Miina E Ollikainen

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

#	Paper	IF	Citations
58	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, 4176-88	5.6	270
57	BRAF screening as a low-cost effective strategy for simplifying HNPCC genetic testing. <i>Journal of Medical Genetics</i> , 2004 , 41, 664-8	5.8	256
56	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, 1395-406	9.7	214
55	Mutations in the beta-tropomyosin (TPM2) genea rare cause of nemaline myopathy. <i>Neuromuscular Disorders</i> , 2002 , 12, 151-8	2.9	182
54	Impaired Mitochondrial Biogenesis in Adipose Tissue in Acquired Obesity. <i>Diabetes</i> , 2015 , 64, 3135-45	0.9	177
53	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	18.3	150
52	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, 4609-16	2.2	113
51	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, 2303-11	5.6	102
50	A Genome-Wide Association Study of a Biomarker of Nicotine Metabolism. <i>PLoS Genetics</i> , 2015 , 11, e10	00 5 498	80
49	Epigenetic signatures of familial cancer are characteristic of tumor type and family category. <i>Cancer Research</i> , 2008 , 68, 4597-605	10.1	72
48	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, 1542-51	9.2	71
47	Expression discordance of monozygotic twins at birth: effect of intrauterine environment and a possible mechanism for fetal programming. <i>Epigenetics</i> , 2011 , 6, 579-92	5.7	64
46	Patterns of PIK3CA alterations in familial colorectal and endometrial carcinoma. <i>International Journal of Cancer</i> , 2007 , 121, 915-20	7.5	58
45	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	7.7	56
44	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. <i>Clinical Epigenetics</i> , 2018 , 10, 126	7.7	56
43	Mechanisms of inactivation of MLH1 in hereditary nonpolyposis colorectal carcinoma: a novel approach. <i>Oncogene</i> , 2007 , 26, 4541-9	9.2	49
42	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, 654-61	5.5	48

(2005-2017)

41	An epigenome-wide association study meta-analysis of educational attainment. <i>Molecular Psychiatry</i> , 2017 , 22, 1680-1690	15.1	46
40	The Peri/postnatal Epigenetic Twins Study (PETS). Twin Research and Human Genetics, 2013, 16, 13-20	2.2	45
39	Cohort profile: The peri/post-natal epigenetic twins study. <i>International Journal of Epidemiology</i> , 2012 , 41, 55-61	7.8	43
38	Epigenome-wide association study of serum cotinine in current smokers reveals novel genetically driven loci. <i>Clinical Epigenetics</i> , 2019 , 11, 1	7.7	40
37	Copy number alterations of the polycomb gene BMI1 in gliomas. <i>Acta Neuropathologica</i> , 2008 , 116, 97-	1 02 .3	36
36	EpiSmokEr: a robust classifier to determine smoking status from DNA methylation data. <i>Epigenomics</i> , 2019 , 11, 1469-1486	4.4	35
35	Making Sense of the Epigenome Using Data Integration Approaches. <i>Frontiers in Pharmacology</i> , 2019 , 10, 126	5.6	35
34	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, 1069-79	5.7	32
33	Epigenetic discordance at imprinting control regions in twins. <i>Epigenomics</i> , 2011 , 3, 295-306	4.4	30
32	Somatic FGF9 mutations in colorectal and endometrial carcinomas associated with membranous beta-catenin. <i>Human Mutation</i> , 2008 , 29, 390-7	4.7	27
31	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021 , 53, 1311-1321	36.3	27
30	Epigenome-wide association study of lung function level and its change. <i>European Respiratory Journal</i> , 2019 , 54,	13.6	25
29	Mendelian randomization in (epi)genetic epidemiology: an effective tool to be handled with care. <i>Genome Biology</i> , 2016 , 17, 156	18.3	24
28	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	5.5	22
27	The Older Finnish Twin Cohort - 45 Years of Follow-up. Twin Research and Human Genetics, 2019, 22, 240	0 <u>-225</u> 4	21
26	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	5.5	21
25	High-throughput DNA methylation analysis in anorexia nervosa confirms TNXB hypermethylation. World Journal of Biological Psychiatry, 2018 , 19, 187-199	3.8	20
24	APC and beta-catenin protein expression patterns in HNPCC-related endometrial and colorectal cancers. <i>Familial Cancer</i> , 2005 , 4, 187-90	3	18

23	Leisure-time physical activity and DNA methylation age-a twin study. Clinical Epigenetics, 2019, 11, 12	7.7	16
22	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, 647-61	2.2	14
21	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021 , 22, 194	18.3	14
20	Biotin-dependent functions in adiposity: a study of monozygotic twin pairs. <i>International Journal of Obesity</i> , 2016 , 40, 788-95	5.5	13
19	Biological clocks and physical functioning in monozygotic female twins. <i>BMC Geriatrics</i> , 2018 , 18, 83	4.1	13
18	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, 463-71	5	13
17	Peripheral blood DNA methylation differences in twin pairs discordant for Alzheimer's disease. <i>Clinical Epigenetics</i> , 2019 , 11, 130	7.7	12
16	Identification, Heritability, and Relation With Gene Expression of Novel DNA Methylation Loci for Blood Pressure. <i>Hypertension</i> , 2020 , 76, 195-205	8.5	12
15	Accuracy of self-reported anthropometric measures - Findings from the Finnish Twin Study. <i>Obesity Research and Clinical Practice</i> , 2019 , 13, 522-528	5.4	11
14	Genetic and Environmental Effects on Gene Expression Signatures of Blood Pressure: A Transcriptome-Wide Twin Study. <i>Hypertension</i> , 2018 , 71, 457-464	8.5	9
13	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	5.5	9
12	Leisure-Time and Occupational Physical Activity Associates Differently with Epigenetic Aging. <i>Medicine and Science in Sports and Exercise</i> , 2021 , 53, 487-495	1.2	8
11	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	15.1	7
10	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021 , 12, 5618	17.4	6
9	Neuregulin signaling pathway in smoking behavior. <i>Translational Psychiatry</i> , 2017 , 7, e1212	8.6	5
8	Does the epigenetic clock GrimAge predict mortality independent of genetic influences: an 18lyear follow-up study in older female twin pairs. <i>Clinical Epigenetics</i> , 2021 , 13, 128	7.7	4
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	3.7	4
6	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health		2

LIST OF PUBLICATIONS

5	The potential of DNA methylation as a biomarker for obesity and smoking <i>Journal of Internal Medicine</i> , 2022 ,	10.8	2
4	Blood and skeletal muscle ageing determined by epigenetic clocks and their associations with physical activity and functioning. <i>Clinical Epigenetics</i> , 2021 , 13, 110	7.7	1
3	Genetic meta-analysis of twin birth weight shows high genetic correlation with singleton birth weight. <i>Human Molecular Genetics</i> , 2021 , 30, 1894-1905	5.6	1
2	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	3.8	1
1	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	3.3	O