Athina Vidaki

List of Publications by Year
in descending order

24 papers	797 citations	687220 13 h-index	677027 22 g-index
25 all docs	25 docs citations	25 times ranked	822 citing authors

#	Article	IF	Citations
1	DNA methylation-based forensic age prediction using artificial neural networks and next generation sequencing. Forensic Science International: Genetics, 2017, 28, 225-236.	1.6	170
2	Recent progress, methods and perspectives in forensic epigenetics. Forensic Science International: Genetics, 2018, 37, 180-195.	1.6	94
3	Forensic DNA methylation profilingâ€"Potential opportunities and challenges. Forensic Science International: Genetics, 2013, 7, 499-507.	1.6	84
4	From forensic epigenetics to forensic epigenomics: broadening DNA investigative intelligence. Genome Biology, 2017, 18, 238.	3.8	64
5	Discovery of potential DNA methylation markers for forensic tissue identification using bisulphite pyrosequencing. Electrophoresis, 2016, 37, 2767-2779.	1.3	49
6	Development and validation of the VISAGE AmpliSeq basic tool to predict appearance and ancestry from DNA. Forensic Science International: Genetics, 2020, 48, 102336.	1.6	43
7	Epigenetic discrimination of identical twins from blood under the forensic scenario. Forensic Science International: Genetics, 2017, 31, 67-80.	1.6	35
8	Novel taxonomy-independent deep learning microbiome approach allows for accurate classification of different forensically relevant human epithelial materials. Forensic Science International: Genetics, 2019, 41, 72-82.	1.6	34
9	Impact of SNP microarray analysis of compromised DNA on kinship classification success in the context of investigative genetic genealogy. Forensic Science International: Genetics, 2022, 56, 102625.	1.6	32
10	Validated inference of smoking habits from blood with a finite DNA methylation marker set. European Journal of Epidemiology, 2019, 34, 1055-1074.	2.5	31
11	Microbiome-based body site of origin classification of forensically relevant blood traces. Forensic Science International: Genetics, 2020, 47, 102280.	1.6	26
12	Estimating the Time Since Deposition of Saliva Stains With a Targeted Bacterial DNA Approach: A Proof-of-Principle Study. Frontiers in Microbiology, 2021, 12, 647933.	1.5	20
13	Equivalent DNA methylation variation between monozygotic co-twins and unrelated individuals reveals universal epigenetic inter-individual dissimilarity. Genome Biology, 2021, 22, 18.	3.8	19
14	Investigating the Epigenetic Discrimination of Identical Twins Using Buccal Swabs, Saliva, and Cigarette Butts in the Forensic Setting. Genes, 2018, 9, 252.	1.0	17
15	Integrating the human microbiome in the forensic toolkit: Current bottlenecks and future solutions. Forensic Science International: Genetics, 2022, 56, 102627.	1.6	17
16	A collaborative exercise on DNA methylation-based age prediction and body fluid typing. Forensic Science International: Genetics, 2022, 57, 102656.	1.6	15
17	Male-specific age estimation based on Y-chromosomal DNA methylation. Aging, 2021, 13, 6442-6458.	1.4	14
18	Differentially methylated embryonal Fyn-associated substrate (EFS) gene as a blood-specific epigenetic marker and its potential application in forensic casework. Forensic Science International: Genetics, 2017, 29, 165-173.	1.6	10

#	Article	IF	Citations
19	Revisiting genetic artifacts on DNA methylation microarrays exposes novel biological implications. Genome Biology, 2021, 22, 274.	3.8	8
20	Validating biomarkers and models for epigenetic inference of alcohol consumption from blood. Clinical Epigenetics, 2021, 13, 198.	1.8	7
21	Prediction of Smoking Habits From Class-Imbalanced Saliva Microbiome Data Using Data Augmentation and Machine Learning. Frontiers in Microbiology, 0, 13, .	1.5	3
22	Breaking the Restriction Barriers and Applying CRISPRi as a Gene Silencing Tool in Pseudoclostridium thermosuccinogenes. Microorganisms, 2022, 10, 698.	1.6	2
23	Epigenetic Fingerprint. , 2015, , 221-243.		1
24	Unsupported claim of significant discrimination between monozygotic twins from multiple pairs based on three age-related DNA methylation markers. Forensic Science International: Genetics, 2019, 39, e1-e2.	1.6	1