

Miina E Ollikainen

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

4,056
citations

168829

31
h-index

145109

60
g-index

80
all docs

80
docs citations

80
times ranked

7464
citing authors

#	ARTICLE	IF	CITATIONS
1	The Association Between Epigenetic Clocks and Physical Functioning in Older Women: A 3-Year Follow-up. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2022, 77, 1569-1576.	1.7	11
2	Modeling dependency structures in 450k DNA methylation data. <i>Bioinformatics</i> , 2022, 38, 885-891.	1.8	2
3	Do Epigenetic Clocks Provide Explanations for Sex Differences in Life Span? A Cross-Sectional Twin Study. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2022, 77, 1898-1906.	1.7	15
4	Multi-Omics Integration in a Twin Cohort and Predictive Modeling of Blood Pressure Values. <i>OMICS A Journal of Integrative Biology</i> , 2022, 26, 130-141.	1.0	6
5	The potential of DNA methylation as a biomarker for obesity and smoking. <i>Journal of Internal Medicine</i> , 2022, 292, 390-408.	2.7	19
6	BMI is positively associated with accelerated epigenetic aging in twin pairs discordant for body mass index. <i>Journal of Internal Medicine</i> , 2022, 292, 627-640.	2.7	15
7	Associations of Alcohol Consumption With Epigenome-Wide DNA Methylation and Epigenetic Age Acceleration: Individual-Level and Co-twin Comparison Analyses. <i>Alcoholism: Clinical and Experimental Research</i> , 2021, 45, 318-328.	1.4	18
8	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. <i>Molecular Psychiatry</i> , 2021, 26, 2148-2162.	4.1	21
9	Blood and skeletal muscle ageing determined by epigenetic clocks and their associations with physical activity and functioning. <i>Clinical Epigenetics</i> , 2021, 13, 110.	1.8	15
10	Genetic meta-analysis of twin birth weight shows high genetic correlation with singleton birth weight. <i>Human Molecular Genetics</i> , 2021, 30, 1894-1905.	1.4	6
11	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	3.8	90
12	Does the epigenetic clock GrimAge predict mortality independent of genetic influences: an 18-year follow-up study in older female twin pairs. <i>Clinical Epigenetics</i> , 2021, 13, 128.	1.8	17
13	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021, 12, 5618.	5.8	26
14	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
15	Leisure-Time and Occupational Physical Activity Associates Differently with Epigenetic Aging. <i>Medicine and Science in Sports and Exercise</i> , 2021, 53, 487-495.	0.2	28
16	Lymphoma-Associated Biomarkers Are Increased in Current Smokers in Twin Pairs Discordant for Smoking. <i>Cancers</i> , 2021, 13, 5395.	1.7	2
17	The mitochondrial protein Opa1 promotes adipocyte browning that is dependent on urea cycle metabolites. <i>Nature Metabolism</i> , 2021, 3, 1633-1647.	5.1	42
18	An integrative machine learning approach to discovering multi-level molecular mechanisms of obesity using data from monozygotic twin pairs. <i>Royal Society Open Science</i> , 2020, 7, 200872.	1.1	4

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19	Identification, Heritability, and Relation With Gene Expression of Novel DNA Methylation Loci for Blood Pressure. <i>Hypertension</i> , 2020, 76, 195-205.	1.3	33
20	Plasma metabolites reveal distinct profiles associating with different metabolic risk factors in monozygotic twin pairs. <i>International Journal of Obesity</i> , 2019, 43, 487-502.	1.6	13
21	Epigenome-wide association study of lung function level and its change. <i>European Respiratory Journal</i> , 2019, 54, 1900457.	3.1	49
22	The Older Finnish Twin Cohort – 45 Years of Follow-up. <i>Twin Research and Human Genetics</i> , 2019, 22, 240-254.	0.3	68
23	Peripheral blood DNA methylation differences in twin pairs discordant for Alzheimer’s disease. <i>Clinical Epigenetics</i> , 2019, 11, 130.	1.8	29
24	EpiSmokEr: a robust classifier to determine smoking status from DNA methylation data. <i>Epigenomics</i> , 2019, 11, 1469-1486.	1.0	85
25	Leisure-time physical activity and DNA methylation age – a twin study. <i>Clinical Epigenetics</i> , 2019, 11, 12.	1.8	34
26	Making Sense of the Epigenome Using Data Integration Approaches. <i>Frontiers in Pharmacology</i> , 2019, 10, 126.	1.6	58
27	Accuracy of self-reported anthropometric measures – Findings from the Finnish Twin Study. <i>Obesity Research and Clinical Practice</i> , 2019, 13, 522-528.	0.8	22
28	Epigenome-wide association study of serum cotinine in current smokers reveals novel genetically driven loci. <i>Clinical Epigenetics</i> , 2019, 11, 1.	1.8	116
29	Genetic and Environmental Effects on Gene Expression Signatures of Blood Pressure. <i>Hypertension</i> , 2018, 71, 457-464.	1.3	16
30	High-throughput DNA methylation analysis in anorexia nervosa confirms <i>TNXB</i> hypermethylation. <i>World Journal of Biological Psychiatry</i> , 2018, 19, 187-199.	1.3	28
31	Subcutaneous adipose tissue gene expression and DNA methylation respond to both short- and long-term weight loss. <i>International Journal of Obesity</i> , 2018, 42, 412-423.	1.6	32
32	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. <i>Clinical Epigenetics</i> , 2018, 10, 126.	1.8	110
33	Biological clocks and physical functioning in monozygotic female twins. <i>BMC Geriatrics</i> , 2018, 18, 83.	1.1	22
34	Abstract 3228: Tobacco smoking and circulating immune-related biomarkers in monozygotic twins. , 2018, , .		0
35	Gene expression profile of subcutaneous adipose tissue in BMI-discordant monozygotic twin pairs unravels molecular and clinical changes associated with sub-types of obesity. <i>International Journal of Obesity</i> , 2017, 41, 1176-1184.	1.6	31
36	Neuregulin signaling pathway in smoking behavior. <i>Translational Psychiatry</i> , 2017, 7, e1212-e1212.	2.4	8

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37	An epigenome-wide association study meta-analysis of educational attainment. <i>Molecular Psychiatry</i> , 2017, 22, 1680-1690.	4.1	70
38	Mendelian randomization in (epi)genetic epidemiology: an effective tool to be handled with care. <i>Genome Biology</i> , 2016, 17, 156.	3.8	29
39	Biotin-dependent functions in adiposity: a study of monozygotic twin pairs. <i>International Journal of Obesity</i> , 2016, 40, 788-795.	1.6	16
40	DNA methylation and gene expression patterns in adipose tissue differ significantly within young adult monozygotic BMI-discordant twin pairs. <i>International Journal of Obesity</i> , 2016, 40, 654-661.	1.6	59
41	Hormone Replacement Therapy Associated White Blood Cell DNA Methylation and Gene Expression are Associated With Within-Pair Differences of Body Adiposity and Bone Mass. <i>Twin Research and Human Genetics</i> , 2015, 18, 647-661.	0.3	16
42	A Genome-Wide Association Study of a Biomarker of Nicotine Metabolism. <i>PLoS Genetics</i> , 2015, 11, e1005498.	1.5	107
43	Genome-wide blood DNA methylation alterations at regulatory elements and heterochromatic regions in monozygotic twins discordant for obesity and liver fat. <i>Clinical Epigenetics</i> , 2015, 7, 39.	1.8	71
44	Impaired Mitochondrial Biogenesis in Adipose Tissue in Acquired Obesity. <i>Diabetes</i> , 2015, 64, 3135-3145.	0.3	263
45	Longitudinal, genome-scale analysis of DNA methylation in twins from birth to 18 months of age reveals rapid epigenetic change in early life and pair-specific effects of discordance. <i>Genome Biology</i> , 2013, 14, R42.	13.9	172
46	Association of maternal and nutrient supply line factors with DNA methylation at the imprinted IGF2/H19 locus in multiple tissues of newborn twins. <i>Epigenetics</i> , 2013, 8, 1069-1079.	1.3	40
47	The Peri/Postnatal Epigenetic Twins Study (PETS). <i>Twin Research and Human Genetics</i> , 2013, 16, 13-20.	0.3	50
48	Cohort Profile: The Peri/post-natal Epigenetic Twins Study. <i>International Journal of Epidemiology</i> , 2012, 41, 55-61.	0.9	48
49	Neonatal DNA methylation profile in human twins is specified by a complex interplay between intrauterine environmental and genetic factors, subject to tissue-specific influence. <i>Genome Research</i> , 2012, 22, 1395-1406.	2.4	246
50	Expression discordance of monozygotic twins at birth: Effect of intrauterine environment and a possible mechanism for fetal programming. <i>Epigenetics</i> , 2011, 6, 579-592.	1.3	70
51	Epigenetic discordance at imprinting control regions in twins. <i>Epigenomics</i> , 2011, 3, 295-306.	1.0	37
52	DNA methylation analysis of multiple tissues from newborn twins reveals both genetic and intrauterine components to variation in the human neonatal epigenome. <i>Human Molecular Genetics</i> , 2010, 19, 4176-4188.	1.4	296
53	Copy number alterations of the polycomb gene BMI1 in gliomas. <i>Acta Neuropathologica</i> , 2008, 116, 97-102.	3.9	44
54	Somatic <i>FGF9</i> mutations in colorectal and endometrial carcinomas associated with membranous β -catenin. <i>Human Mutation</i> , 2008, 29, 390-397.	1.1	31

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55	Epigenetic Signatures of Familial Cancer Are Characteristic of Tumor Type and Family Category. <i>Cancer Research</i> , 2008, 68, 4597-4605.	0.4	79
56	Patterns of PIK3CA alterations in familial colorectal and endometrial carcinoma. <i>International Journal of Cancer</i> , 2007, 121, 915-920.	2.3	61
57	Mechanisms of inactivation of MLH1 in hereditary nonpolyposis colorectal carcinoma: a novel approach. <i>Oncogene</i> , 2007, 26, 4541-4549.	2.6	56
58	Comprehensive characterization of HNPCC-related colorectal cancers reveals striking molecular features in families with no germline mismatch repair gene mutations. <i>Oncogene</i> , 2005, 24, 1542-1551.	2.6	79
59	APC and β -catenin protein expression patterns in HNPCC-related endometrial and colorectal cancers. <i>Familial Cancer</i> , 2005, 4, 187-190.	0.9	19
60	Molecular Analysis of Familial Endometrial Carcinoma: A Manifestation of Hereditary Nonpolyposis Colorectal Cancer or a Separate Syndrome?. <i>Journal of Clinical Oncology</i> , 2005, 23, 4609-4616.	0.8	125
61	Distinct patterns of KRAS mutations in colorectal carcinomas according to germline mismatch repair defects and hMLH1 methylation status. <i>Human Molecular Genetics</i> , 2004, 13, 2303-2311.	1.4	127
62	BRAF screening as a low-cost effective strategy for simplifying HNPCC genetic testing. <i>Journal of Medical Genetics</i> , 2004, 41, 664-668.	1.5	305
63	Mutations in the β -tropomyosin (TPM2) gene – a rare cause of nemaline myopathy. <i>Neuromuscular Disorders</i> , 2002, 12, 151-158.	0.3	210
64	Frequency-related effects in the optimization of coils for the magnetic stimulation of the nervous system. <i>IEEE Transactions on Biomedical Engineering</i> , 2002, 49, 463-471.	2.5	16