	1.3	1
4	DNA mixture interpretation based on the continuous model. <i>Japanese Journal of Forensic Science and Technology</i> , 2020, 25, 1-14.	0.1	2
5	Development of a software for kinship analysis considering linkage and mutation based on a Bayesian network. <i>Forensic Science International: Genetics</i> , 2020, 47, 102279.	3.1	5
6	Distinct spectrum of microRNA expression in forensically relevant body fluids and probabilistic discriminant approach. <i>Scientific Reports</i> , 2019, 9, 14332.	3.3	27
7	Discrimination of relationships with the same degree of kinship using chromosomal sharing patterns estimated from high-density SNPs. <i>Forensic Science International: Genetics</i> , 2018, 33, 10-16.	3.1	15
8	Optimal small-molecular reference RNA for RT-qPCR-based body fluid identification. <i>Forensic Science International: Genetics</i> , 2018, 37, 135-142.	3.1	13
9	Forensic age prediction for saliva samples using methylation-sensitive high resolution melting: exploratory application for cigarette butts. <i>Scientific Reports</i> , 2017, 7, 10444.	3.3	39
10	Development and validation of open-source software for DNA mixture interpretation based on a quantitative continuous model. <i>PLoS ONE</i> , 2017, 12, e0188183.	2.5	42
11	Forensic age prediction for dead or living samples by use of methylation-sensitive high resolution melting. <i>Legal Medicine</i> , 2016, 21, 5-10.	1.3	55
12	New stutter ratio distribution for DNA mixture interpretation based on a continuous model. <i>Legal Medicine</i> , 2016, 19, 16-21.	1.3	5
13	Pairwise Kinship Analysis by the Index of Chromosome Sharing Using High-Density Single Nucleotide Polymorphisms. <i>PLoS ONE</i> , 2016, 11, e0160287.	2.5	13
14	Development of new peak-height models for a continuous method of mixture interpretation. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e104-e106.	0.3	2
15	Subdural hemorrhage: A unique case involving secondary vitamin K deficiency bleeding due to biliary atresia. <i>Forensic Science International</i> , 2012, 221, e25-e29.	2.2	10
16	Transmesenteric hernia due to double-loop formation in the small intestine: A fatal case involving a toddler. <i>Forensic Science International</i> , 2012, 214, e39-e42.	2.2	8