

# David J Ballard

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

1,832  
citations

304602

22  
h-index

414303

32  
g-index

33  
all docs

33  
docs citations

33  
times ranked

1568  
citing authors

#	ARTICLE	IF	CITATIONS
1	Combining current knowledge on DNA methylation-based age estimation towards the development of a superior forensic DNA intelligence tool. <i>Forensic Science International: Genetics</i> , 2022, 57, 102637.	1.6	15
2	Predicting Chronological Age from DNA Methylation Data: A Machine Learning Approach for Small Datasets and Limited Predictors. <i>Methods in Molecular Biology</i> , 2022, 2432, 187-200.	0.4	3
3	Classification of STR allelic variation using massively parallel sequencing and assessment of flanking region power. <i>Forensic Science International: Genetics</i> , 2020, 48, 102356.	1.6	17
4	Massive parallel sequencing in forensics: advantages, issues, technicalities, and prospects. <i>International Journal of Legal Medicine</i> , 2020, 134, 1291-1303.	1.2	77
5	Biowarfare, bioterrorism and biocrime: A historical overview on microbial harmful applications. <i>Forensic Science International</i> , 2020, 314, 110366.	1.3	45
6	UK and Irish Y-STR population data – A catalogue of variant alleles. <i>Forensic Science International: Genetics</i> , 2018, 34, e1-e6.	1.6	20
7	“The devil’s in the detail” Release of an expanded, enhanced and dynamically revised forensic STR Sequence Guide. <i>Forensic Science International: Genetics</i> , 2018, 34, 162-169.	1.6	73
8	Concordance of the ForenSeq <sup>™</sup> system and characterisation of sequence-specific autosomal STR alleles across two major population groups. <i>Forensic Science International: Genetics</i> , 2018, 34, 57-61.	1.6	67
9	DNA methylation-based age prediction using massively parallel sequencing data and multiple machine learning models. <i>Forensic Science International: Genetics</i> , 2018, 37, 215-226.	1.6	81
10	Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA. <i>Forensic Science International: Genetics</i> , 2018, 37, 241-251.	1.6	38
11	Global patterns of STR sequence variation: Sequencing the CEPH human genome diversity panel for 58 forensic STRs using the Illumina ForenSeq DNA Signature Prep Kit. <i>Electrophoresis</i> , 2018, 39, 2708-2724.	1.3	51
12	Implementing a biogeographic ancestry inference service for forensic casework. <i>Electrophoresis</i> , 2018, 39, 2757-2765.	1.3	17
13	DNA methylation-based forensic age prediction using artificial neural networks and next generation sequencing. <i>Forensic Science International: Genetics</i> , 2017, 28, 225-236.	1.6	170
14	STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci. <i>Forensic Science International: Genetics</i> , 2017, 31, 111-117.	1.6	77
15	A collaborative EDNAP exercise on SNaPshot <sup>™</sup> -based mtDNA control region typing. <i>Forensic Science International: Genetics</i> , 2017, 26, 77-84.	1.6	5
16	Analysis of Mitochondrial Control Region Using Sanger Sequencing. <i>Methods in Molecular Biology</i> , 2016, 1420, 143-155.	0.4	4
17	Inter-laboratory evaluation of the EUROFORGEN Global ancestry-informative SNP panel by massively parallel sequencing using the Ion PGM <sup>™</sup> . <i>Forensic Science International: Genetics</i> , 2016, 23, 178-189.	1.6	65
18	Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements. <i>Forensic Science International: Genetics</i> , 2016, 22, 54-63.	1.6	190

#	ARTICLE	IF	CITATIONS
19	Evaluation of DNA Variants Associated with Androgenetic Alopecia and Their Potential to Predict Male Pattern Baldness. PLoS ONE, 2015, 10, e0127852.	1.1	51
20	Brief Report: Isogenic Induced Pluripotent Stem Cell Lines From an Adult With Mosaic Down Syndrome Model Accelerated Neuronal Ageing and Neurodegeneration. Stem Cells, 2015, 33, 2077-2084.	1.4	56
21	Forensic ancestry analysis with two capillary electrophoresis ancestry informative marker (AIM) panels: Results of a collaborative EDNAP exercise. Forensic Science International: Genetics, 2015, 19, 56-67.	1.6	27
22	Inter-laboratory evaluation of SNP-based forensic identification by massively parallel sequencing using the Ion PGM. Forensic Science International: Genetics, 2015, 17, 110-121.	1.6	105
23	Evaluation of the predictive capacity of DNA variants associated with straight hair in Europeans. Forensic Science International: Genetics, 2015, 19, 280-288.	1.6	36
24	Enhancing the capabilities of forensic short tandem repeat analysis. Electrophoresis, 2014, 35, 3173-3187.	1.3	31
25	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. Forensic Science International: Genetics, 2014, 12, 12-23.	1.6	214
26	Collaborative EDNAP exercise on the IrisPlex system for DNA-based prediction of human eye colour. Forensic Science International: Genetics, 2014, 11, 241-251.	1.6	23
27	Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. Human Mutation, 2014, 35, 1021-1032.	1.1	151
28	Supplementary markers for deficient immigration cases: Additional STRs or SNPs?. Forensic Science International: Genetics Supplement Series, 2009, 2, 153-154.	0.1	1
29	Identification of West Eurasian mitochondrial haplogroups by mtDNA SNP screening: Results of the 2006-2007 EDNAP collaborative exercise. Forensic Science International: Genetics, 2008, 2, 61-68.	1.6	13
30	Forensic validation of the Genplex SNP typing system. Results of an inter-laboratory study. Forensic Science International: Genetics Supplement Series, 2008, 1, 389-393.	0.1	4
31	Forensic validation of the SNPforID 52-plex assay. Forensic Science International: Genetics, 2007, 1, 186-190.	1.6	74
32	The beneficial effect of extending the Y chromosome STR haplotype. International Congress Series, 2006, 1288, 151-153.	0.2	0