

Ewelina PoÅ>piech

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

1,617
citations

279798

23
h-index

315739

38
g-index

47
all docs

47
docs citations

47
times ranked

1979
citing authors

#	ARTICLE	IF	CITATIONS
1	A collaborative exercise on DNA methylation-based age prediction and body fluid typing. <i>Forensic Science International: Genetics</i> , 2022, 57, 102656.	3.1	15
2	Predicting Physical Appearance from DNA Data – Towards Genomic Solutions. <i>Genes</i> , 2022, 13, 121.	2.4	8
3	miR-378 affects metabolic disturbances in the mdx model of Duchenne muscular dystrophy. <i>Scientific Reports</i> , 2022, 12, 3945.	3.3	7
4	Overlapping association signals in the genetics of hair-related phenotypes in humans and their relevance to predictive DNA analysis. <i>Forensic Science International: Genetics</i> , 2022, 59, 102693.	3.1	5
5	Testing the impact of trait prevalence priors in Bayesian-based genetic prediction modeling of human appearance traits. <i>Forensic Science International: Genetics</i> , 2021, 50, 102412.	3.1	3
6	Role of Heme-Oxygenase-1 in Biology of Cardiomyocytes Derived from Human Induced Pluripotent Stem Cells. <i>Cells</i> , 2021, 10, 522.	4.1	5
7	Development of the VISAGE enhanced tool and statistical models for epigenetic age estimation in blood, buccal cells and bones. <i>Aging</i> , 2021, 13, 6459-6484.	3.1	49
8	Deletion of <i>Mcpip1</i> in <i>Mcpip1^{fl/fl}AlbCre</i> mice recapitulates the phenotype of human primary biliary cholangitis. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021, 1867, 166086.	3.8	12
9	DNA methylation-based age clocks: From age prediction to age reversion. <i>Ageing Research Reviews</i> , 2021, 68, 101314.	10.9	60
10	Searching for improvements in predicting human eye colour from DNA. <i>International Journal of Legal Medicine</i> , 2021, 135, 2175-2187.	2.2	5
11	Epigenetic age prediction in semen – marker selection and model development. <i>Aging</i> , 2021, 13, 19145-19164.	3.1	23
12	Impact of excessive alcohol abuse on age prediction using the VISAGE enhanced tool for epigenetic age estimation in blood. <i>International Journal of Legal Medicine</i> , 2021, 135, 2209-2219.	2.2	9
13	MCPIP1 inhibits Wnt/ β -catenin signaling pathway activity and modulates epithelial-mesenchymal transition during clear cell renal cell carcinoma progression by targeting miRNAs. <i>Oncogene</i> , 2021, 40, 6720-6735.	5.9	21
14	Exploring the possibility of predicting human head hair greying from DNA using whole-exome and targeted NGS data. <i>BMC Genomics</i> , 2020, 21, 538.	2.8	20
15	Angiotensin converting enzyme: A review on expression profile and its association with human disorders with special focus on SARS-CoV-2 infection. <i>Vascular Pharmacology</i> , 2020, 130, 106680.	2.1	44
16	Effects of host genetic variations on response to, susceptibility and severity of respiratory infections. <i>Biomedicine and Pharmacotherapy</i> , 2020, 128, 110296.	5.6	50
17	The challenge of predicting human pigmentation traits in degraded bone samples with the MPS-based HrisPlex-S system. <i>Forensic Science International: Genetics</i> , 2020, 47, 102301.	3.1	19
18	Development and validation of the VISAGE AmpliSeq basic tool to predict appearance and ancestry from DNA. <i>Forensic Science International: Genetics</i> , 2020, 48, 102336.	3.1	43

#	ARTICLE	IF	CITATIONS
19	Altered cytokine levels and immune responses in patients with SARS-CoV-2 infection and related conditions. <i>Cytokine</i> , 2020, 133, 155143.	3.2	64
20	DNA-based predictive models for the presence of freckles. <i>Forensic Science International: Genetics</i> , 2019, 42, 252-259.	3.1	27
21	Non-CYP2D6 Variants Selected by a GWAS Improve the Prediction of Impaired Tamoxifen Metabolism in Patients with Breast Cancer. <i>Journal of Clinical Medicine</i> , 2019, 8, 1087.	2.4	6
22	HlrPlex-S system for eye, hair, and skin color prediction from DNA: Massively parallel sequencing solutions for two common forensically used platforms. <i>Forensic Science International: Genetics</i> , 2019, 43, 102152.	3.1	45
23	RNase MCP1P1 regulates hepatic peroxisome proliferator-activated receptor gamma via TXNIP/PGC-1alpha pathway. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2019, 1864, 1458-1471.	2.4	11
24	GWAS links variants in neuronal development and actin remodeling related loci with pseudoexfoliation syndrome without glaucoma. <i>Experimental Eye Research</i> , 2018, 168, 138-148.	2.6	22
25	Meta-analysis of genome-wide association studies identifies 8 novel loci involved in shape variation of human head hair. <i>Human Molecular Genetics</i> , 2018, 27, 559-575.	2.9	51
26	The HlrPlex-S system for eye, hair and skin colour prediction from DNA: Introduction and forensic developmental validation. <i>Forensic Science International: Genetics</i> , 2018, 35, 123-135.	3.1	199
27	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.	3.1	38
28	Variation in the RPTN gene may facilitate straight hair formation in Europeans and East Asians. <i>Journal of Dermatological Science</i> , 2018, 91, 331-334.	1.9	11
29	Investigating the impact of age-dependent hair colour darkening during childhood on DNA-based hair colour prediction with the HlrPlex system. <i>Forensic Science International: Genetics</i> , 2018, 36, 26-33.	3.1	25
30	Modified aging of elite athletes revealed by analysis of epigenetic age markers. <i>Aging</i> , 2018, 10, 241-252.	3.1	25
31	Global skin colour prediction from DNA. <i>Human Genetics</i> , 2017, 136, 847-863.	3.8	99
32	Hot on the Trail of Genes that Shape Our Fingerprints. <i>Journal of Investigative Dermatology</i> , 2016, 136, 740-742.	0.7	4
33	Further evidence for population specific differences in the effect of DNA markers and gender on eye colour prediction in forensics. <i>International Journal of Legal Medicine</i> , 2016, 130, 923-934.	2.2	20
34	Evaluation of DNA Variants Associated with Androgenetic Alopecia and Their Potential to Predict Male Pattern Baldness. <i>PLoS ONE</i> , 2015, 10, e0127852.	2.5	51
35	Variants of SCARB1 and VDR Involved in Complex Genetic Interactions May Be Implicated in the Genetic Susceptibility to Clear Cell Renal Cell Carcinoma. <i>BioMed Research International</i> , 2015, 2015, 1-11.	1.9	11
36	Evaluation of the predictive capacity of DNA variants associated with straight hair in Europeans. <i>Forensic Science International: Genetics</i> , 2015, 19, 280-288.	3.1	36

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37	A new dimension of the forensic DNA expertise – the need for training experts and expertise recipients. <i>Archiwum Medycyny Sadowej I Kryminologii</i> , 2014, 3, 175-194.	0.3	4
38	Increased risk of developing cutaneous malignant melanoma is associated with variation in pigmentation genes and VDR, and may involve epistatic effects. <i>Melanoma Research</i> , 2014, 24, 388-396.	1.2	24
39	The common occurrence of epistasis in the determination of human pigmentation and its impact on DNA-based pigmentation phenotype prediction. <i>Forensic Science International: Genetics</i> , 2014, 11, 64-72.	3.1	53
40	Bona fide colour: DNA prediction of human eye and hair colour from ancient and contemporary skeletal remains. <i>Investigative Genetics</i> , 2013, 4, 3.	3.3	58
41	Prediction of eye color in the Slovenian population using the IrisPlex SNPs. <i>Croatian Medical Journal</i> , 2013, 54, 381-386.	0.7	37
42	Prediction of Eye Color from Genetic Data Using Bayesian Approach*. <i>Journal of Forensic Sciences</i> , 2012, 57, 880-886.	1.6	30
43	Potential association of single nucleotide polymorphisms in pigmentation genes with the development of basal cell carcinoma. <i>Journal of Dermatology</i> , 2012, 39, 693-698.	1.2	12
44	Gene-gene interactions contribute to eye colour variation in humans. <i>Journal of Human Genetics</i> , 2011, 56, 447-455.	2.3	57
45	The Impact of Mitochondrial and Nuclear DNA Variants on Late-Onset Alzheimer's Disease Risk. <i>Journal of Alzheimer's Disease</i> , 2011, 27, 197-210.	2.6	43
46	Model-based prediction of human hair color using DNA variants. <i>Human Genetics</i> , 2011, 129, 443-454.	3.8	151