

Eilis J Hannon

List of Publications by Year in descending order

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Version: 2024-02-01

95
papers

10,483
citations

71061

41
h-index

43868

91
g-index

145
all docs

145
docs citations

145
times ranked

16371
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	9.4	2,224
2	De novo mutations in schizophrenia implicate synaptic networks. <i>Nature</i> , 2014, 506, 179-184.	13.7	1,510
3	Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. <i>Nature Neuroscience</i> , 2014, 17, 1164-1170.	7.1	488
4	Association of Lifestyle and Genetic Risk With Incidence of Dementia. <i>JAMA - Journal of the American Medical Association</i> , 2019, 322, 430.	3.8	421
5	Interindividual methylomic variation across blood, cortex, and cerebellum: implications for epigenetic studies of neurological and neuropsychiatric phenotypes. <i>Epigenetics</i> , 2015, 10, 1024-1032.	1.3	393
6	Methylation QTLs in the developing brain and their enrichment in schizophrenia risk loci. <i>Nature Neuroscience</i> , 2016, 19, 48-54.	7.1	306
7	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.	3.8	287
8	Methylomic trajectories across human fetal brain development. <i>Genome Research</i> , 2015, 25, 338-352.	2.4	250
9	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.	9.4	223
10	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
11	DunedinPACE, a DNA methylation biomarker of the pace of aging. <i>ELife</i> , 2022, 11, .	2.8	214
12	Guidance for DNA methylation studies: statistical insights from the Illumina EPIC array. <i>BMC Genomics</i> , 2019, 20, 366.	1.2	201
13	Characterizing genetic and environmental influences on variable DNA methylation using monozygotic and dizygotic twins. <i>PLoS Genetics</i> , 2018, 14, e1007544.	1.5	153
14	Methylomic profiling of human brain tissue supports a neurodevelopmental origin for schizophrenia. <i>Genome Biology</i> , 2014, 15, 483.	3.8	141
15	Elevated DNA methylation across a 48 kb region spanning the <i>HOXA</i> gene cluster is associated with Alzheimer's disease neuropathology. <i>Alzheimer's and Dementia</i> , 2018, 14, 1580-1588.	0.4	138
16	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.	7.1	138
17	Expression quantitative trait loci in the developing human brain and their enrichment in neuropsychiatric disorders. <i>Genome Biology</i> , 2018, 19, 194.	3.8	126
18	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.	2.6	126

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19	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.	4.0	114
20	Recalibrating the epigenetic clock: implications for assessing biological age in the human cortex. <i>Brain</i> , 2020, 143, 3763-3775.	3.7	100
21	Systematic underestimation of the epigenetic clock and age acceleration in older subjects. <i>Genome Biology</i> , 2019, 20, 283.	3.8	97
22	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. <i>Nature Communications</i> , 2017, 8, 15353.	5.8	92
23	Elevated polygenic burden for autism is associated with differential DNA methylation at birth. <i>Genome Medicine</i> , 2018, 10, 19.	3.6	88
24	Parallel profiling of DNA methylation and hydroxymethylation highlights neuropathology-associated epigenetic variation in Alzheimer's disease. <i>Clinical Epigenetics</i> , 2019, 11, 52.	1.8	84
25	Variation in 5-hydroxymethylcytosine across human cortex and cerebellum. <i>Genome Biology</i> , 2016, 17, 27.	3.8	83
26	Socioeconomic Position and DNA Methylation Age Acceleration Across the Life Course. <i>American Journal of Epidemiology</i> , 2018, 187, 2346-2354.	1.6	81
27	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.	1.5	79
28	Full-length transcript sequencing of human and mouse cerebral cortex identifies widespread isoform diversity and alternative splicing. <i>Cell Reports</i> , 2021, 37, 110022.	2.9	79
29	Patterns of Reliability: Assessing the Reproducibility and Integrity of DNA Methylation Measurement. <i>Patterns</i> , 2020, 1, 100014.	3.1	78
30	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.	2.6	77
31	Schizophrenia-associated methylomic variation: molecular signatures of disease and polygenic risk burden across multiple brain regions. <i>Human Molecular Genetics</i> , 2017, 26, ddw373.	1.4	74
32	Genetic variation at 16q24.2 is associated with small vessel stroke. <i>Annals of Neurology</i> , 2017, 81, 383-394.	2.8	73
33	DNA methylation meta-analysis reveals cellular alterations in psychosis and markers of treatment-resistant schizophrenia. <i>ELife</i> , 2021, 10, .	2.8	72
34	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.	5.8	72
35	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.	1.4	70
36	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016, 7, 10561.	5.8	69

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37	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018, 23, 2133-2144.	4.1	68
38	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-e989.	2.4	64
39	5-hydroxymethylcytosine is highly dynamic across human fetal brain development. <i>BMC Genomics</i> , 2017, 18, 738.	1.2	63
40	Establishing a generalized polyepigenetic biomarker for tobacco smoking. <i>Translational Psychiatry</i> , 2019, 9, 92.	2.4	51
41	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.	1.5	51
42	Bigmelon: tools for analysing large DNA methylation datasets. <i>Bioinformatics</i> , 2019, 35, 981-986.	1.8	49
43	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , 2021, 22, 90.	3.8	49
44	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. <i>Biological Psychiatry</i> , 2019, 86, 599-607.	0.7	47
45	DNA methylation and inflammation marker profiles associated with a history of depression. <i>Human Molecular Genetics</i> , 2018, 27, 2840-2850.	1.4	46
46	Which Risk Factors Causally Influence Dementia? A Systematic Review of Mendelian Randomization Studies. <i>Journal of Alzheimer's Disease</i> , 2018, 64, 181-193.	1.2	46
47	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.	1.8	46
48	Transcriptional Signatures of Tau and Amyloid Neuropathology. <i>Cell Reports</i> , 2020, 30, 2040-2054.e5.	2.9	45
49	Methylomic analysis of monozygotic twins discordant for childhood psychotic symptoms. <i>Epigenetics</i> , 2015, 10, 1014-1023.	1.3	40
50	Methylomic markers of persistent childhood asthma: a longitudinal study of asthma-discordant monozygotic twins. <i>Clinical Epigenetics</i> , 2015, 7, 130.	1.8	38
51	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. <i>Science Translational Medicine</i> , 2022, 14, eabj0264.	5.8	38
52	Dynamic expression of genes associated with schizophrenia and bipolar disorder across development. <i>Translational Psychiatry</i> , 2019, 9, 74.	2.4	37
53	Age-associated changes in DNA methylation across multiple tissues in an inbred mouse model. <i>Mechanisms of Ageing and Development</i> , 2016, 154, 20-23.	2.2	34
54	Regional differences in mitochondrial DNA methylation in human post-mortem brain tissue. <i>Clinical Epigenetics</i> , 2017, 9, 47.	1.8	34

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55	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.	1.5	33
56	Genome-wide DNA methylation meta-analysis in the brains of suicide completers. <i>Translational Psychiatry</i> , 2020, 10, 69.	2.4	32
57	Major surgery induces acute changes in measured DNA methylation associated with immune response pathways. <i>Scientific Reports</i> , 2020, 10, 5743.	1.6	31
58	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021, 12, 5618.	5.8	26
59	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. <i>Npj Genomic Medicine</i> , 2020, 5, 10.	1.7	25
60	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.	1.1	25
61	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. <i>Nature Communications</i> , 2018, 9, 3738.	5.8	24
62	Genetic risk variants for brain disorders are enriched in cortical H3K27ac domains. <i>Molecular Brain</i> , 2019, 12, 7.	1.3	21
63	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
64	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.	1.3	19
65	Genome-wide methylomic analysis in individuals with HNF1B intragenic mutation and 17q12 microdeletion. <i>Clinical Epigenetics</i> , 2018, 10, 97.	1.8	18
66	Integrated genetic and methylomic analyses identify shared biology between autism and autistic traits. <i>Molecular Autism</i> , 2019, 10, 31.	2.6	17
67	Methylation age acceleration does not predict mortality in schizophrenia. <i>Translational Psychiatry</i> , 2019, 9, 157.	2.4	17
68	A machine learning caseâ€“control classifier for schizophrenia based on DNA methylation in blood. <i>Translational Psychiatry</i> , 2021, 11, 412.	2.4	16
69	Independent Methylome-Wide Association Studies of Schizophrenia Detect Consistent Caseâ€“Control Differences. <i>Schizophrenia Bulletin</i> , 2020, 46, 319-327.	2.3	15
70	Epigenome-wide association study of attention-deficit/hyperactivity disorder in adults. <i>Translational Psychiatry</i> , 2020, 10, 199.	2.4	14
71	Clozapine-induced transcriptional changes in the zebrafish brain. <i>NPJ Schizophrenia</i> , 2020, 6, 3.	2.0	14
72	DNA methylation signatures of adolescent victimization: analysis of a longitudinal monozygotic twin sample. <i>Epigenetics</i> , 2021, 16, 1169-1186.	1.3	14

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73	Longitudinal investigation of DNA methylation changes preceding adolescent psychotic experiences. <i>Translational Psychiatry</i> , 2019, 9, 69.	2.4	13
74	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.	1.5	13
75	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. <i>Human Molecular Genetics</i> , 2016, 25, 4339-4349.	1.4	11
76	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.	1.2	11
77	DNA methylation-based sex classifier to predict sex and identify sex chromosome aneuploidy. <i>BMC Genomics</i> , 2021, 22, 484.	1.2	9
78	Genetic risk for Alzheimer's disease influences neuropathology via multiple biological pathways. <i>Brain Communications</i> , 2020, 2, fcaa167.	1.5	9
79	Interaction between genetic predisposition, smoking, and dementia risk: a population-based cohort study. <i>Scientific Reports</i> , 2021, 11, 12953.	1.6	8
80	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.	1.1	8
81	Methylome analysis of ALS patients and presymptomatic mutation carriers in blood cells. <i>Neurobiology of Aging</i> , 2022, 116, 16-24.	1.5	8
82	Evaluation of nanopore sequencing for epigenetic epidemiology: a comparison with DNA methylation microarrays. <i>Human Molecular Genetics</i> , 2022, 31, 3181-3190.	1.4	5
83	A role for CaV1 and calcineurin signaling in depolarization-induced changes in neuronal DNA methylation. <i>Neuroepigenetics</i> , 2015, 3, 1-6.	2.8	4
84	THE AUTHORS REPLY. <i>American Journal of Epidemiology</i> , 2019, 188, 488-489.	1.6	3
85	Functional characterization of the schizophrenia associated gene <i>AS3MT</i> identifies a role in neuronal development. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 0, , .	1.1	2
86	Longitudinal Epigenetic Analysis Of Clozapine Use In Treatment-Resistant Schizophrenia: Data From The Crestar Consortium. <i>European Neuropsychopharmacology</i> , 2017, 27, S463-S464.	0.3	1
87	[P3529]: A SYSTEMATIC REVIEW OF MENDELIAN RANDOMIZATION STUDIES INVESTIGATING CAUSAL ASSOCIATIONS BETWEEN RISK FACTORS AND DEMENTIA. <i>Alzheimer's and Dementia</i> , 2017, 13, P1180.	0.4	1
88	O3-04-03: CROSS-TISSUE METHYLOMIC PROFILING IN ALZHEIMER'S DISEASE. , 2014, 10, P215-P215.		0
89	O3-05-01: Systems-level evidence for epigenetic dysfunction in Alzheimer's disease. , 2015, 11, P228-P228.		0
90	O20605: Hydroxymethylomic Profiling Implicates Cortical Deregulation of <i>ANK1</i> and <i>APP</i> in the Alzheimer's Disease Brain. <i>Alzheimer's and Dementia</i> , 2016, 12, P240.	0.4	0

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91	PLEIOTROPIC EFFECTS OF GENETIC VARIATION ASSOCIATED WITH PSYCHIATRIC DISORDERS ON DNA METHYLATION. <i>European Neuropsychopharmacology</i> , 2019, 29, S984-S985.	0.3	0
92	SU123PREDICTION OF MORTALITY USING DNA METHYLATION AGE IN SCHIZOPHRENIA. <i>European Neuropsychopharmacology</i> , 2019, 29, S1332-S1333.	0.3	0
93	A ZEBRAFISH MODEL OF CLOZAPINE EXPOSURE: DRUG-INDUCED TRANSCRIPTOMIC CHANGES IN THE BRAIN. <i>European Neuropsychopharmacology</i> , 2019, 29, S782.	0.3	0
94	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>Alzheimer's and Dementia</i> , 2020, 16, e042868.	0.4	0
95	An integrated epigenetic-genetic study of neuropathology in the Brains for Dementia Research cohort. <i>Alzheimer's and Dementia</i> , 2020, 16, e043388.	0.4	0