## Wojciech Branicki

## List of Publications by Citations

Source: https://exaly.com/author-pdf/5942786/wojciech-branicki-publications-by-citations.pdf

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

102<br/>papers3,305<br/>citations32<br/>h-index55<br/>g-index110<br/>ext. papers4,077<br/>ext. citations4.2<br/>avg, IF5.07<br/>L-index

#	Paper	IF	Citations
102	The HIrisPlex system for simultaneous prediction of hair and eye colour from DNA. <i>Forensic Science International: Genetics</i> , <b>2013</b> , 7, 98-115	4.3	289
101	Ecological factors influence population genetic structure of European grey wolves. <i>Molecular Ecology</i> , <b>2006</b> , 15, 4533-53	5.7	169
100	Development of a forensically useful age prediction method based on DNA methylation analysis. <i>Forensic Science International: Genetics</i> , <b>2015</b> , 17, 173-179	4.3	159
99	Phylogeography of two European newt speciesdiscordance between mtDNA and morphology. <i>Molecular Ecology</i> , <b>2005</b> , 14, 2475-91	5.7	156
98	Model-based prediction of human hair color using DNA variants. <i>Human Genetics</i> , <b>2011</b> , 129, 443-54	6.3	123
97	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> , <b>2015</b> , 14, 161-7	4.3	121
96	Developmental validation of the HIrisPlex system: DNA-based eye and hair colour prediction for forensic and anthropological usage. <i>Forensic Science International: Genetics</i> , <b>2014</b> , 9, 150-61	4.3	110
95	The HIrisPlex-S system for eye, hair and skin colour prediction from DNA: Introduction and forensic developmental validation. <i>Forensic Science International: Genetics</i> , <b>2018</b> , 35, 123-135	4.3	106
94	Mitochondrial phylogeography of the moor frog, Rana arvalis. <i>Molecular Ecology</i> , <b>2004</b> , 13, 1469-80	5.7	98
93	Phylogeographic history of grey wolves in Europe. BMC Evolutionary Biology, 2010, 10, 104	3	94
92	Interactions between HERC2, OCA2 and MC1R may influence human pigmentation phenotype. <i>Annals of Human Genetics</i> , <b>2009</b> , 73, 160-70	2.2	87
91	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> , <b>2016</b> , 24, 65-74	4.3	86
90	Homogeneity and distinctiveness of Polish paternal lineages revealed by Y chromosome microsatellite haplotype analysis. <i>Human Genetics</i> , <b>2002</b> , 110, 592-600	6.3	84
89	Validation of Cytochrome b Sequence Analysis as a Method of Species Identification. <i>Journal of Forensic Sciences</i> , <b>2003</b> , 48, 2002128	1.8	79
88	MC1R variants increased the risk of sporadic cutaneous melanoma in darker-pigmented Caucasians: a pooled-analysis from the M-SKIP project. <i>International Journal of Cancer</i> , <b>2015</b> , 136, 618-31	7.5	67
87	Global skin colour prediction from DNA. <i>Human Genetics</i> , <b>2017</b> , 136, 847-863	6.3	63
86	Determination of phenotype associated SNPs in the MC1R gene. <i>Journal of Forensic Sciences</i> , <b>2007</b> , 52, 349-54	1.8	57

85	MCPIP1 contributes to clear cell renal cell carcinomas development. <i>Angiogenesis</i> , <b>2017</b> , 20, 325-340	10.6	54
84	Genetic diversity and relatedness within packs in an intensely hunted population of wolvesCanis lupus. <i>Acta Theriologica</i> , <b>2005</b> , 50, 3-22		53
83	Gene-gene interactions contribute to eye colour variation in humans. <i>Journal of Human Genetics</i> , <b>2011</b> , 56, 447-55	4.3	52
82	Bona fide colour: DNA prediction of human eye and hair colour from ancient and contemporary skeletal remains. <i>Investigative Genetics</i> , <b>2013</b> , 4, 3		46
81	Association of the SLC45A2 gene with physiological human hair colour variation. <i>Journal of Human Genetics</i> , <b>2008</b> , 53, 966-971	4.3	45
80	DNA methylation in ELOVL2 and C1orf132 correctly predicted chronological age of individuals from three disease groups. <i>International Journal of Legal Medicine</i> , <b>2018</b> , 132, 1-11	3.1	43
79	Body fluid identification using a targeted mRNA massively parallel sequencing approach - results of a EUROFORGEN/EDNAP collaborative exercise. <i>Forensic Science International: Genetics</i> , <b>2018</b> , 34, 105-1	1 <del>\$</del> ·3	42
78	The SARS-CoV-2 ORF10 is not essential in vitro or in vivo in humans. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e100895	<b>9</b> 7.6	42
77	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> , <b>2014</b> , 11, 64-72	4.3	39
76	Altered cytokine levels and immune responses in patients with SARS-CoV-2 infection and related conditions. <i>Cytokine</i> , <b>2020</b> , 133, 155143	4	39
75	Replication of Severe Acute Respiratory Syndrome Coronavirus 2 in Human Respiratory Epithelium. Journal of Virology, <b>2020</b> , 94,	6.6	37
74	The impact of mitochondrial and nuclear DNA variants on late-onset Alzheimer's disease risk. Journal of Alzheimer's Disease, <b>2011</b> , 27, 197-210	4.3	36
73	Genetic identification of putative remains of the famous astronomer Nicolaus Copernicus.  Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12279-82	11.5	36
72	Evaluation of DNA variants associated with androgenetic alopecia and their potential to predict male pattern baldness. <i>PLoS ONE</i> , <b>2015</b> , 10, e0127852	3.7	34
71	Meta-analysis of genome-wide association studies identifies 8 novel loci involved in shape variation of human head hair. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 559-575	5.6	33
70	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> , <b>2020</b> , 130, 106680	5.9	31
69	Non-coding RNA profile in lung cancer. Experimental and Molecular Pathology, 2020, 114, 104411	4.4	31
68	Prediction of eye color in the Slovenian population using the IrisPlex SNPs. <i>Croatian Medical Journal</i> , <b>2013</b> , 54, 381-6	1.6	29

67	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> , <b>2009</b> , 18, 167-74	4	28
66	Association of polymorphic sites in the OCA2 gene with eye colour using the tree scanning method. <i>Annals of Human Genetics</i> , <b>2008</b> , 72, 184-92	2.2	28
65	MC1R gene variants and non-melanoma skin cancer: a pooled-analysis from the M-SKIP project. <i>British Journal of Cancer</i> , <b>2015</b> , 113, 354-63	8.7	26
64	Evaluation of the predictive capacity of DNA variants associated with straight hair in Europeans. <i>Forensic Science International: Genetics</i> , <b>2015</b> , 19, 280-288	4.3	26
63	Prediction of eye color from genetic data using Bayesian approach. <i>Journal of Forensic Sciences</i> , <b>2012</b> , 57, 880-6	1.8	26
62	Effects of host genetic variations on response to, susceptibility and severity of respiratory infections. <i>Biomedicine and Pharmacotherapy</i> , <b>2020</b> , 128, 110296	7.5	25
61	HIrisPlex-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> , <b>2019</b> , 43, 102152	4.3	24
60	Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA. <i>Forensic Science International: Genetics</i> , <b>2018</b> , 37, 241-251	4.3	24
59	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> , <b>2014</b> , 24, 388-96	3.3	23
58	Development and validation of the VISAGE AmpliSeq basic tool to predict appearance and ancestry from DNA. <i>Forensic Science International: Genetics</i> , <b>2020</b> , 48, 102336	4.3	22
57	Biowarfare, bioterrorism and biocrime: A historical overview on microbial harmful applications. <i>Forensic Science International</i> , <b>2020</b> , 314, 110366	2.6	20
56	Forensic ancestry analysis with two capillary electrophoresis ancestry informative marker (AIM) panels: Results of a collaborative EDNAP exercise. <i>Forensic Science International: Genetics</i> , <b>2015</b> , 19, 56-	6 <del>1</del> .3	18
55	Hypermethylation of and Influences Cell Death Signaling in Familial Alzheimer's Disease. <i>Oxidative Medicine and Cellular Longevity</i> , <b>2018</b> , 2018, 6918797	6.7	18
54	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> , <b>2016</b> , 130, 923-934	3.1	17
53	Investigating the impact of age-depended hair colour darkening during childhood on DNA-based hair colour prediction with the HIrisPlex system. <i>Forensic Science International: Genetics</i> , <b>2018</b> , 36, 26-33	3 4.3	17
52	Collaborative EDNAP exercise on the IrisPlex system for DNA-based prediction of human eye colour. <i>Forensic Science International: Genetics</i> , <b>2014</b> , 11, 241-51	4.3	17
51	Genetic variation of 15 autosomal STR loci in a population sample from Poland. <i>Legal Medicine</i> , <b>2010</b> , 12, 246-8	1.9	16
50	Modified aging of elite athletes revealed by analysis of epigenetic age markers. <i>Aging</i> , <b>2018</b> , 10, 241-25	5 <b>2</b> 5.6	16

## (2021-2021)

49	DNA methylation-based age clocks: From age prediction to age reversion. <i>Ageing Research Reviews</i> , <b>2021</b> , 68, 101314	12	16
48	Development and optimization of the VISAGE basic prototype tool for forensic age estimation. <i>Forensic Science International: Genetics</i> , <b>2020</b> , 48, 102322	4.3	13
47	Association of Melanocortin-1 Receptor Variants with Pigmentary Traits in Humans: AlPooled Analysis from the M-Skip Project. <i>Journal of Investigative Dermatology</i> , <b>2016</b> , 136, 1914-1917	4.3	12
46	Potential association of single nucleotide polymorphisms in pigmentation genes with the development of basal cell carcinoma. <i>Journal of Dermatology</i> , <b>2012</b> , 39, 693-8	1.6	12
45	DNA-based predictive models for the presence of freckles. <i>Forensic Science International: Genetics</i> , <b>2019</b> , 42, 252-259	4.3	11
44	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> , <b>2019</b> , 11, 185-188	1.1	11
43	Development of the VISAGE enhanced tool and statistical models for epigenetic age estimation in blood, buccal cells and bones. <i>Aging</i> , <b>2021</b> , 13, 6459-6484	5.6	11
42	The challenge of predicting human pigmentation traits in degraded bone samples with the MPS-based HIrisPlex-S system. <i>Forensic Science International: Genetics</i> , <b>2020</b> , 47, 102301	4.3	10
41	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> , <b>2012</b> , 12, 116	4.7	10
40	MicroRNA Signature in Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , <b>2020</b> , 10, 596359	5.3	10
39	MicroRNA Signature in Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , <b>2020</b> , 10, 596359  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> , <b>2015</b> , 2015, 860405	5·3 3	9
	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> , <b>2015</b> ,		9
39	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> , <b>2015</b> , 2015, 860405  MC1R variants in childhood and adolescent melanoma: a retrospective pooled analysis of a	3	9
39	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> , <b>2015</b> , 2015, 860405  MC1R variants in childhood and adolescent melanoma: a retrospective pooled analysis of a multicentre cohort. <i>The Lancet Child and Adolescent Health</i> , <b>2019</b> , 3, 332-342  A population data for 17 Y-chromosome STR loci in South Poland population samplesome	3	9
39 38 37	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> , <b>2015</b> , 2015, 860405  MC1R variants in childhood and adolescent melanoma: a retrospective pooled analysis of a multicentre cohort. <i>The Lancet Child and Adolescent Health</i> , <b>2019</b> , 3, 332-342  A population data for 17 Y-chromosome STR loci in South Poland population samplesome DYS458.2 variants uncovered and sequenced. <i>Forensic Science International: Genetics</i> , <b>2009</b> , 4, e43-4  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:</i>	3 14.5 4.3	9 8 8
39 38 37 36	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> , <b>2015</b> , 2015, 860405  MC1R variants in childhood and adolescent melanoma: a retrospective pooled analysis of a multicentre cohort. <i>The Lancet Child and Adolescent Health</i> , <b>2019</b> , 3, 332-342  A population data for 17 Y-chromosome STR loci in South Poland population samplesome DYS458.2 variants uncovered and sequenced. <i>Forensic Science International: Genetics</i> , <b>2009</b> , 4, e43-4  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> , <b>2018</b> , 34, e15-e17  STR data for SGM Plus and penta E and D loci in a population sample from south Poland. <i>Forensic</i>	3 14.5 4.3	9 8 8 7
39 38 37 36 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, 860405  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  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, e43-4  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  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, 237-9  Exploring the possibility of predicting human head hair greying from DNA using whole-exome and	3 14.5 4.3 4.3	9 8 8 7 7

31	Variation in the RPTN gene may facilitate straight hair formation in Europeans and East Asians. Journal of Dermatological Science, <b>2018</b> , 91, 331-334	4.3	6
30	Distribution of mtDNA Haplogroups in a Population Sample from Poland. <i>Journal of Forensic Sciences</i> , <b>2005</b> , 50, 1-2	1.8	5
29	Expression profile of lncRNAs and miRNAs in esophageal cancer: Implications in diagnosis, prognosis, and therapeutic response. <i>Journal of Cellular Physiology</i> , <b>2020</b> , 235, 9269-9290	7	4
28	Genetic examination of the putative skull of Jan Kochanowski reveals its female sex. <i>Croatian Medical Journal</i> , <b>2011</b> , 52, 403-9	1.6	4
27	Y-chromosomal polymorphic loci DYS19, DYS390, DYS393 in a population sample from northern Poland. <i>Electrophoresis</i> , <b>1999</b> , 20, 1702-6	3.6	4
26	Assessment of expression profile of microRNAs in multiple sclerosis patients treated with fingolimod. <i>Journal of Molecular Neuroscience</i> , <b>2020</b> , 70, 1274-1281	3.3	3
25	A cautionary note on using binary calls for analysis of DNA methylation. <i>Bioinformatics</i> , <b>2015</b> , 31, 1519-3	2 <del>9</del> .2	3
24	A new dimension of the forensic DNA expertise - the need for training experts and expertise recipients. <i>Archiwum Medycyny Sadowej I Kryminologii</i> , <b>2014</b> , 64, 175-94	0.3	3
23	Application of BioRobot M48 to forensic DNA extraction. <i>Forensic Science International: Genetics Supplement Series</i> , <b>2008</b> , 1, 58-59	0.5	3
22	STR data for AmpF/STR Profiler Plus loci in south Poland. Forensic Science International, 2001, 122, 173-	42.6	3
21	Replication of SARS-CoV-2 in human respiratory epithelium		3
20	Evaluation of supervised machine-learning methods for predicting appearance traits from DNA. <i>Forensic Science International: Genetics</i> , <b>2021</b> , 53, 102507	4.3	3
19	Hot on the Trail of Genes that Shape Our Fingerprints. <i>Journal of Investigative Dermatology</i> , <b>2016</b> , 136, 740-742	4.3	3
18	Identification of Cellular Factors Required for SARS-CoV-2 Replication. <i>Cells</i> , <b>2021</b> , 10,	7.9	2
17	Recommendations of the Polish Speaking Working Group of the International Society for Forensic Genetics on forensic Y chromosome typing. <i>Archiwum Medycyny Sadowej I Kryminologii</i> , <b>2020</b> , 70, 1-18	0.3	2
16	Development and Evaluation of the Ancestry Informative Marker Panel of the VISAGE Basic Tool. <i>Genes</i> , <b>2021</b> , 12,	4.2	2
15	Examples of combining genetic evidence <b>B</b> ayesian network approach. <i>Forensic Science International: Genetics Supplement Series</i> , <b>2008</b> , 1, 669-670	0.5	1
14	Determination of forensically relevant SNPs in the MC1R gene. <i>International Congress Series</i> , <b>2006</b> , 1288, 816-818		1

## LIST OF PUBLICATIONS

13	A collaborative exercise on DNA methylation-based age prediction and body fluid typing <i>Forensic Science International: Genetics</i> , <b>2021</b> , 57, 102656	4.3	1
12	The SARS-CoV-2 ORF10 is not essential in vitro or in vivo in humans		1
11	The impact of correlations between pigmentation phenotypes and underlying genotypes on genetic prediction of pigmentation traits. <i>Forensic Science International: Genetics</i> , <b>2021</b> , 50, 102395	4.3	1
10	Recommendations of the Polish Speaking Working Group of the International Society for Forensic Genetics for forensic mitochondrial DNA testing. <i>Archiwum Medycyny Sadowej I Kryminologii</i> , <b>2018</b> , 68, 242-258	0.3	1
9	Epigenetic age prediction in semen - marker selection and model development. <i>Aging</i> , <b>2021</b> , 13, 19145	-1 <u>9</u> .664	1
8	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> , <b>2021</b> , 135, 2209-2219	3.1	1
7	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). <i>Archiwum Medycyny Sadowej I Kryminologii</i> , <b>2020</b> , 70, 103-123	0.3	O
6	Testing the impact of trait prevalence priors in Bayesian-based genetic prediction modeling of human appearance traits. <i>Forensic Science International: Genetics</i> , <b>2021</b> , 50, 102412	4.3	O
5	Searching for improvements in predicting human eye colour from DNA. <i>International Journal of Legal Medicine</i> , <b>2021</b> , 135, 2175-2187	3.1	O
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> , <b>2022</b> , 59, 102693	4.3	O
3	Prediction of Human Pigmentation Traits from DNA Polymorphisms 2015, 1-10		
2	The OCA2 gene as a marker for eye colour prediction. <i>Forensic Science International: Genetics Supplement Series</i> , <b>2008</b> , 1, 536-537	0.5	
1	Beyond HV1 and HV2Identification of valuable mitochondrial DNA single nucleotide polymorphisms. <i>International Congress Series</i> , <b>2004</b> , 1261, 100-102		