Miina E Ollikainen

List of Publications by Year in Descending Order

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

58 papers	2,747 citations	27 h-index	52 g-index
80 ext. papers	3,389 ext. citations	7.5 avg, IF	4.49 L-index

#	Paper	IF	Citations
58	Multi-Omics Integration in a Twin Cohort and Predictive Modeling of Blood Pressure Values.. *OMICS A Journal of Integrative Biology*, **2022**, 26, 130-141	3.8	1
57	The potential of DNA methylation as a biomarker for obesity and smoking.. *Journal of Internal Medicine*, **2022**,	10.8	2
56	Leisure-Time and Occupational Physical Activity Associates Differently with Epigenetic Aging. *Medicine and Science in Sports and Exercise*, **2021**, 53, 487-495	1.2	8
55	Blood and skeletal muscle ageing determined by epigenetic clocks and their associations with physical activity and functioning. *Clinical Epigenetics*, **2021**, 13, 110	7.7	1
54	Genetic meta-analysis of twin birth weight shows high genetic correlation with singleton birth weight. *Human Molecular Genetics*, **2021**, 30, 1894-1905	5.6	1
53	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. *Genome Biology*, **2021**, 22, 194	18.3	14
52	Does the epigenetic clock GrimAge predict mortality independent of genetic influences: an 18‐year follow-up study in older female twin pairs. *Clinical Epigenetics*, **2021**, 13, 128	7.7	4
51	Associations of Alcohol Consumption With Epigenome-Wide DNA Methylation and Epigenetic Age Acceleration: Individual-Level and Co-twin Comparison Analyses. *Alcoholism: Clinical and Experimental Research*, **2021**, 45, 318-328	3.7	4
50	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. *Molecular Psychiatry*, **2021**, 26, 2148-2162	15.1	7
49	Identical twins carry a persistent epigenetic signature of early genome programming. *Nature Communications*, **2021**, 12, 5618	17.4	6
48	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. *Nature Genetics*, **2021**, 53, 1311-1321	36.3	27
47	Identification, Heritability, and Relation With Gene Expression of Novel DNA Methylation Loci for Blood Pressure. *Hypertension*, **2020**, 76, 195-205	8.5	12
46	An integrative machine learning approach to discovering multi-level molecular mechanisms of obesity using data from monozygotic twin pairs. *Royal Society Open Science*, **2020**, 7, 200872	3.3	0
45	The Older Finnish Twin Cohort - 45 Years of Follow-up. *Twin Research and Human Genetics*, **2019**, 22, 240-254	2.2	21
44	Peripheral blood DNA methylation differences in twin pairs discordant for Alzheimer's disease. *Clinical Epigenetics*, **2019**, 11, 130	7.7	12
43	EpiSmokEr: a robust classifier to determine smoking status from DNA methylation data. *Epigenomics*, **2019**, 11, 1469-1486	4.4	35
42	Leisure-time physical activity and DNA methylation age-a twin study. *Clinical Epigenetics*, **2019**, 11, 12	7.7	16

(2015-2019)

41	Making Sense of the Epigenome Using Data Integration Approaches. *Frontiers in Pharmacology*, **2019**, 10, 126	5.6	35
40	Plasma metabolites reveal distinct profiles associating with different metabolic risk factors in monozygotic twin pairs. *International Journal of Obesity*, **2019**, 43, 487-502	5.5	9
39	Epigenome-wide association study of lung function level and its change. *European Respiratory Journal*, **2019**, 54,	13.6	25
38	Accuracy of self-reported anthropometric measures - Findings from the Finnish Twin Study. *Obesity Research and Clinical Practice*, **2019**, 13, 522-528	5.4	11
37	Epigenome-wide association study of serum cotinine in current smokers reveals novel genetically driven loci. *Clinical Epigenetics*, **2019**, 11, 1	7.7	40
36	Genetic and Environmental Effects on Gene Expression Signatures of Blood Pressure: A Transcriptome-Wide Twin Study. *Hypertension*, **2018**, 71, 457-464	8.5	9
35	High-throughput DNA methylation analysis in anorexia nervosa confirms TNXB hypermethylation. *World Journal of Biological Psychiatry*, **2018**, 19, 187-199	3.8	20
34	Subcutaneous adipose tissue gene expression and DNA methylation respond to both short- and long-term weight loss. *International Journal of Obesity*, **2018**, 42, 412-423	5.5	21
33	Biological clocks and physical functioning in monozygotic female twins. *BMC Geriatrics*, **2018**, 18, 83	4.1	13
32	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. *Clinical Epigenetics*, **2018**, 10, 126	7.7	56
31	Gene expression profile of subcutaneous adipose tissue in BMI-discordant monozygotic twin pairs unravels molecular and clinical changes associated with sub-types of obesity. *International Journal of Obesity*, **2017**, 41, 1176-1184	5.5	22
30	Neuregulin signaling pathway in smoking behavior. *Translational Psychiatry*, **2017**, 7, e1212	8.6	5
29	An epigenome-wide association study meta-analysis of educational attainment. *Molecular Psychiatry*, **2017**, 22, 1680-1690	15.1	46
28	Biotin-dependent functions in adiposity: a study of monozygotic twin pairs. *International Journal of Obesity*, **2016**, 40, 788-95	5.5	13
27	DNA methylation and gene expression patterns in adipose tissue differ significantly within young adult monozygotic BMI-discordant twin pairs. *International Journal of Obesity*, **2016**, 40, 654-61	5.5	48
26	Mendelian randomization in (epi)genetic epidemiology: an effective tool to be handled with care. *Genome Biology*, **2016**, 17, 156	18.3	24
25	Genome-wide blood DNA methylation alterations at regulatory elements and heterochromatic regions in monozygotic twins discordant for obesity and liver fat. *Clinical Epigenetics*, **2015**, 7, 39	7.7	56
24	Impaired Mitochondrial Biogenesis in Adipose Tissue in Acquired Obesity. *Diabetes*, **2015**, 64, 3135-45	0.9	177

23	Hormone Replacement Therapy Associated White Blood Cell DNA Methylation and Gene Expression are Associated With Within-Pair Differences of Body Adiposity and Bone Mass. *Twin Research and Human Genetics*, **2015**, 18, 647-61	2.2	14
22	A Genome-Wide Association Study of a Biomarker of Nicotine Metabolism. *PLoS Genetics*, **2015**, 11, e1005498	6	80
21	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. *Genome Biology*, **2013**, 14, R42	18.3	150
20	Association of maternal and nutrient supply line factors with DNA methylation at the imprinted IGF2/H19 locus in multiple tissues of newborn twins. *Epigenetics*, **2013**, 8, 1069-79	5.7	32
19	The Peri/postnatal Epigenetic Twins Study (PETS). *Twin Research and Human Genetics*, **2013**, 16, 13-20	2.2	45
18	Neonatal DNA methylation profile in human twins is specified by a complex interplay between intrauterine environmental and genetic factors, subject to tissue-specific influence. *Genome Research*, **2012**, 22, 1395-406	9.7	214
17	Cohort profile: The peri/post-natal epigenetic twins study. *International Journal of Epidemiology*, **2012**, 41, 55-61	7.8	43
16	Expression discordance of monozygotic twins at birth: effect of intrauterine environment and a possible mechanism for fetal programming. *Epigenetics*, **2011**, 6, 579-92	5.7	64
15	Epigenetic discordance at imprinting control regions in twins. *Epigenomics*, **2011**, 3, 295-306	4.4	30
14	DNA methylation analysis of multiple tissues from newborn twins reveals both genetic and intrauterine components to variation in the human neonatal epigenome. *Human Molecular Genetics* , **2010**, 19, 4176-88	5.6	270
13	Epigenetic signatures of familial cancer are characteristic of tumor type and family category. *Cancer Research*, **2008**, 68, 4597-605	10.1	72
12	Copy number alterations of the polycomb gene BMI1 in gliomas. *Acta Neuropathologica*, **2008**, 116, 97-102	14.3	36
11	Somatic FGF9 mutations in colorectal and endometrial carcinomas associated with membranous beta-catenin. *Human Mutation*, **2008**, 29, 390-7	4.7	27
10	Patterns of PIK3CA alterations in familial colorectal and endometrial carcinoma. *International Journal of Cancer*, **2007**, 121, 915-20	7.5	58
9	Mechanisms of inactivation of MLH1 in hereditary nonpolyposis colorectal carcinoma: a novel approach. *Oncogene*, **2007**, 26, 4541-9	9.2	49
8	Comprehensive characterization of HNPCC-related colorectal cancers reveals striking molecular features in families with no germline mismatch repair gene mutations. *Oncogene*, **2005**, 24, 1542-51	9.2	71
7	APC and beta-catenin protein expression patterns in HNPCC-related endometrial and colorectal cancers. *Familial Cancer*, **2005**, 4, 187-90	3	18
6	Molecular analysis of familial endometrial carcinoma: a manifestation of hereditary nonpolyposis colorectal cancer or a separate syndrome?. *Journal of Clinical Oncology*, **2005**, 23, 4609-16	2.2	113

5	Distinct patterns of KRAS mutations in colorectal carcinomas according to germline mismatch repair defects and hMLH1 methylation status. *Human Molecular Genetics*, **2004**, 13, 2303-11	5.6	102
4	BRAF screening as a low-cost effective strategy for simplifying HNPCC genetic testing. *Journal of Medical Genetics*, **2004**, 41, 664-8	5.8	256
3	Frequency-related effects in the optimization of coils for the magnetic stimulation of the nervous system. *IEEE Transactions on Biomedical Engineering*, **2002**, 49, 463-71	5	13
2	Mutations in the beta-tropomyosin (TPM2) gene--a rare cause of nemaline myopathy. *Neuromuscular Disorders*, **2002**, 12, 151-8	2.9	182
1	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health		2