

Eilis J Hannon

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/880420/publications.pdf>

Version: 2024-02-01

95
papers

10,483
citations

70961

41
h-index

43802

91
g-index

145
all docs

145
docs citations

145
times ranked

16371
citing authors

#	ARTICLE	IF	CITATIONS
1	DunedinPACE, a DNA methylation biomarker of the pace of aging. <i>ELife</i> , 2022, 11, .	2.8	214
2	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
3	Methylome analysis of ALS patients and presymptomatic mutation carriers in blood cells. <i>Neurobiology of Aging</i> , 2022, 116, 16-24.	1.5	8
4	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
5	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
6	DNA methylation meta-analysis reveals cellular alterations in psychosis and markers of treatment-resistant schizophrenia. <i>ELife</i> , 2021, 10, .	2.8	72
7	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , 2021, 22, 90.	3.8	49
8	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
9	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
10	DNA methylation-based sex classifier to predict sex and identify sex chromosome aneuploidy. <i>BMC Genomics</i> , 2021, 22, 484.	1.2	9
11	Interaction between genetic predisposition, smoking, and dementia risk: a population-based cohort study. <i>Scientific Reports</i> , 2021, 11, 12953.	1.6	8
12	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
13	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
14	A machine learning case-control classifier for schizophrenia based on DNA methylation in blood. <i>Translational Psychiatry</i> , 2021, 11, 412.	2.4	16
15	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021, 12, 5618.	5.8	26
16	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
17	DNA methylation signatures of adolescent victimization: analysis of a longitudinal monozygotic twin sample. <i>Epigenetics</i> , 2021, 16, 1169-1186.	1.3	14
18	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

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19	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
20	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
21	Independent Methylome-Wide Association Studies of Schizophrenia Detect Consistent Caseâ€“Control Differences. <i>Schizophrenia Bulletin</i> , 2020, 46, 319-327.	2.3	15
22	Patterns of Reliability: Assessing the Reproducibility and Integrity of DNA Methylation Measurement. <i>Patterns</i> , 2020, 1, 100014.	3.1	78
23	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
24	Assessment of the contribution of common genetic variants associated with Alzheimerâ€™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
25	An integrated epigeneticâ€“genetic study of neuropathology in the Brains for Dementia Research cohort. <i>Alzheimer's and Dementia</i> , 2020, 16, e043388.	0.4	0
26	Recalibrating the epigenetic clock: implications for assessing biological age in the human cortex. <i>Brain</i> , 2020, 143, 3763-3775.	3.7	100
27	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. <i>Npj Genomic Medicine</i> , 2020, 5, 10.	1.7	25
28	Epigenome-wide association study of attention-deficit/hyperactivity disorder in adults. <i>Translational Psychiatry</i> , 2020, 10, 199.	2.4	14
29	Genome-wide DNA methylation meta-analysis in the brains of suicide completers. <i>Translational Psychiatry</i> , 2020, 10, 69.	2.4	32
30	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
31	Major surgery induces acute changes in measured DNA methylation associated with immune response pathways. <i>Scientific Reports</i> , 2020, 10, 5743.	1.6	31
32	Transcriptional Signatures of Tau and Amyloid Neuropathology. <i>Cell Reports</i> , 2020, 30, 2040-2054.e5.	2.9	45
33	Clozapine-induced transcriptional changes in the zebrafish brain. <i>NPJ Schizophrenia</i> , 2020, 6, 3.	2.0	14
34	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
35	Genetic risk for Alzheimerâ€™s disease influences neuropathology via multiple biological pathways. <i>Brain Communications</i> , 2020, 2, fcaa167.	1.5	9
36	PLEIOTROPIC EFFECTS OF GENETIC VARIATION ASSOCIATED WITH PSYCHIATRIC DISORDERS ON DNA METHYLATION. <i>European Neuropsychopharmacology</i> , 2019, 29, S984-S985.	0.3	0

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37	Association of Lifestyle and Genetic Risk With Incidence of Dementia. JAMA - Journal of the American Medical Association, 2019, 322, 430.	3.8	421
38	Integrated genetic and methylomic analyses identify shared biology between autism and autistic traits. Molecular Autism, 2019, 10, 31.	2.6	17
39	SU123PREDICTION OF MORTALITY USING DNA METHYLATION AGE IN SCHIZOPHRENIA. European Neuropsychopharmacology, 2019, 29, S1332-S1333.	0.3	0
40	Methylation age acceleration does not predict mortality in schizophrenia. Translational Psychiatry, 2019, 9, 157.	2.4	17
41	A ZEBRAFISH MODEL OF CLOZAPINE EXPOSURE: DRUG-INDUCED TRANSCRIPTOMIC CHANGES IN THE BRAIN. European Neuropsychopharmacology, 2019, 29, S782.	0.3	0
42	Guidance for DNA methylation studies: statistical insights from the Illumina EPIC array. BMC Genomics, 2019, 20, 366.	1.2	201
43	Parallel profiling of DNA methylation and hydroxymethylation highlights neuropathology-associated epigenetic variation in Alzheimer's disease. Clinical Epigenetics, 2019, 11, 52.	1.8	84
44	Genome-wide DNA methylation profiling identifies convergent molecular signatures associated with idiopathic and syndromic autism in post-mortem human brain tissue. Human Molecular Genetics, 2019, 28, 2201-2211.	1.4	70
45	Variable DNA methylation in neonates mediates the association between prenatal smoking and birth weight. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180120.	1.8	46
46	Dynamic expression of genes associated with schizophrenia and bipolar disorder across development. Translational Psychiatry, 2019, 9, 74.	2.4	37
47	Genetic risk variants for brain disorders are enriched in cortical H3K27ac domains. Molecular Brain, 2019, 12, 7.	1.3	21
48	Longitudinal investigation of DNA methylation changes preceding adolescent psychotic experiences. Translational Psychiatry, 2019, 9, 69.	2.4	13
49	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. Biological Psychiatry, 2019, 86, 599-607.	0.7	47
50	Establishing a generalized polyepigenetic biomarker for tobacco smoking. Translational Psychiatry, 2019, 9, 92.	2.4	51
51	Systematic underestimation of the epigenetic clock and age acceleration in older subjects. Genome Biology, 2019, 20, 283.	3.8	97
52	THE AUTHORS REPLY. American Journal of Epidemiology, 2019, 188, 488-489.	1.6	3
53	Bigmelon: tools for analysing large DNA methylation datasets. Bioinformatics, 2019, 35, 981-986.	1.8	49
54	Analysis of DNA Methylation in Young People: Limited Evidence for an Association Between Victimization Stress and Epigenetic Variation in Blood. American Journal of Psychiatry, 2018, 175, 517-529.	4.0	114

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55	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018, 23, 2133-2144.	4.1	68
56	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
57	Elevated DNA methylation across a 48â€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
58	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
59	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
60	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
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	DNA methylation and inflammation marker profiles associated with a history of depression. <i>Human Molecular Genetics</i> , 2018, 27, 2840-2850.	1.4	46
63	Genome-wide methylomic analysis in individuals with HNF1B intragenic mutation and 17q12 microdeletion. <i>Clinical Epigenetics</i> , 2018, 10, 97.	1.8	18
64	Socioeconomic Position and DNA Methylation Age Acceleration Across the Life Course. <i>American Journal of Epidemiology</i> , 2018, 187, 2346-2354.	1.6	81
65	Elevated polygenic burden for autism is associated with differential DNA methylation at birth. <i>Genome Medicine</i> , 2018, 10, 19.	3.6	88
66	Characterizing genetic and environmental influences on variable DNA methylation using monozygotic and dizygotic twins. <i>PLoS Genetics</i> , 2018, 14, e1007544.	1.5	153
67	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
68	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
69	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
70	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. <i>Nature Communications</i> , 2017, 8, 15353.	5.8	92
71	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
72	Genetic variation at 16q24.2 is associated with small vessel stroke. <i>Annals of Neurology</i> , 2017, 81, 383-394.	2.8	73

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73	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
74	[P3â€“529]: 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
75	Regional differences in mitochondrial DNA methylation in human post-mortem brain tissue. <i>Clinical Epigenetics</i> , 2017, 9, 47.	1.8	34
76	5-hydroxymethylcytosine is highly dynamic across human fetal brain development. <i>BMC Genomics</i> , 2017, 18, 738.	1.2	63
77	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. <i>Human Molecular Genetics</i> , 2016, 25, 4339-4349.	1.4	11
78	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016, 7, 10561.	5.8	69
79	O2â€“06â€“05: 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
80	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
81	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
82	Variation in 5-hydroxymethylcytosine across human cortex and cerebellum. <i>Genome Biology</i> , 2016, 17, 27.	3.8	83
83	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
84	Methylation QTLs in the developing brain and their enrichment in schizophrenia risk loci. <i>Nature Neuroscience</i> , 2016, 19, 48-54.	7.1	306
85	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
86	Methylomic markers of persistent childhood asthma: a longitudinal study of asthma-discordant monozygotic twins. <i>Clinical Epigenetics</i> , 2015, 7, 130.	1.8	38
87	O3-05-01: Systems-level evidence for epigenetic dysfunction in Alzheimer's disease. , 2015, 11, P228-P228.		0
88	Methylomic trajectories across human fetal brain development. <i>Genome Research</i> , 2015, 25, 338-352.	2.4	250
89	Methylomic analysis of monozygotic twins discordant for childhood psychotic symptoms. <i>Epigenetics</i> , 2015, 10, 1014-1023.	1.3	40
90	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

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91	Methylomic profiling of human brain tissue supports a neurodevelopmental origin for schizophrenia. <i>Genome Biology</i> , 2014, 15, 483.	3.8	141
92	De novo mutations in schizophrenia implicate synaptic networks. <i>Nature</i> , 2014, 506, 179-184.	13.7	1,510
93	Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. <i>Nature Neuroscience</i> , 2014, 17, 1164-1170.	7.1	488
94	O3-04-03: CROSS-TISSUE METHYLOMIC PROFILING IN ALZHEIMER'S DISEASE. , 2014, 10, P215-P215.		0
95	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