

# Wojciech Branicki

## List of Publications by Year in descending order

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Version: 2024-02-01

101  
papers

4,768  
citations

76294

40  
h-index

106281

65  
g-index

110  
all docs

110  
docs citations

110  
times ranked

5568  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | The HirisPlex system for simultaneous prediction of hair and eye colour from DNA. <i>Forensic Science International: Genetics</i> , 2013, 7, 98-115.   | 1.6 | 365       |
| 2  | Development of a forensically useful age prediction method based on DNA methylation analysis. <i>Forensic Science International: Genetics</i> , 2015, 17, 173-179.   | 1.6 | 236       |
| 3  | Ecological factors influence population genetic structure of European grey wolves. <i>Molecular Ecology</i> , 2006, 15, 4533-4553.   | 2.0 | 204       |
| 4  | The HirisPlex-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.                         | 1.6 | 199       |
| 5  | Phylogeography of two European newt species - discordance between mtDNA and morphology. <i>Molecular Ecology</i> , 2005, 14, 2475-2491.  | 2.0 | 173       |
| 6  | Developmental validation of the HirisPlex system: DNA-based eye and hair colour prediction for forensic and anthropological usage. <i>Forensic Science International: Genetics</i> , 2014, 9, 150-161.                     | 1.6 | 164       |
| 7  | Examination of DNA methylation status of the ELOVL2 marker may be useful for human age prediction in forensic science. <i>Forensic Science International: Genetics</i> , 2015, 14, 161-167.                                | 1.6 | 163       |
| 8  | Model-based prediction of human hair color using DNA variants. <i>Human Genetics</i> , 2011, 129, 443-454.   | 1.8 | 151       |
| 9  | Development of a methylation marker set for forensic age estimation using analysis of public methylation data and the Agena Bioscience EpiTYPER system. <i>Forensic Science International: Genetics</i> , 2016, 24, 65-74. | 1.6 | 127       |
| 10 | Phylogeographic history of grey wolves in Europe. <i>BMC Evolutionary Biology</i> , 2010, 10, 104.   | 3.2 | 116       |
| 11 | Mitochondrial phylogeography of the moor frog, <i>Rana arvalis</i> . <i>Molecular Ecology</i> , 2004, 13, 1469-1480.   | 2.0 | 108       |
| 12 | Validation of <i>Cytochrome b</i> Sequence Analysis as a Method of Species Identification. <i>Journal of Forensic Sciences</i> , 2003, 48, 1-5.  | 0.9 | 101       |
| 13 | Global skin colour prediction from DNA. <i>Human Genetics</i> , 2017, 136, 847-863.  | 1.8 | 99        |
| 14 | Interactions Between <i>HERC2</i> , <i>OCA2</i> and <i>MC1R</i> May Influence Human Pigmentation Phenotype. <i>Annals of Human Genetics</i> , 2009, 73, 160-170.   | 0.3 | 96        |
| 15 | <i>MC1R</i> variants increased the risk of sporadic cutaneous melanoma in darker pigmented Caucasians: A pooled analysis from the SKIP project. <i>International Journal of Cancer</i> , 2015, 136, 618-631.               | 2.3 | 92        |
| 16 | Homogeneity and distinctiveness of Polish paternal lineages revealed by Y chromosome microsatellite haplotype analysis. <i>Human Genetics</i> , 2002, 110, 592-600.  | 1.8 | 91        |
| 17 | DNA methylation in <i>ELOVL2</i> and <i>C1orf132</i> correctly predicted chronological age of individuals from three disease groups. <i>International Journal of Legal Medicine</i> , 2018, 132, 1-11.                     | 1.2 | 73        |
| 18 | Role of miRNA and lncRNAs in organ fibrosis and aging. <i>Biomedicine and Pharmacotherapy</i> , 2021, 143, 112132.   | 2.5 | 72        |

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|----|---|-----|-----------|
| 19 | The SARS-CoV-2 ORF10 is not essential in vitro or in vivo in humans. <i>PLoS Pathogens</i> , 2020, 16, e1008959.  | 2.1 | 71        |
| 20 | Genetic diversity and relatedness within packs in an intensely hunted population of wolves <i>Canis lupus</i> . <i>Acta Theriologica</i> , 2005, 50, 3-22.  | 1.1 | 69        |
| 21 | Determination of Phenotype Associated SNPs in the MC1R Gene. <i>Journal of Forensic Sciences</i> , 2007, 52, 349-354.   | 0.9 | 64        |
| 22 | Body fluid identification using a targeted mRNA massively parallel sequencing approach – results of a EUROFORGEN/EDNAP collaborative exercise. <i>Forensic Science International: Genetics</i> , 2018, 34, 105-115. | 1.6 | 64        |
| 23 | Altered cytokine levels and immune responses in patients with SARS-CoV-2 infection and related conditions. <i>Cytokine</i> , 2020, 133, 155143.   | 1.4 | 64        |
| 24 | MCPIP1 contributes to clear cell renal cell carcinomas development. <i>Angiogenesis</i> , 2017, 20, 325-340.  | 3.7 | 61        |
| 25 | Association of the SLC45A2 gene with physiological human hair colour variation. <i>Journal of Human Genetics</i> , 2008, 53, 966-971.   | 1.1 | 60        |
| 26 | DNA methylation-based age clocks: From age prediction to age reversion. <i>Ageing Research Reviews</i> , 2021, 68, 101314.  | 5.0 | 60        |
| 27 | 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        |
| 28 | Gene-gene interactions contribute to eye colour variation in humans. <i>Journal of Human Genetics</i> , 2011, 56, 447-455.  | 1.1 | 57        |
| 29 | 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.     | 1.6 | 53        |
| 30 | Evaluation of DNA Variants Associated with Androgenetic Alopecia and Their Potential to Predict Male Pattern Baldness. <i>PLoS ONE</i> , 2015, 10, e0127852.  | 1.1 | 51        |
| 31 | 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.                                       | 1.4 | 51        |
| 32 | Replication of Severe Acute Respiratory Syndrome Coronavirus 2 in Human Respiratory Epithelium. <i>Journal of Virology</i> , 2020, 94, .  | 1.5 | 51        |
| 33 | Effects of host genetic variations on response to, susceptibility and severity of respiratory infections. <i>Biomedicine and Pharmacotherapy</i> , 2020, 128, 110296.   | 2.5 | 50        |
| 34 | 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.  | 1.4 | 49        |
| 35 | Non-coding RNA profile in lung cancer. <i>Experimental and Molecular Pathology</i> , 2020, 114, 104411.   | 0.9 | 47        |
| 36 | Genetic identification of putative remains of the famous astronomer Nicolaus Copernicus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12279-12282.           | 3.3 | 46        |

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|----|--|-----|-----------|
| 37 | 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.                            | 1.6 | 45        |
| 38 | Biowarfare, bioterrorism and biocrime: A historical overview on microbial harmful applications. <i>Forensic Science International</i> , 2020, 314, 110366.   | 1.3 | 45        |
| 39 | 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.   | 1.0 | 44        |
| 40 | 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.  | 1.2 | 43        |
| 41 | MC1R gene variants and non-melanoma skin cancer: a pooled-analysis from the M-SKIP project. <i>British Journal of Cancer</i> , 2015, 113, 354-363.   | 2.9 | 43        |
| 42 | 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.  | 1.6 | 43        |
| 43 | 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        |
| 44 | Prediction of eye color in the Slovenian population using the IrisPlex SNPs. <i>Croatian Medical Journal</i> , 2013, 54, 381-386.  | 0.2 | 37        |
| 45 | Evaluation of the predictive capacity of DNA variants associated with straight hair in Europeans. <i>Forensic Science International: Genetics</i> , 2015, 19, 280-288.   | 1.6 | 36        |
| 46 | MicroRNA Signature in Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 596359.   | 1.3 | 32        |
| 47 | Prediction of Eye Color from Genetic Data Using Bayesian Approach*. <i>Journal of Forensic Sciences</i> , 2012, 57, 880-886.   | 0.9 | 30        |
| 48 | Association of Polymorphic Sites in the <i>OCA2</i> Gene with Eye Colour Using the Tree Scanning Method. <i>Annals of Human Genetics</i> , 2008, 72, 184-192.  | 0.3 | 29        |
| 49 | The contribution of melanocortin 1 receptor gene polymorphisms and the agouti signalling protein gene 8818A>G polymorphism to cutaneous melanoma and basal cell carcinoma in a Polish population. <i>Experimental Dermatology</i> , 2009, 18, 167-174. | 1.4 | 28        |
| 50 | Forensic ancestry analysis with two capillary electrophoresis ancestry informative marker (AIM) panels: Results of a collaborative EDNAP exercise. <i>Forensic Science International: Genetics</i> , 2015, 19, 56-67.                                  | 1.6 | 27        |
| 51 | DNA-based predictive models for the presence of freckles. <i>Forensic Science International: Genetics</i> , 2019, 42, 252-259.   | 1.6 | 27        |
| 52 | 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.                                       | 1.6 | 25        |
| 53 | Development and optimization of the VISAGE basic prototype tool for forensic age estimation. <i>Forensic Science International: Genetics</i> , 2020, 48, 102322.   | 1.6 | 25        |
| 54 | Modified aging of elite athletes revealed by analysis of epigenetic age markers. <i>Aging</i> , 2018, 10, 241-252.   | 1.4 | 25        |

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|----|---|-----|-----------|
| 55 | 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.  | 0.6 | 24        |
| 56 | Collaborative EDNAP exercise on the IrisPlex system for DNA-based prediction of human eye colour. <i>Forensic Science International: Genetics</i> , 2014, 11, 241-251.  | 1.6 | 23        |
| 57 | Hypermethylation of TRIM59 and KLF14 Influences Cell Death Signaling in Familial Alzheimer's Disease. <i>Oxidative Medicine and Cellular Longevity</i> , 2018, 2018, 1-11.  | 1.9 | 23        |
| 58 | Epigenetic age prediction in semen " marker selection and model development. <i>Aging</i> , 2021, 13, 19145-19164.  | 1.4 | 23        |
| 59 | What's new in the pathophysiology of alopecia areata? the possible contribution of skin and gut microbiome in the pathogenesis of alopecia " Big opportunities, big challenges, and novel perspectives. <i>International Journal of Trichology</i> , 2019, 11, 185. | 0.1 | 21        |
| 60 | 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.  | 1.2 | 20        |
| 61 | 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.  | 1.2 | 20        |
| 62 | Development and Evaluation of the Ancestry Informative Marker Panel of the VISAGE Basic Tool. <i>Genes</i> , 2021, 12, 1284.  | 1.0 | 20        |
| 63 | The challenge of predicting human pigmentation traits in degraded bone samples with the MPS-based HirisPlex-S system. <i>Forensic Science International: Genetics</i> , 2020, 47, 102301.   | 1.6 | 19        |
| 64 | Expression profile of lncRNAs and miRNAs in esophageal cancer: Implications in diagnosis, prognosis, and therapeutic response. <i>Journal of Cellular Physiology</i> , 2020, 235, 9269-9290.  | 2.0 | 17        |
| 65 | A population data for 17 Y-chromosome STR loci in South Poland population sample " Some DYS458.2 variants uncovered and sequenced. <i>Forensic Science International: Genetics</i> , 2009, 4, e43-e44.  | 1.6 | 16        |
| 66 | Genetic variation of 15 autosomal STR loci in a population sample from Poland. <i>Legal Medicine</i> , 2010, 12, 246-248.   | 0.6 | 16        |
| 67 | Association of Melanocortin-1 Receptor Variants with Pigmentary Traits in Humans: A Pooled Analysis from the M-Skip Project. <i>Journal of Investigative Dermatology</i> , 2016, 136, 1914-1917.  | 0.3 | 16        |
| 68 | MC1R variants in childhood and adolescent melanoma: a retrospective pooled analysis of a multicentre cohort. <i>The Lancet Child and Adolescent Health</i> , 2019, 3, 332-342.  | 2.7 | 16        |
| 69 | A collaborative exercise on DNA methylation-based age prediction and body fluid typing. <i>Forensic Science International: Genetics</i> , 2022, 57, 102656.   | 1.6 | 15        |
| 70 | DNA methylation signature in blood does not predict calendar age in patients with chronic lymphocytic leukemia but may alert to the presence of disease. <i>Forensic Science International: Genetics</i> , 2018, 34, e15-e17.                                       | 1.6 | 13        |
| 71 | Melanocortin-1 receptor, skin cancer and phenotypic characteristics (M-SKIP) project: study design and methods for pooling results of genetic epidemiological studies. <i>BMC Medical Research Methodology</i> , 2012, 12, 116.                                     | 1.4 | 12        |
| 72 | 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.   | 0.6 | 12        |

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|----|--|-----|-----------|
| 73 | Donor age and C1orf132/MIR29B2C determine age-related methylation signature of blood after allogeneic hematopoietic stem cell transplantation. <i>Clinical Epigenetics</i> , 2016, 8, 93.                        | 1.8 | 12        |
| 74 | 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. | 0.9 | 11        |
| 75 | 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.  | 1.0 | 11        |
| 76 | Evaluation of supervised machine-learning methods for predicting appearance traits from DNA. <i>Forensic Science International: Genetics</i> , 2021, 53, 102507.   | 1.6 | 11        |
| 77 | 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.                | 1.2 | 9         |
| 78 | STR data for SGM Plus and penta E and D loci in a population sample from south Poland. <i>Forensic Science International</i> , 2002, 127, 237-239.   | 1.3 | 8         |
| 79 | Identification of Cellular Factors Required for SARS-CoV-2 Replication. <i>Cells</i> , 2021, 10, 3159.   | 1.8 | 8         |
| 80 | Predicting Physical Appearance from DNA Data – Towards Genomic Solutions. <i>Genes</i> , 2022, 13, 121.  | 1.0 | 8         |
| 81 | The impact of correlations between pigmentation phenotypes and underlying genotypes on genetic prediction of pigmentation traits. <i>Forensic Science International: Genetics</i> , 2021, 50, 102395.            | 1.6 | 7         |
| 82 | Y-Chromosomal polymorphic loci DYS19, DYS390, DYS393 in a population sample from northern Poland. <i>Electrophoresis</i> , 1999, 20, 1702-1706.  | 1.3 | 5         |
| 83 | Genetic examination of the putative skull of Jan Kochanowski reveals its female sex. <i>Croatian Medical Journal</i> , 2011, 52, 403-409.  | 0.2 | 5         |
| 84 | Assessment of expression profile of microRNAs in multiple sclerosis patients treated with fingolimod. <i>Journal of Molecular Neuroscience</i> , 2020, 70, 1274-1281.  | 1.1 | 5         |
| 85 | Searching for improvements in predicting human eye colour from DNA. <i>International Journal of Legal Medicine</i> , 2021, 135, 2175-2187.   | 1.2 | 5         |
| 86 | Distribution of mtDNA Haplogroups in a Population Sample from Poland. <i>Journal of Forensic Sciences</i> , 2005, 50, 1-2.   | 0.9 | 5         |
| 87 | 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.         | 1.6 | 5         |
| 88 | 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         |
| 89 | Hot on the Trail of Genes that Shape Our Fingerprints. <i>Journal of Investigative Dermatology</i> , 2016, 136, 740-742.   | 0.3 | 4         |
| 90 | STR data for AmpF/STR Profiler Plus loci in south Poland. <i>Forensic Science International</i> , 2001, 122, 173-174.  | 1.3 | 3         |

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|-----|--|-----|-----------|
| 91  | Application of BioRobot M48 to forensic DNA extraction. Forensic Science International: Genetics Supplement Series, 2008, 1, 58-59.  | 0.1 | 3         |
| 92  | A cautionary note on using binary calls for analysis of DNA methylation. Bioinformatics, 2015, 31, 1519-1520.  | 1.8 | 3         |
| 93  | Testing the impact of trait prevalence priors in Bayesian-based genetic prediction modeling of human appearance traits. Forensic Science International: Genetics, 2021, 50, 102412.  | 1.6 | 3         |
| 94  | The OCA2 gene as a marker for eye colour prediction. Forensic Science International: Genetics Supplement Series, 2008, 1, 536-537.   | 0.1 | 2         |
| 95  | Recommendations of the Polish Speaking Working Group of the International Society for Forensic Genetics on forensic Y chromosome typing. Archiwum Medycyny Sadowej I Kryminologii, 2020, 70, 1-18.   | 0.3 | 2         |
| 96  | Examination of LT-DNA traces – literature overview and general recommendations of the Polish Speaking Working Group of the International Society for Forensic Genetics (ISFG-PL). Archiwum Medycyny Sadowej I Kryminologii, 2020, 70, 103-123. | 0.3 | 2         |
| 97  | Determination of forensically relevant SNPs in the MC1R gene. International Congress Series, 2006, 1288, 816-818.  | 0.2 | 1         |
| 98  | Examples of combining genetic evidence – Bayesian network approach. Forensic Science International: Genetics Supplement Series, 2008, 1, 669-670.  | 0.1 | 1         |
| 99  | Recommendations of the Polish Speaking Working Group of the International Society for Forensic Genetics for forensic mitochondrial DNA testing. Archiwum Medycyny Sadowej I Kryminologii, 2018, 68, 242-258.                                   | 0.3 | 1         |
| 100 | Beyond HV1 and HV2 – identification of valuable mitochondrial DNA single nucleotide polymorphisms. International Congress Series, 2004, 1261, 100-102.   | 0.2 | 0         |
| 101 | Prediction of Hair Color from Genetic Data. Materials and Methods, 0, 1, .   | 0.0 | 0         |