

Jonathan S Mill

List of Publications by Year in descending order

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Version: 2024-02-01

266
papers

39,412
citations

5896

81
h-index

3182

186
g-index

329
all docs

329
docs citations

329
times ranked

37328
citing authors

#	ARTICLE	IF	CITATIONS
1	Influence of Life Stress on Depression: Moderation by a Polymorphism in the 5-HTT Gene. <i>Science</i> , 2003, 301, 386-389.	12.6	7,147
2	Role of Genotype in the Cycle of Violence in Maltreated Children. <i>Science</i> , 2002, 297, 851-854.	12.6	4,118
3	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	21.4	2,224
4	Transcriptomic analysis of autistic brain reveals convergent molecular pathology. <i>Nature</i> , 2011, 474, 380-384.	27.8	1,654
5	Non-neuronal expression of SARS-CoV-2 entry genes in the olfactory system suggests mechanisms underlying COVID-19-associated anosmia. <i>Science Advances</i> , 2020, 6, .	10.3	865
6	A data-driven approach to preprocessing Illumina 450K methylation array data. <i>BMC Genomics</i> , 2013, 14, 293.	2.8	850
7	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. <i>Nature Neuroscience</i> , 2014, 17, 1156-1163.	14.8	800
8	Epigenomic Profiling Reveals DNA-Methylation Changes Associated with Major Psychosis. <i>American Journal of Human Genetics</i> , 2008, 82, 696-711.	6.2	725
9	Epigenome-Wide Scans Identify Differentially Methylated Regions for Age and Age-Related Phenotypes in a Healthy Ageing Population. <i>PLoS Genetics</i> , 2012, 8, e1002629.	3.5	620
10	Functional annotation of the human brain methylome identifies tissue-specific epigenetic variation across brain and blood. <i>Genome Biology</i> , 2012, 13, R43.	9.6	585
11	Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. <i>Nature Neuroscience</i> , 2014, 17, 1164-1170.	14.8	488
12	Disease-associated epigenetic changes in monozygotic twins discordant for schizophrenia and bipolar disorder. <i>Human Molecular Genetics</i> , 2011, 20, 4786-4796.	2.9	407
13	Exposure to violence during childhood is associated with telomere erosion from 5 to 10 years of age: a longitudinal study. <i>Molecular Psychiatry</i> , 2013, 18, 576-581.	7.9	400
14	Interindividual methylomic variation across blood, cortex, and cerebellum: implications for epigenetic studies of neurological and neuropsychiatric phenotypes. <i>Epigenetics</i> , 2015, 10, 1024-1032.	2.7	393
15	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712.	14.8	371
16	From promises to practical strategies in epigenetic epidemiology. <i>Nature Reviews Genetics</i> , 2013, 14, 585-594.	16.3	314
17	Expression of the dopamine transporter gene is regulated by the 3' UTR VNTR: Evidence from brain and lymphocytes using quantitative RT-PCR. <i>American Journal of Medical Genetics Part A</i> , 2002, 114, 975-979.	2.4	310
18	Methylation QTLs in the developing brain and their enrichment in schizophrenia risk loci. <i>Nature Neuroscience</i> , 2016, 19, 48-54.	14.8	306

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19	A Common Haplotype of the Dopamine Transporter Gene Associated With Attention-Deficit/Hyperactivity Disorder and Interacting With Maternal Use of Alcohol During Pregnancy. Archives of General Psychiatry, 2006, 63, 74.	12.3	288
20	An integrated genetic-epigenetic analysis of schizophrenia: evidence for co-localization of genetic associations and differential DNA methylation. Genome Biology, 2016, 17, 176.	8.8	287
21	DNA from buccal swabs recruited by mail: evaluation of storage effects on long-term stability and suitability for multiplex polymerase chain reaction genotyping. Behavior Genetics, 2003, 33, 67-72.	2.1	286
22	A longitudinal study of epigenetic variation in twins. Epigenetics, 2010, 5, 516-526.	2.7	286
23	Methylomic analysis of monozygotic twins discordant for autism spectrum disorder and related behavioural traits. Molecular Psychiatry, 2014, 19, 495-503.	7.9	280
24	Quantification of the pace of biological aging in humans through a blood test, the DunedinPoAm DNA methylation algorithm. ELife, 2020, 9, .	6.0	268
25	Molecular studies of major depressive disorder: the epigenetic perspective. Molecular Psychiatry, 2007, 12, 799-814.	7.9	260
26	Methylomic trajectories across human fetal brain development. Genome Research, 2015, 25, 338-352.	5.5	250
27	Histone Acetylome-wide Association Study of Autism Spectrum Disorder. Cell, 2016, 167, 1385-1397.e11.	28.9	237
28	Allelic Skewing of DNA Methylation Is Widespread across the Genome. American Journal of Human Genetics, 2010, 86, 196-212.	6.2	228
29	Epigenetic Mediation of Environmental Influences in Major Psychotic Disorders. Schizophrenia Bulletin, 2009, 35, 1045-1056.	4.3	224
30	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. Nature Genetics, 2021, 53, 1636-1648.	21.4	223
31	Dynamic changes in DNA methylation of stress-associated genes (OXTR, BDNF) after acute psychosocial stress. Translational Psychiatry, 2012, 2, e150-e150.	4.8	220
32	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
33	Integrated Genetic and Epigenetic Analysis Identifies Haplotype-Specific Methylation in the FTO Type 2 Diabetes and Obesity Susceptibility Locus. PLoS ONE, 2010, 5, e14040.	2.5	215
34	DunedinPACE, a DNA methylation biomarker of the pace of aging. ELife, 2022, 11, .	6.0	214
35	Guidance for DNA methylation studies: statistical insights from the Illumina EPIC array. BMC Genomics, 2019, 20, 366.	2.8	201
36	Differential epigenomic and transcriptomic responses in subcutaneous adipose tissue between low and high responders to caloric restriction. American Journal of Clinical Nutrition, 2010, 91, 309-320.	4.7	193

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37	Environmental risk, Oxytocin Receptor Gene (OXTR) methylation and youth callous-unemotional traits: a 13-year longitudinal study. <i>Molecular Psychiatry</i> , 2014, 19, 1071-1077.	7.9	192
38	Pre- and perinatal environmental risks for attention-deficit hyperactivity disorder (ADHD): the potential role of epigenetic processes in mediating susceptibility. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2008, 49, 1020-1030.	5.2	190
39	Increased serotonin transporter gene (<i>SERT</i>) DNA methylation is associated with bullying victimization and blunted cortisol response to stress in childhood: a longitudinal study of discordant monozygotic twins. <i>Psychological Medicine</i> , 2013, 43, 1813-1823.	4.5	186
40	Commentary: The seven plagues of epigenetic epidemiology. <i>International Journal of Epidemiology</i> , 2012, 41, 74-78.	1.9	182
41	Genetic and epigenetic associations of MAOA and NR3C1 with depression and childhood adversities. <i>International Journal of Neuropsychopharmacology</i> , 2013, 16, 1513-1528.	2.1	182
42	Genome-wide DNA methylation levels and altered cortisol stress reactivity following childhood trauma in humans. <i>Nature Communications</i> , 2016, 7, 10967.	12.8	175
43	Is treatment-resistant schizophrenia categorically distinct from treatment-responsive schizophrenia? a systematic review. <i>BMC Psychiatry</i> , 2017, 17, 12.	2.6	170
44	Joint Analysis of the DRD5 Marker Concludes Association with Attention-Deficit/Hyperactivity Disorder Confined to the Predominantly Inattentive and Combined Subtypes. <i>American Journal of Human Genetics</i> , 2004, 74, 348-356.	6.2	168
45	Characterizing genetic and environmental influences on variable DNA methylation using monozygotic and dizygotic twins. <i>PLoS Genetics</i> , 2018, 14, e1007544.	3.5	153
46	Bisphenol A causes reproductive toxicity, decreases <i>dnmt1</i> transcription, and reduces global DNA methylation in breeding zebrafish <i>(Danio rerio)</i>. <i>Epigenetics</i> , 2016, 11, 526-538.	2.7	149
47	Association study of a dopamine transporter polymorphism and attention deficit hyperactivity disorder in UK and Turkish samples. <i>Molecular Psychiatry</i> , 2001, 6, 425-428.	7.9	143
48	Methylomic profiling of human brain tissue supports a neurodevelopmental origin for schizophrenia. <i>Genome Biology</i> , 2014, 15, 483.	8.8	141
49	Elevated DNA methylation across a 48&nb 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.	0.8	138
50	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.	14.8	138
51	Differential methylation of the TRPA1 promoter in pain sensitivity. <i>Nature Communications</i> , 2014, 5, 2978.	12.8	132
52	Allele-specific methylation in the human genome. <i>Epigenetics</i> , 2010, 5, 578-582.	2.7	129
53	Drugs and addiction: an introduction to epigenetics. <i>Addiction</i> , 2011, 106, 480-489.	3.3	128
54	Expression quantitative trait loci in the developing human brain and their enrichment in neuropsychiatric disorders. <i>Genome Biology</i> , 2018, 19, 194.	8.8	126

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55	Leveraging DNA-Methylation Quantitative-Trait Loci to Characterize the Relationship between Methylomic Variation, Gene Expression, and Complex Traits. American Journal of Human Genetics, 2018, 103, 654-665.	6.2	126
56	Epigenetic profiling of ADHD symptoms trajectories: a prospective, methylome-wide study. Molecular Psychiatry, 2017, 22, 250-256.	7.9	124
57	Maternal separation is associated with strain-specific responses to stress and epigenetic alterations to <i>Nr3c1</i> , <i>Avp</i> , and <i>Nr4a1</i> in mouse. Brain and Behavior, 2012, 2, 455-467.	2.2	123
58	Evidence for monozygotic twin (MZ) discordance in methylation level at two CpG sites in the promoter region of the catechol-O-methyltransferase (<i>COMT</i>) gene. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2006, 141B, 421-425.	1.7	119
59	A multi-tissue analysis identifies HLA complex group 9 gene methylation differences in bipolar disorder. Molecular Psychiatry, 2012, 17, 728-740.	7.9	117
60	Haplotype analysis of SNAP-25 suggests a role in the aetiology of ADHD. Molecular Psychiatry, 2004, 9, 801-810.	7.9	115
61	DNA Methylation Profiling in Inflammatory Bowel Disease Provides New Insights into Disease Pathogenesis. Journal of Crohn's and Colitis, 2016, 10, 77-86.	1.3	115
62	Cross-region reduction in 5-hydroxymethylcytosine in Alzheimer's disease brain. Neurobiology of Aging, 2014, 35, 1850-1854.	3.1	114
63	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.	7.2	114
64	Epigenetic Research in Neuropsychiatric Disorders: the "Tissue Issue". Current Behavioral Neuroscience Reports, 2016, 3, 264-274.	1.3	113
65	Genome-wide Methylomic Analysis of Monozygotic Twins Discordant for Adolescent Depression. Biological Psychiatry, 2014, 76, 977-983.	1.3	112
66	The dopamine transporter gene is associated with attention deficit hyperactivity disorder in a Taiwanese sample. Molecular Psychiatry, 2003, 8, 393-396.	7.9	111
67	The quantification of COMT mRNA in post mortem cerebellum tissue: diagnosis, genotype, methylation and expression. BMC Medical Genetics, 2006, 7, 10.	2.1	110
68	Association of DRD4 in children with ADHD and comorbid conduct problems. American Journal of Medical Genetics Part A, 2002, 114, 150-153.	2.4	109
69	Eating disorders, gene-environment interactions and epigenetics. Neuroscience and Biobehavioral Reviews, 2011, 35, 784-793.	6.1	108
70	Epigenetically regulated microRNAs in Alzheimer's disease. Neurobiology of Aging, 2014, 35, 731-745.	3.1	105
71	Epigenetic Studies of Psychosis: Current Findings, Methodological Approaches, and Implications for Postmortem Research. Biological Psychiatry, 2011, 69, 146-156.	1.3	104
72	Functional effects of a tandem duplication polymorphism in the 5' flanking region of the DRD4 gene. Biological Psychiatry, 2004, 56, 691-697.	1.3	100

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73	Prediction of Heterogeneity in Intelligence and Adult Prognosis by Genetic Polymorphisms in the Dopamine System Among Children With Attention-Deficit/Hyperactivity Disorder. Archives of General Psychiatry, 2006, 63, 462.	12.3	100
74	Stress-induced gene expression and behavior are controlled by DNA methylation and methyl donor availability in the dentate gyrus. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4830-4835.	7.1	100
75	Recalibrating the epigenetic clock: implications for assessing biological age in the human cortex. Brain, 2020, 143, 3763-3775.	7.6	100
76	Epigenetic signatures of childhood abuse and neglect: Implications for psychiatric vulnerability. Journal of Psychiatric Research, 2016, 83, 184-194.	3.1	99
77	Methylomic analysis of salivary <scp>DNA</scp> in childhood <scp>ADHD</scp> identifies altered <scp>DNA</scp> methylation in <i><scp>VIPR</scp>2</i>. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2016, 57, 152-160.	5.2	99
78	Sleep quality and diurnal preference in a sample of young adults: Associations with <i>5HTTLPR</i>, <i>PER3</i>, and <i>CLOCK 3111</i>. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2011, 156, 681-690.	1.7	98
79	Longitudinal analyses of the DNA methylome in deployed military servicemen identify susceptibility loci for post-traumatic stress disorder. Molecular Psychiatry, 2018, 23, 1145-1156.	7.9	98
80	Systematic underestimation of the epigenetic clock and age acceleration in older subjects. Genome Biology, 2019, 20, 283.	8.8	97
81	Advanced paternal age effects in neurodevelopmental disordersâ€”review of potential underlying mechanisms. Translational Psychiatry, 2017, 7, e1019-e1019.	4.8	94
82	Schizophrenia is associated with dysregulation of a Cdk5 activator that regulates synaptic protein expression and cognition. Brain, 2011, 134, 2408-2421.	7.6	92
83	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. Nature Communications, 2017, 8, 15353.	12.8	92
84	Intermediate DNA methylation is a conserved signature of genome regulation. Nature Communications, 2015, 6, 6363.	12.8	91
85	Measuring adolescents' exposure to victimization: The Environmental Risk (E-Risk) Longitudinal Twin Study. Development and Psychopathology, 2015, 27, 1399-1416.	2.3	90
86	Prenatal maternal immune activation causes epigenetic differences in adolescent mouse brain. Translational Psychiatry, 2014, 4, e434-e434.	4.8	88
87	Elevated polygenic burden for autism is associated with differential DNA methylation at birth. Genome Medicine, 2018, 10, 19.	8.2	88
88	Alzheimerâ€™s disease-associated (hydroxy)methylomic changes in the brain and blood. Clinical Epigenetics, 2019, 11, 164.	4.1	88
89	Long-lasting regulation of hippocampal <i>Bdnf</i> gene transcription after contextual fear conditioning. Genes, Brain and Behavior, 2012, 11, 651-659.	2.2	87
90	Hypermethylation in the ZBTB20 gene is associated with major depressive disorder. Genome Biology, 2014, 15, R56.	9.6	87

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91	DNA methylation and substance-use risk: a prospective, genome-wide study spanning gestation to adolescence. <i>Translational Psychiatry</i> , 2016, 6, e976-e976.	4.8	86
92	Parallel profiling of DNA methylation and hydroxymethylation highlights neuropathology-associated epigenetic variation in Alzheimer's disease. <i>Clinical Epigenetics</i> , 2019, 11, 52.	4.1	84
93	Variation in 5-hydroxymethylcytosine across human cortex and cerebellum. <i>Genome Biology</i> , 2016, 17, 27.	8.8	83
94	Current status and future prospects for epigenetic psychopharmacology. <i>Epigenetics</i> , 2012, 7, 20-28.	2.7	82
95	Socioeconomic Position and DNA Methylation Age Acceleration Across the Life Course. <i>American Journal of Epidemiology</i> , 2018, 187, 2346-2354.	3.4	81
96	An epigenome-wide association meta-analysis of prenatal maternal stress in neonates: A model approach for replication. <i>Epigenetics</i> , 2016, 11, 140-149.	2.7	80
97	Association study of a SNAP-25 microsatellite and attention deficit hyperactivity disorder. <i>American Journal of Medical Genetics Part A</i> , 2002, 114, 269-271.	2.4	79
98	Quantitative trait locus analysis of candidate gene alleles associated with attention deficit hyperactivity disorder (ADHD) in five genes: DRD4, DAT1, DRD5, SNAP-25, and 5HT1B. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2005, 133B, 68-73.	1.7	79
99	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.	3.1	79
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.	6.4	79
101	Patterns of Reliability: Assessing the Reproducibility and Integrity of DNA Methylation Measurement. <i>Patterns</i> , 2020, 1, 100014.	5.9	78
102	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.	6.2	77
103	Advancing Paternal Age Is Associated with Deficits in Social and Exploratory Behaviors in the Offspring: A Mouse Model. <i>PLoS ONE</i> , 2009, 4, e8456.	2.5	77
104	Transient expression analysis of allelic variants of a VNTR in the dopamine transporter gene (DAT1). <i>BMC Genetics</i> , 2005, 6, 3.	2.7	75
105	Epigenetic Studies of Schizophrenia: Progress, Predicaments, and Promises for the Future. <i>Schizophrenia Bulletin</i> , 2013, 39, 11-16.	4.3	75
106	Schizophrenia-associated methylomic variation: molecular signatures of disease and polygenic risk burden across multiple brain regions. <i>Human Molecular Genetics</i> , 2017, 26, ddw373.	2.9	74
107	Evidence of causal effect of major depression on alcohol dependence: findings from the psychiatric genomics consortium. <i>Psychological Medicine</i> , 2019, 49, 1218-1226.	4.5	74
108	Epigenetics in health and disease: heralding the EWAS era. <i>Lancet</i> , The, 2014, 383, 1952-1954.	13.7	73

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109	Genetic variation at 16q24.2 is associated with small vessel stroke. <i>Annals of Neurology</i> , 2017, 81, 383-394.	5.3	73
110	Attention deficit hyperactivity disorder (ADHD) and the dopamine D4 receptor gene: evidence of association but no linkage in a UK sample. <i>Molecular Psychiatry</i> , 2001, 6, 440-444.	7.9	72
111	DNA methylation meta-analysis reveals cellular alterations in psychosis and markers of treatment-resistant schizophrenia. <i>ELife</i> , 2021, 10, .	6.0	72
112	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.	12.8	72
113	DNA methylation in interleukin-11 predicts clinical response to antidepressants in GENDEP. <i>Translational Psychiatry</i> , 2013, 3, e300-e300.	4.8	71
114	Trajectories leading to autism spectrum disorders are affected by paternal age: findings from two nationally representative twin studies. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2010, 51, 850-856.	5.2	70
115	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.	2.9	70
116	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016, 7, 10561.	12.8	69
117	Epigenetic studies in Alzheimer's disease: Current findings, caveats, and considerations for future studies. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2013, 162, 789-799.	1.7	68
118	Association of Protein Phosphatase 1G With Alcohol Use Disorder and Brain Activity During Behavioral Control in a Genome-Wide Methylation Analysis. <i>American Journal of Psychiatry</i> , 2015, 172, 543-552.	7.2	68
119	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018, 23, 2133-2144.	7.9	68
120	DNA Modification Study of Major Depressive Disorder: Beyond Locus-by-Locus Comparisons. <i>Biological Psychiatry</i> , 2015, 77, 246-255.	1.3	66
121	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.	4.8	64
122	5-hydroxymethylcytosine is highly dynamic across human fetal brain development. <i>BMC Genomics</i> , 2017, 18, 738.	2.8	63
123	Integrative genomics identifies a convergent molecular subtype that links epigenomic with transcriptomic differences in autism. <i>Nature Communications</i> , 2020, 11, 4873.	12.8	62
124	Severe psychosocial deprivation in early childhood is associated with increased DNA methylation across a region spanning the transcription start site of CYP2E1. <i>Translational Psychiatry</i> , 2016, 6, e830-e830.	4.8	61
125	Bisulfite-based epityping on pooled genomic DNA provides an accurate estimate of average group DNA methylation. <i>Epigenetics and Chromatin</i> , 2009, 2, 3.	3.9	60
126	SORL1 and SIRT1 mRNA expression and promoter methylation levels in aging and Alzheimer's Disease. <i>Neurochemistry International</i> , 2012, 61, 973-975.	3.8	58

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127	A cross-brain regions study of ANK1 DNA methylation in different neurodegenerative diseases. <i>Neurobiology of Aging</i> , 2019, 74, 70-76.	3.1	58
128	Epigenetic regulation of adult neural stem cells: implications for Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2014, 9, 25.	10.8	55
129	Family-based association study between brain-derived neurotrophic factor gene polymorphisms and attention deficit hyperactivity disorder in UK and Taiwanese samples. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2007, 144B, 83-86.	1.7	54
130	Association of Neighborhood Disadvantage in Childhood With DNA Methylation in Young Adulthood. <i>JAMA Network Open</i> , 2020, 3, e206095.	5.9	54
131	Large epigenome-wide association study of childhood ADHD identifies peripheral DNA methylation associated with disease and polygenic risk burden. <i>Translational Psychiatry</i> , 2020, 10, 8.	4.8	54
132	Stochastic Choice of Allelic Expression in Human Neural Stem Cells. <i>Stem Cells</i> , 2012, 30, 1938-1947.	3.2	53
133	Analysis of HSPA8 and HSPA9 mRNA Expression and Promoter Methylation in the Brain and Blood of Alzheimer's Disease Patients. <i>Journal of Alzheimer's Disease</i> , 2013, 38, 165-170.	2.6	53
134	Epigenomic and transcriptomic signatures of a Klinefelter syndrome (47,XXY) karyotype in the brain. <i>Epigenetics</i> , 2014, 9, 587-599.	2.7	53
135	Establishing a generalized polyepigenetic biomarker for tobacco smoking. <i>Translational Psychiatry</i> , 2019, 9, 92.	4.8	51
136	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.	3.1	51
137	QTL association analysis of the DRD4 exon 3 VNTR polymorphism in a population sample of children screened with a parent rating scale for ADHD symptoms. <i>American Journal of Medical Genetics Part A</i> , 2001, 105, 387-393.	2.4	50
138	Peripheral DNA methylation, cognitive decline and brain aging: pilot findings from the Whitehall II imaging study. <i>Epigenomics</i> , 2018, 10, 585-595.	2.1	50
139	DNA pooling analysis of 21 norepinephrine transporter gene SNPs with attention deficit hyperactivity disorder: No evidence for association. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2005, 134B, 115-118.	1.7	49
140	Analysis of SNAP25 mRNA expression and promoter DNA methylation in brain areas of Alzheimer's Disease patients. <i>Neuroscience</i> , 2012, 220, 41-46.	2.3	49
141	Bigmelon: tools for analysing large DNA methylation datasets. <i>Bioinformatics</i> , 2019, 35, 981-986.	4.1	49
142	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , 2021, 22, 90.	8.8	49
143	Genetics and the geography of health, behaviour and attainment. <i>Nature Human Behaviour</i> , 2019, 3, 576-586.	12.0	47
144	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. <i>Biological Psychiatry</i> , 2019, 86, 599-607.	1.3	47

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145	DNA methylation and inflammation marker profiles associated with a history of depression. Human Molecular Genetics, 2018, 27, 2840-2850.	2.9	46
146	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.	4.0	46
147	Transcriptional Signatures of Tau and Amyloid Neuropathology. Cell Reports, 2020, 30, 2040-2054.e5.	6.4	45
148	Sequence analysis of Drd2, Drd4, and Dat1 in SHR and WKY rat strains. Behavioral and Brain Functions, 2005, 1, 24.	3.3	44
149	DNA methylation profiling using bisulfite-based epityping of pooled genomic DNA. Methods, 2010, 52, 255-258.	3.8	43
150	A Longitudinal Twin Study of Skewed X Chromosome-Inactivation. PLoS ONE, 2011, 6, e17873.	2.5	42
151	Toward an integrated genetic and epigenetic approach to Alzheimer's disease. Neurobiology of Aging, 2011, 32, 1188-1191.	3.1	41
152	Methylomic analysis of monozygotic twins discordant for childhood psychotic symptoms. Epigenetics, 2015, 10, 1014-1023.	2.7	40
153	Polymorphisms in the dopamine D4 receptor gene and attention-deficit hyperactivity disorder. NeuroReport, 2003, 14, 1463-1466.	1.2	38
154	Methylomic markers of persistent childhood asthma: a longitudinal study of asthma-discordant monozygotic twins. Clinical Epigenetics, 2015, 7, 130.	4.1	38
155	Growth disrupting mutations in epigenetic regulatory molecules are associated with abnormalities of epigenetic aging. Genome Research, 2019, 29, 1057-1066.	5.5	38
156	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. Science Translational Medicine, 2022, 14, eabj0264.	12.4	38
157	Rapid Down-Regulation of Glucocorticoid Receptor Gene Expression in the Dentate Gyrus after Acute Stress in vivo: Role of DNA Methylation and MicroRNA Activity. Neuroendocrinology, 2017, 104, 157-169.	2.5	37
158	Epigenetics, genomic mutations and cognitive function. Cognitive Neuropsychiatry, 2009, 14, 377-390.	1.3	36
159	A genetic association study of DNA methylation levels in the DRD4 gene region finds associations with nearby SNPs. Behavioral and Brain Functions, 2012, 8, 31.	3.3	36
160	The mitochondrial epigenome: a role in Alzheimer's disease?. Epigenomics, 2014, 6, 665-675.	2.1	36
161	The association of epigenetic clocks in brain tissue with brain pathologies and common aging phenotypes. Neurobiology of Disease, 2021, 157, 105428.	4.4	36
162	Application of microarrays to the analysis of the inactivation status of human X-linked genes expressed in lymphocytes. European Journal of Human Genetics, 2004, 12, 639-646.	2.8	35

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163	Prenatal immune activation alters the adult neural epigenome but can be partly stabilised by a n-3 polyunsaturated fatty acid diet. <i>Translational Psychiatry</i> , 2018, 8, 125.	4.8	35
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