

Eilis J Hannon

List of Publications by Year in Descending Order

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Version: 2024-04-27

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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.

104
papers

5,981
citations

33
h-index

77
g-index

145
ext. papers

8,613
ext. citations

9.9
avg, IF

5.36
L-index

#	Paper	IF	Citations
104	DunedinPACE, a DNA methylation biomarker of the pace of aging.. <i>ELife</i> , 2022 , 11,	8.9	9
103	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS.. <i>Science Translational Medicine</i> , 2022 , 14, eabj0264	17.5	4
102	Methylome analysis of ALS patients and presymptomatic mutation carriers in blood cells.. <i>Neurobiology of Aging</i> , 2022 , 116, 16-24	5.6	0
101	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. <i>Nature Genetics</i> , 2021 , 53, 1636-1648	36.3	19
100	Full-length transcript sequencing of human and mouse cerebral cortex identifies widespread isoform diversity and alternative splicing. <i>Cell Reports</i> , 2021 , 37, 110022	10.6	5
99	Sites of active gene regulation in the prenatal frontal cortex and their role in neuropsychiatric disorders. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2021 , 186, 376-388	3.5	1
98	DNA methylation signatures of adolescent victimization: analysis of a longitudinal monozygotic twin sample. <i>Epigenetics</i> , 2021 , 16, 1169-1186	5.7	2
97	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , 2021 , 22, 90	18.3	6
96	Assessing the co-variability of DNA methylation across peripheral cells and tissues: Implications for the interpretation of findings in epigenetic epidemiology. <i>PLoS Genetics</i> , 2021 , 17, e1009443	6	11
95	A meta-analysis of epigenome-wide association studies in Alzheimer's disease highlights novel differentially methylated loci across cortex. <i>Nature Communications</i> , 2021 , 12, 3517	17.4	8
94	DNA methylation-based sex classifier to predict sex and identify sex chromosome aneuploidy. <i>BMC Genomics</i> , 2021 , 22, 484	4.5	2
93	Interaction between genetic predisposition, smoking, and dementia risk: a population-based cohort study. <i>Scientific Reports</i> , 2021 , 11, 12953	4.9	1
92	Characterizing the properties of bisulfite sequencing data: maximizing power and sensitivity to identify between-group differences in DNA methylation. <i>BMC Genomics</i> , 2021 , 22, 446	4.5	3
91	Novel epigenetic clock for fetal brain development predicts prenatal age for cellular stem cell models and derived neurons. <i>Molecular Brain</i> , 2021 , 14, 98	4.5	3
90	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
89	DNA methylation meta-analysis reveals cellular alterations in psychosis and markers of treatment-resistant schizophrenia. <i>ELife</i> , 2021 , 10,	8.9	15
88	A machine learning case-control classifier for schizophrenia based on DNA methylation in blood. <i>Translational Psychiatry</i> , 2021 , 11, 412	8.6	3

87	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021 , 12, 5618	17.4	6
86	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021 , 53, 1311-1321	36.3	27
85	Independent Methylome-Wide Association Studies of Schizophrenia Detect Consistent Case-Control Differences. <i>Schizophrenia Bulletin</i> , 2020 , 46, 319-327	1.3	3
84	Assessment of the contribution of common genetic variants associated with Alzheimer's disease on neuropathological burden and clinical characteristics in the Brains for Dementia Research cohort. <i>Alzheimers and Dementia</i> , 2020 , 16, e042868	1.2	
83	An integrated epigenetic-genetic study of neuropathology in the Brains for Dementia Research cohort. <i>Alzheimers and Dementia</i> , 2020 , 16, e043388	1.2	
82	Recalibrating the epigenetic clock: implications for assessing biological age in the human cortex. <i>Brain</i> , 2020 , 143, 3763-3775	11.2	32
81	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. <i>Npj Genomic Medicine</i> , 2020 , 5, 10	6.2	11
80	Epigenome-wide association study of attention-deficit/hyperactivity disorder in adults. <i>Translational Psychiatry</i> , 2020 , 10, 199	8.6	4
79	Genome-wide DNA methylation meta-analysis in the brains of suicide completers. <i>Translational Psychiatry</i> , 2020 , 10, 69	8.6	17
78	Genome-Wide DNA Methylation Patterns in Persistent Attention-Deficit/Hyperactivity Disorder and in Association With Impulsive and Callous Traits. <i>Frontiers in Genetics</i> , 2020 , 11, 16	4.5	6
77	Major surgery induces acute changes in measured DNA methylation associated with immune response pathways. <i>Scientific Reports</i> , 2020 , 10, 5743	4.9	8
76	Genetic risk for Alzheimer's disease influences neuropathology via multiple biological pathways. <i>Brain Communications</i> , 2020 , 2, fcaa167	4.5	1
75	Transcriptional Signatures of Tau and Amyloid Neuropathology. <i>Cell Reports</i> , 2020 , 30, 2040-2054.e5	10.6	20
74	Clozapine-induced transcriptional changes in the zebrafish brain. <i>NPJ Schizophrenia</i> , 2020 , 6, 3	5.5	5
73	Cross-reactive probes on Illumina DNA methylation arrays: a large study on ALS shows that a cautionary approach is warranted in interpreting epigenome-wide association studies. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa105	3.7	3
72	Patterns of Reliability: Assessing the Reproducibility and Integrity of DNA Methylation Measurement. <i>Patterns</i> , 2020 , 1,	5.1	24
71	An epigenome-wide association study of Alzheimer's disease blood highlights robust DNA hypermethylation in the HOXB6 gene. <i>Neurobiology of Aging</i> , 2020 , 95, 26-45	5.6	17
70	Methylation age acceleration does not predict mortality in schizophrenia. <i>Translational Psychiatry</i> , 2019 , 9, 157	8.6	9

69	Guidance for DNA methylation studies: statistical insights from the Illumina EPIC array. <i>BMC Genomics</i> , 2019 , 20, 366	4.5	87
68	Parallel profiling of DNA methylation and hydroxymethylation highlights neuropathology-associated epigenetic variation in Alzheimer's disease. <i>Clinical Epigenetics</i> , 2019 , 11, 52	7.7	49
67	Genome-wide DNA methylation profiling identifies convergent molecular signatures associated with idiopathic and syndromic autism in post-mortem human brain tissue. <i>Human Molecular Genetics</i> , 2019 , 28, 2201-2211	5.6	43
66	Variable DNA methylation in neonates mediates the association between prenatal smoking and birth weight. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019 , 374, 20180120	5.8	28
65	Dynamic expression of genes associated with schizophrenia and bipolar disorder across development. <i>Translational Psychiatry</i> , 2019 , 9, 74	8.6	18
64	Genetic risk variants for brain disorders are enriched in cortical H3K27ac domains. <i>Molecular Brain</i> , 2019 , 12, 7	4.5	11
63	Longitudinal investigation of DNA methylation changes preceding adolescent psychotic experiences. <i>Translational Psychiatry</i> , 2019 , 9, 69	8.6	10
62	Association of Lifestyle and Genetic Risk With Incidence of Dementia. <i>JAMA - Journal of the American Medical Association</i> , 2019 , 322, 430-437	27.4	150
61	Integrated genetic and methylomic analyses identify shared biology between autism and autistic traits. <i>Molecular Autism</i> , 2019 , 10, 31	6.5	12
60	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. <i>Biological Psychiatry</i> , 2019 , 86, 599-607	7.9	24
59	Establishing a generalized polyepigenetic biomarker for tobacco smoking. <i>Translational Psychiatry</i> , 2019 , 9, 92	8.6	34
58	Systematic underestimation of the epigenetic clock and age acceleration in older subjects. <i>Genome Biology</i> , 2019 , 20, 283	18.3	41
57	THE AUTHORS REPLY. <i>American Journal of Epidemiology</i> , 2019 , 188, 488-489	3.8	1
56	Bigmelon: tools for analysing large DNA methylation datasets. <i>Bioinformatics</i> , 2019 , 35, 981-986	7.2	20
55	Analysis of DNA Methylation in Young People: Limited Evidence for an Association Between Victimization Stress and Epigenetic Variation in Blood. <i>American Journal of Psychiatry</i> , 2018 , 175, 517-529	11.9	83
54	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018 , 23, 2133-2144	15.1	46
53	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018 , 50, 668-681	36.3	1301
52	Elevated DNA methylation across a 48-kb region spanning the HOXA gene cluster is associated with Alzheimer's disease neuropathology. <i>Alzheimers and Dementia</i> , 2018 , 14, 1580-1588	1.2	73

51	Genome-wide methylomic analysis in individuals with HNF1B intragenic mutation and 17q12 microdeletion. <i>Clinical Epigenetics</i> , 2018 , 10, 97	7.7	10
50	Socioeconomic Position and DNA Methylation Age Acceleration Across the Life Course. <i>American Journal of Epidemiology</i> , 2018 , 187, 2346-2354	3.8	49
49	Elevated polygenic burden for autism is associated with differential DNA methylation at birth. <i>Genome Medicine</i> , 2018 , 10, 19	14.4	58
48	Characterizing genetic and environmental influences on variable DNA methylation using monozygotic and dizygotic twins. <i>PLoS Genetics</i> , 2018 , 14, e1007544	6	92
47	Which Risk Factors Causally Influence Dementia? A Systematic Review of Mendelian Randomization Studies. <i>Journal of Alzheimerts Disease</i> , 2018 , 64, 181-193	4.3	20
46	Expression quantitative trait loci in the developing human brain and their enrichment in neuropsychiatric disorders. <i>Genome Biology</i> , 2018 , 19, 194	18.3	69
45	Leveraging DNA-Methylation Quantitative-Trait Loci to Characterize the Relationship between Methylomic Variation, Gene Expression, and Complex Traits. <i>American Journal of Human Genetics</i> , 2018 , 103, 654-665	11	61
44	A histone acetylome-wide association study of Alzheimer's disease identifies disease-associated H3K27ac differences in the entorhinal cortex. <i>Nature Neuroscience</i> , 2018 , 21, 1618-1627	25.5	72
43	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. <i>Nature Communications</i> , 2018 , 9, 3738	17.4	12
42	DNA methylation and inflammation marker profiles associated with a history of depression. <i>Human Molecular Genetics</i> , 2018 , 27, 2840-2850	5.6	23
41	Pleiotropic Effects of Trait-Associated Genetic Variation on DNA Methylation: Utility for Refining GWAS Loci. <i>American Journal of Human Genetics</i> , 2017 , 100, 954-959	11	61
40	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. <i>Nature Communications</i> , 2017 , 8, 15353	17.4	57
39	Methylomic profiling of cortex samples from completed suicide cases implicates a role for PSORS1C3 in major depression and suicide. <i>Translational Psychiatry</i> , 2017 , 7, e989	8.6	48
38	Genetic variation at 16q24.2 is associated with small vessel stroke. <i>Annals of Neurology</i> , 2017 , 81, 383-394	9.4	51
37	5-hydroxymethylcytosine is highly dynamic across human fetal brain development. <i>BMC Genomics</i> , 2017 , 18, 738	4.5	43
36	[P3B29]: A SYSTEMATIC REVIEW OF MENDELIAN RANDOMIZATION STUDIES INVESTIGATING CAUSAL ASSOCIATIONS BETWEEN RISK FACTORS AND DEMENTIA 2017 , 13, P1180-P1180		0
35	Regional differences in mitochondrial DNA methylation in human post-mortem brain tissue. <i>Clinical Epigenetics</i> , 2017 , 9, 47	7.7	22
34	Schizophrenia-associated methylomic variation: molecular signatures of disease and polygenic risk burden across multiple brain regions. <i>Human Molecular Genetics</i> , 2017 , 26, 210-225	5.6	60

33	An integrated genetic-epigenetic analysis of schizophrenia: evidence for co-localization of genetic associations and differential DNA methylation. <i>Genome Biology</i> , 2016 , 17, 176	18.3	189
32	Increased DNA methylation near TREM2 is consistently seen in the superior temporal gyrus in Alzheimer's disease brain. <i>Neurobiology of Aging</i> , 2016 , 47, 35-40	5.6	60
31	Variation in 5-hydroxymethylcytosine across human cortex and cerebellum. <i>Genome Biology</i> , 2016 , 17, 27	18.3	67
30	Age-associated changes in DNA methylation across multiple tissues in an inbred mouse model. <i>Mechanisms of Ageing and Development</i> , 2016 , 154, 20-3	5.6	27
29	Methylation QTLs in the developing brain and their enrichment in schizophrenia risk loci. <i>Nature Neuroscience</i> , 2016 , 19, 48-54	25.5	227
28	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. <i>Human Molecular Genetics</i> , 2016 , 25, 4339-4349	5.6	7
27	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016 , 7, 10561	17.4	55
26	O2-06-05: Hydroxymethylomic Profiling Implicates Cortical Deregulation of ANK1 and APP in the Alzheimer's Disease Brain 2016 , 12, P240-P241		
25	Methylomic trajectories across human fetal brain development. <i>Genome Research</i> , 2015 , 25, 338-52	9.7	188
24	Methylomic analysis of monozygotic twins discordant for childhood psychotic symptoms. <i>Epigenetics</i> , 2015 , 10, 1014-23	5.7	36
23	Interindividual methylomic variation across blood, cortex, and cerebellum: implications for epigenetic studies of neurological and neuropsychiatric phenotypes. <i>Epigenetics</i> , 2015 , 10, 1024-32	5.7	272
22	A role for Ca1 and calcineurin signaling in depolarization-induced changes in neuronal DNA methylation. <i>Neuroepigenetics</i> , 2015 , 3, 1-6		2
21	Methylomic markers of persistent childhood asthma: a longitudinal study of asthma-discordant monozygotic twins. <i>Clinical Epigenetics</i> , 2015 , 7, 130	7.7	33
20	O3-05-01: Systems-level evidence for epigenetic dysfunction in Alzheimer's disease 2015 , 11, P228-P228		
19	De novo mutations in schizophrenia implicate synaptic networks. <i>Nature</i> , 2014 , 506, 179-84	50.4	1163
18	Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. <i>Nature Neuroscience</i> , 2014 , 17, 1164-70	25.5	356
17	O3-04-03: CROSS-TISSUE METHYLOMIC PROFILING IN ALZHEIMER'S DISEASE 2014 , 10, P215-P215		
16	Methylomic profiling of human brain tissue supports a neurodevelopmental origin for schizophrenia. <i>Genome Biology</i> , 2014 , 15, 483	18.3	114

15	Sex differences in gene expression in the human fetal brain	3
14	Epigenetic age is accelerated in schizophrenia with age- and sex-specific effects and associated with polygenic disease risk	2
13	A comparison of blood and brain-derived ageing and inflammation-related DNA methylation signatures and their association with microglial burdens	1
12	5-hydroxymethylcytosine is highly dynamic across human fetal brain development	1
11	A meta-analysis of epigenome-wide association studies in Alzheimer's disease highlights novel differentially methylated loci across cortex	8
10	Large-scale analysis of DNA methylation identifies cellular alterations in blood from psychosis patients and molecular biomarkers of treatment-resistant schizophrenia	1
9	Recalibrating the Epigenetic Clock: Implications for Assessing Biological Age in the Human Cortex	6
8	Assessing the co-variability of DNA methylation across peripheral cells and tissues: implications for the interpretation of findings in epigenetic epidemiology	2
7	Genomic and phenomic insights from an atlas of genetic effects on DNA methylation	7
6	Novel epigenetic clock for fetal brain development predicts prenatal age for cellular stem cell models and derived neurons	1
5	Properties of the epigenetic clock and age acceleration	4
4	Genome-wide DNA methylation profiling identifies convergent molecular signatures associated with idiopathic and syndromic forms of autism in post-mortem human brain tissue	1
3	A histone acetylome-wide association study of Alzheimer's disease: neuropathology-associated regulatory variation in the human entorhinal cortex	1
2	Genome-wide study of DNA methylation in Amyotrophic Lateral Sclerosis identifies differentially methylated loci and implicates metabolic, inflammatory and cholesterol pathways	1
1	Quantification of the pace of biological aging in humans through a blood test: the DunedinPACE DNA methylation algorithm	3