Keiji Tamaki

List of Publications by Year
in descending order

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