

Jonathan S Mill

List of Publications by Year in descending order

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Version: 2024-02-01

266
papers

39,412
citations

5876

81
h-index

3173

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.	6.0	7,147
2	Role of Genotype in the Cycle of Violence in Maltreated Children. <i>Science</i> , 2002, 297, 851-854.	6.0	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.	9.4	2,224
4	Transcriptomic analysis of autistic brain reveals convergent molecular pathology. <i>Nature</i> , 2011, 474, 380-384.	13.7	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, .	4.7	865
6	A data-driven approach to preprocessing Illumina 450K methylation array data. <i>BMC Genomics</i> , 2013, 14, 293.	1.2	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.	7.1	800
8	Epigenomic Profiling Reveals DNA-Methylation Changes Associated with Major Psychosis. <i>American Journal of Human Genetics</i> , 2008, 82, 696-711.	2.6	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.	1.5	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.	13.9	585
11	Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. <i>Nature Neuroscience</i> , 2014, 17, 1164-1170.	7.1	488
12	Disease-associated epigenetic changes in monozygotic twins discordant for schizophrenia and bipolar disorder. <i>Human Molecular Genetics</i> , 2011, 20, 4786-4796.	1.4	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.	4.1	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.	1.3	393
15	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712.	7.1	371
16	From promises to practical strategies in epigenetic epidemiology. <i>Nature Reviews Genetics</i> , 2013, 14, 585-594.	7.7	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.	7.1	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. <i>Archives of General Psychiatry</i> , 2006, 63, 74.	13.8	288
20	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
21	DNA from buccal swabs recruited by mail: evaluation of storage effects on long-term stability and suitability for multiplex polymerase chain reaction genotyping. <i>Behavior Genetics</i> , 2003, 33, 67-72.	1.4	286
22	A longitudinal study of epigenetic variation in twins. <i>Epigenetics</i> , 2010, 5, 516-526.	1.3	286
23	Methylomic analysis of monozygotic twins discordant for autism spectrum disorder and related behavioural traits. <i>Molecular Psychiatry</i> , 2014, 19, 495-503.	4.1	280
24	Quantification of the pace of biological aging in humans through a blood test, the DunedinPoAm DNA methylation algorithm. <i>ELife</i> , 2020, 9, .	2.8	268
25	Molecular studies of major depressive disorder: the epigenetic perspective. <i>Molecular Psychiatry</i> , 2007, 12, 799-814.	4.1	260
26	Methylomic trajectories across human fetal brain development. <i>Genome Research</i> , 2015, 25, 338-352.	2.4	250
27	Histone Acetylome-wide Association Study of Autism Spectrum Disorder. <i>Cell</i> , 2016, 167, 1385-1397.e11.	13.5	237
28	Allelic Skewing of DNA Methylation Is Widespread across the Genome. <i>American Journal of Human Genetics</i> , 2010, 86, 196-212.	2.6	228
29	Epigenetic Mediation of Environmental Influences in Major Psychotic Disorders. <i>Schizophrenia Bulletin</i> , 2009, 35, 1045-1056.	2.3	224
30	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. <i>Nature Genetics</i> , 2021, 53, 1636-1648.	9.4	223
31	Dynamic changes in DNA methylation of stress-associated genes (OXTR, BDNF) after acute psychosocial stress. <i>Translational Psychiatry</i> , 2012, 2, e150-e150.	2.4	220
32	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
33	Integrated Genetic and Epigenetic Analysis Identifies Haplotype-Specific Methylation in the FTO Type 2 Diabetes and Obesity Susceptibility Locus. <i>PLoS ONE</i> , 2010, 5, e14040.	1.1	215
34	DunedinPACE, a DNA methylation biomarker of the pace of aging. <i>ELife</i> , 2022, 11, .	2.8	214
35	Guidance for DNA methylation studies: statistical insights from the Illumina EPIC array. <i>BMC Genomics</i> , 2019, 20, 366.	1.2	201
36	Differential epigenomic and transcriptomic responses in subcutaneous adipose tissue between low and high responders to caloric restriction. <i>American Journal of Clinical Nutrition</i> , 2010, 91, 309-320.	2.2	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.	4.1	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.	3.1	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.	2.7	186
40	Commentary: The seven plagues of epigenetic epidemiology. <i>International Journal of Epidemiology</i> , 2012, 41, 74-78.	0.9	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.	1.0	182
42	Genome-wide DNA methylation levels and altered cortisol stress reactivity following childhood trauma in humans. <i>Nature Communications</i> , 2016, 7, 10967.	5.8	175
43	Is treatment-resistant schizophrenia categorically distinct from treatment-responsive schizophrenia? a systematic review. <i>BMC Psychiatry</i> , 2017, 17, 12.	1.1	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.	2.6	168
45	Characterizing genetic and environmental influences on variable DNA methylation using monozygotic and dizygotic twins. <i>PLoS Genetics</i> , 2018, 14, e1007544.	1.5	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.	1.3	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.	4.1	143
48	Methylomic profiling of human brain tissue supports a neurodevelopmental origin for schizophrenia. <i>Genome Biology</i> , 2014, 15, 483.	3.8	141
49	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
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.	7.1	138
51	Differential methylation of the TRPA1 promoter in pain sensitivity. <i>Nature Communications</i> , 2014, 5, 2978.	5.8	132
52	Allele-specific methylation in the human genome. <i>Epigenetics</i> , 2010, 5, 578-582.	1.3	129
53	Drugs and addiction: an introduction to epigenetics. <i>Addiction</i> , 2011, 106, 480-489.	1.7	128
54	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

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55	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
56	Epigenetic profiling of ADHD symptoms trajectories: a prospective, methylome-wide study. <i>Molecular Psychiatry</i> , 2017, 22, 250-256.	4.1	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. <i>Brain and Behavior</i> , 2012, 2, 455-467.	1.0	123
58	Evidence for monozygotic twin (MZ) discordance in methylation level at two CpG sites in the promoter region of the catechol-O-methyltransferase (COMT) gene. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2006, 141B, 421-425.	1.1	119
59	A multi-tissue analysis identifies HLA complex group 9 gene methylation differences in bipolar disorder. <i>Molecular Psychiatry</i> , 2012, 17, 728-740.	4.1	117
60	Haplotype analysis of SNAP-25 suggests a role in the aetiology of ADHD. <i>Molecular Psychiatry</i> , 2004, 9, 801-810.	4.1	115
61	DNA Methylation Profiling in Inflammatory Bowel Disease Provides New Insights into Disease Pathogenesis. <i>Journal of Crohn's and Colitis</i> , 2016, 10, 77-86.	0.6	115
62	Cross-region reduction in 5-hydroxymethylcytosine in Alzheimer's disease brain. <i>Neurobiology of Aging</i> , 2014, 35, 1850-1854.	1.5	114
63	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
64	Epigenetic Research in Neuropsychiatric Disorders: the "Tissue Issue". <i>Current Behavioral Neuroscience Reports</i> , 2016, 3, 264-274.	0.6	113
65	Genome-wide Methylomic Analysis of Monozygotic Twins Discordant for Adolescent Depression. <i>Biological Psychiatry</i> , 2014, 76, 977-983.	0.7	112
66	The dopamine transporter gene is associated with attention deficit hyperactivity disorder in a Taiwanese sample. <i>Molecular Psychiatry</i> , 2003, 8, 393-396.	4.1	111
67	The quantification of COMT mRNA in post mortem cerebellum tissue: diagnosis, genotype, methylation and expression. <i>BMC Medical Genetics</i> , 2006, 7, 10.	2.1	110
68	Association of DRD4 in children with ADHD and comorbid conduct problems. <i>American Journal of Medical Genetics Part A</i> , 2002, 114, 150-153.	2.4	109
69	Eating disorders, gene-environment interactions and epigenetics. <i>Neuroscience and Biobehavioral Reviews</i> , 2011, 35, 784-793.	2.9	108
70	Epigenetically regulated microRNAs in Alzheimer's disease. <i>Neurobiology of Aging</i> , 2014, 35, 731-745.	1.5	105
71	Epigenetic Studies of Psychosis: Current Findings, Methodological Approaches, and Implications for Postmortem Research. <i>Biological Psychiatry</i> , 2011, 69, 146-156.	0.7	104
72	Functional effects of a tandem duplication polymorphism in the 5' flanking region of the DRD4 gene. <i>Biological Psychiatry</i> , 2004, 56, 691-697.	0.7	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. <i>Archives of General Psychiatry</i> , 2006, 63, 462.	13.8	100
74	Stress-induced gene expression and behavior are controlled by DNA methylation and methyl donor availability in the dentate gyrus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4830-4835.	3.3	100
75	Recalibrating the epigenetic clock: implications for assessing biological age in the human cortex. <i>Brain</i> , 2020, 143, 3763-3775.	3.7	100
76	Epigenetic signatures of childhood abuse and neglect: Implications for psychiatric vulnerability. <i>Journal of Psychiatric Research</i> , 2016, 83, 184-194.	1.5	99
77	Methylomic analysis of salivary DNA in childhood ADHD identifies altered DNA methylation in VIPR2. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2016, 57, 152-160.	3.1	99
78	Sleep quality and diurnal preference in a sample of young adults: Associations with 5HTTLPR, PER3, and CLOCK 3111. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2011, 156, 681-690.	1.1	98
79	Longitudinal analyses of the DNA methylome in deployed military servicemen identify susceptibility loci for post-traumatic stress disorder. <i>Molecular Psychiatry</i> , 2018, 23, 1145-1156.	4.1	98
80	Systematic underestimation of the epigenetic clock and age acceleration in older subjects. <i>Genome Biology</i> , 2019, 20, 283.	3.8	97
81	Advanced paternal age effects in neurodevelopmental disorders—review of potential underlying mechanisms. <i>Translational Psychiatry</i> , 2017, 7, e1019-e1019.	2.4	94
82	Schizophrenia is associated with dysregulation of a Cdk5 activator that regulates synaptic protein expression and cognition. <i>Brain</i> , 2011, 134, 2408-2421.	3.7	92
83	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. <i>Nature Communications</i> , 2017, 8, 15353.	5.8	92
84	Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015, 6, 6363.	5.8	91
85	Measuring adolescents' exposure to victimization: The Environmental Risk (E-Risk) Longitudinal Twin Study. <i>Development and Psychopathology</i> , 2015, 27, 1399-1416.	1.4	90
86	Prenatal maternal immune activation causes epigenetic differences in adolescent mouse brain. <i>Translational Psychiatry</i> , 2014, 4, e434-e434.	2.4	88
87	Elevated polygenic burden for autism is associated with differential DNA methylation at birth. <i>Genome Medicine</i> , 2018, 10, 19.	3.6	88
88	Alzheimer's disease-associated (hydroxy)methylomic changes in the brain and blood. <i>Clinical Epigenetics</i> , 2019, 11, 164.	1.8	88
89	Long-lasting regulation of hippocampal Bdnf gene transcription after contextual fear conditioning. <i>Genes, Brain and Behavior</i> , 2012, 11, 651-659.	1.1	87
90	Hypermethylation in the ZBTB20 gene is associated with major depressive disorder. <i>Genome Biology</i> , 2014, 15, R56.	13.9	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.	2.4	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.	1.8	84
93	Variation in 5-hydroxymethylcytosine across human cortex and cerebellum. <i>Genome Biology</i> , 2016, 17, 27.	3.8	83
94	Current status and future prospects for epigenetic psychopharmacology. <i>Epigenetics</i> , 2012, 7, 20-28.	1.3	82
95	Socioeconomic Position and DNA Methylation Age Acceleration Across the Life Course. <i>American Journal of Epidemiology</i> , 2018, 187, 2346-2354.	1.6	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.	1.3	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.	1.1	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.	1.5	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.	2.9	79
101	Patterns of Reliability: Assessing the Reproducibility and Integrity of DNA Methylation Measurement. <i>Patterns</i> , 2020, 1, 100014.	3.1	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.	2.6	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.	1.1	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.	2.3	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.	1.4	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.	2.7	74
108	Epigenetics in health and disease: heralding the EWAS era. <i>Lancet</i> , The, 2014, 383, 1952-1954.	6.3	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.	2.8	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.	4.1	72
111	DNA methylation meta-analysis reveals cellular alterations in psychosis and markers of treatment-resistant schizophrenia. <i>ELife</i> , 2021, 10, .	2.8	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.	5.8	72
113	DNA methylation in interleukin-11 predicts clinical response to antidepressants in GENDEP. <i>Translational Psychiatry</i> , 2013, 3, e300-e300.	2.4	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.	3.1	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.	1.4	70
116	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016, 7, 10561.	5.8	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.	1.1	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.	4.0	68
119	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018, 23, 2133-2144.	4.1	68
120	DNA Modification Study of Major Depressive Disorder: Beyond Locus-by-Locus Comparisons. <i>Biological Psychiatry</i> , 2015, 77, 246-255.	0.7	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.	2.4	64
122	5-hydroxymethylcytosine is highly dynamic across human fetal brain development. <i>BMC Genomics</i> , 2017, 18, 738.	1.2	63
123	Integrative genomics identifies a convergent molecular subtype that links epigenomic with transcriptomic differences in autism. <i>Nature Communications</i> , 2020, 11, 4873.	5.8	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.	2.4	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.	1.8	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.	1.9	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.	1.5	58
128	Epigenetic regulation of adult neural stem cells: implications for Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2014, 9, 25.	4.4	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.	1.1	54
130	Association of Neighborhood Disadvantage in Childhood With DNA Methylation in Young Adulthood. <i>JAMA Network Open</i> , 2020, 3, e206095.	2.8	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.	2.4	54
132	Stochastic Choice of Allelic Expression in Human Neural Stem Cells. <i>Stem Cells</i> , 2012, 30, 1938-1947.	1.4	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.	1.2	53
134	Epigenomic and transcriptomic signatures of a Klinefelter syndrome (47,XXY) karyotype in the brain. <i>Epigenetics</i> , 2014, 9, 587-599.	1.3	53
135	Establishing a generalized polyepigenetic biomarker for tobacco smoking. <i>Translational Psychiatry</i> , 2019, 9, 92.	2.4	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.	1.5	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.	1.0	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.	1.1	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.	1.1	49
141	Bigmelon: tools for analysing large DNA methylation datasets. <i>Bioinformatics</i> , 2019, 35, 981-986.	1.8	49
142	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , 2021, 22, 90.	3.8	49
143	Genetics and the geography of health, behaviour and attainment. <i>Nature Human Behaviour</i> , 2019, 3, 576-586.	6.2	47
144	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. <i>Biological Psychiatry</i> , 2019, 86, 599-607.	0.7	47

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145	DNA methylation and inflammation marker profiles associated with a history of depression. <i>Human Molecular Genetics</i> , 2018, 27, 2840-2850.	1.4	46
146	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
147	Transcriptional Signatures of Tau and Amyloid Neuropathology. <i>Cell Reports</i> , 2020, 30, 2040-2054.e5.	2.9	45
148	Sequence analysis of <i>Drd2</i> , <i>Drd4</i> , and <i>Dat1</i> in SHR and WKY rat strains. <i>Behavioral and Brain Functions</i> , 2005, 1, 24.	1.4	44
149	DNA methylation profiling using bisulfite-based epityping of pooled genomic DNA. <i>Methods</i> , 2010, 52, 255-258.	1.9	43
150	A Longitudinal Twin Study of Skewed X Chromosome-Inactivation. <i>PLoS ONE</i> , 2011, 6, e17873.	1.1	42
151	Toward an integrated genetic and epigenetic approach to Alzheimer's disease. <i>Neurobiology of Aging</i> , 2011, 32, 1188-1191.	1.5	41
152	Methylomic analysis of monozygotic twins discordant for childhood psychotic symptoms. <i>Epigenetics</i> , 2015, 10, 1014-1023.	1.3	40
153	Polymorphisms in the dopamine D4 receptor gene and attention-deficit hyperactivity disorder. <i>NeuroReport</i> , 2003, 14, 1463-1466.	0.6	38
154	Methylomic markers of persistent childhood asthma: a longitudinal study of asthma-discordant monozygotic twins. <i>Clinical Epigenetics</i> , 2015, 7, 130.	1.8	38
155	Growth disrupting mutations in epigenetic regulatory molecules are associated with abnormalities of epigenetic aging. <i>Genome Research</i> , 2019, 29, 1057-1066.	2.4	38
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