

# 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	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	A comparison of blood and brain-derived ageing and inflammation-related DNA methylation signatures and their association with microglial burdens. <i>European Journal of Neuroscience</i> , 2022, 56, 5637-5649.	1.2	9
4	Methylome analysis of ALS patients and presymptomatic mutation carriers in blood cells. <i>Neurobiology of Aging</i> , 2022, 116, 16-24.	1.5	8
5	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
6	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
7	DNA methylation meta-analysis reveals cellular alterations in psychosis and markers of treatment-resistant schizophrenia. <i>ELife</i> , 2021, 10, .	2.8	72
8	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , 2021, 22, 90.	3.8	49
9	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
10	The histone modification H3K4me3 is altered at the <i>ANK1</i> locus in Alzheimer's disease brain. <i>Future Science OA</i> , 2021, 7, FSO665.	0.9	10
11	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
12	DNA methylation-based sex classifier to predict sex and identify sex chromosome aneuploidy. <i>BMC Genomics</i> , 2021, 22, 484.	1.2	9
13	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
14	A central role for anterior cingulate cortex in the control of pathological aggression. <i>Current Biology</i> , 2021, 31, 2321-2333.e5.	1.8	17
15	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
16	A machine learning case-control classifier for schizophrenia based on DNA methylation in blood. <i>Translational Psychiatry</i> , 2021, 11, 412.	2.4	16
17	The association of epigenetic clocks in brain tissue with brain pathologies and common aging phenotypes. <i>Neurobiology of Disease</i> , 2021, 157, 105428.	2.1	36
18	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021, 12, 5618.	5.8	26

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19	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
20	DNA methylation signatures of adolescent victimization: analysis of a longitudinal monozygotic twin sample. <i>Epigenetics</i> , 2021, 16, 1169-1186.	1.3	14
21	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
22	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
23	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
24	Independent Methylome-Wide Association Studies of Schizophrenia Detect Consistent Caseâ€“Control Differences. <i>Schizophrenia Bulletin</i> , 2020, 46, 319-327.	2.3	15
25	Psychosis-associated DNA methylomic variation in Alzheimer's disease cortex. <i>Neurobiology of Aging</i> , 2020, 89, 83-88.	1.5	13
26	Patterns of Reliability: Assessing the Reproducibility and Integrity of DNA Methylation Measurement. <i>Patterns</i> , 2020, 1, 100014.	3.1	78
27	Tissue-Biased Expansion of DNMT3A-Mutant Clones in a Mosaic Individual Is Associated with Conserved Epigenetic Erosion. <i>Cell Stem Cell</i> , 2020, 27, 326-335.e4.	5.2	25
28	The Molecular Etiology of Alzheimerâ€™s disease. <i>Brain Pathology</i> , 2020, 30, 964-965.	2.1	11
29	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
30	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
31	P.118 Longitudinal DNA methylation changes associated with improvement of psychotic symptoms during clozapine treatment. <i>European Neuropsychopharmacology</i> , 2020, 31, S13-S14.	0.3	0
32	Whole transcriptome in silico screening implicates cardiovascular and infectious disease in the mechanism of action underlying atypical antipsychotic side effects. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , 2020, 6, e12078.	1.8	7
33	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
34	Recalibrating the epigenetic clock: implications for assessing biological age in the human cortex. <i>Brain</i> , 2020, 143, 3763-3775.	3.7	100
35	Association of Neighborhood Disadvantage in Childhood With DNA Methylation in Young Adulthood. <i>JAMA Network Open</i> , 2020, 3, e206095.	2.8	54
36	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. <i>Npj Genomic Medicine</i> , 2020, 5, 10.	1.7	25

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37	Epigenome-wide association study of attention-deficit/hyperactivity disorder in adults. <i>Translational Psychiatry</i> , 2020, 10, 199.	2.4	14
38	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
39	Genome-wide DNA methylation meta-analysis in the brains of suicide completers. <i>Translational Psychiatry</i> , 2020, 10, 69.	2.4	32
40	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
41	Major surgery induces acute changes in measured DNA methylation associated with immune response pathways. <i>Scientific Reports</i> , 2020, 10, 5743.	1.6	31
42	Transcriptional Signatures of Tau and Amyloid Neuropathology. <i>Cell Reports</i> , 2020, 30, 2040-2054.e5.	2.9	45
43	Clozapine-induced transcriptional changes in the zebrafish brain. <i>NPJ Schizophrenia</i> , 2020, 6, 3.	2.0	14
44	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
45	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
46	Correlation between the Expression of Somatic ACE (190KDa) and of its Soluble Nâ€ŒDomain Isoforms (90KDa and 65KDa) with Different Nutritional Status and Cardiovascular Risk Profile. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.2	0
47	Genetic risk for Alzheimerâ€™s disease influences neuropathology via multiple biological pathways. <i>Brain Communications</i> , 2020, 2, fcaa167.	1.5	9
48	PLEIOTROPIC EFFECTS OF GENETIC VARIATION ASSOCIATED WITH PSYCHIATRIC DISORDERS ON DNA METHYLATION. <i>European Neuropsychopharmacology</i> , 2019, 29, S984-S985.	0.3	0
49	S50MAPPING CELL-TYPE SPECIFIC MARKERS OF GENOMIC REGULATION IN THE HUMAN BRAIN. <i>European Neuropsychopharmacology</i> , 2019, 29, S139-S140.	0.3	0
50	T40. Alzheimerâ€™s Disease DNA (Hydroxy)Methylome in the Brain and Blood: Evidence for OXT Methylation as a Preclinical Marker. <i>Biological Psychiatry</i> , 2019, 85, S144.	0.7	1
51	T48LARGE-SCALE EWAS AND METHYLATION QTL ANALYSIS IN ADHD. <i>European Neuropsychopharmacology</i> , 2019, 29, S242.	0.3	0
52	SU123PREDICTION OF MORTALITY USING DNA METHYLATION AGE IN SCHIZOPHRENIA. <i>European Neuropsychopharmacology</i> , 2019, 29, S1332-S1333.	0.3	0
53	Epigenetic studies of schizophrenia: current status and future directions. <i>Current Opinion in Behavioral Sciences</i> , 2019, 25, 102-110.	2.0	8
54	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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55	Methylation age acceleration does not predict mortality in schizophrenia. <i>Translational Psychiatry</i> , 2019, 9, 157.	2.4	17
56	A ZEBRAFISH MODEL OF CLOZAPINE EXPOSURE: DRUG-INDUCED TRANSCRIPTOMIC CHANGES IN THE BRAIN. <i>European Neuropsychopharmacology</i> , 2019, 29, S782.	0.3	0
57	Guidance for DNA methylation studies: statistical insights from the Illumina EPIC array. <i>BMC Genomics</i> , 2019, 20, 366.	1.2	201
58	20.3 DNA METHYLATION PROFILING MIGHT SHED LIGHT ON THE BIOLOGY OF CANNABIS ASSOCIATED PSYCHOSIS. <i>Schizophrenia Bulletin</i> , 2019, 45, S122-S122.	2.3	0
59	Functional Genomic Regulation In The Brain: (Epi)Genetic Variation, Neurodevelopment and Psychiatric Disease. <i>European Neuropsychopharmacology</i> , 2019, 29, S771-S772.	0.3	1
60	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
61	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
62	Genetics and the geography of health, behaviour and attainment. <i>Nature Human Behaviour</i> , 2019, 3, 576-586.	6.2	47
63	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
64	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
65	Genetic risk variants for brain disorders are enriched in cortical H3K27ac domains. <i>Molecular Brain</i> , 2019, 12, 7.	1.3	21
66	Longitudinal investigation of DNA methylation changes preceding adolescent psychotic experiences. <i>Translational Psychiatry</i> , 2019, 9, 69.	2.4	13
67	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. <i>Biological Psychiatry</i> , 2019, 86, 599-607.	0.7	47
68	Establishing a generalized polyepigenetic biomarker for tobacco smoking. <i>Translational Psychiatry</i> , 2019, 9, 92.	2.4	51
69	Systematic underestimation of the epigenetic clock and age acceleration in older subjects. <i>Genome Biology</i> , 2019, 20, 283.	3.8	97
70	RNA sequencing of identical twins discordant for autism reveals blood-based signatures implicating immune and transcriptional dysregulation. <i>Molecular Autism</i> , 2019, 10, 38.	2.6	14
71	F13FUNCTIONAL ANALYSIS OF THE SCHIZOPHRENIA ASSOCIATED GENE AS3MT IN SH-SY5Y NEUROBLASTOMA CELLS. <i>European Neuropsychopharmacology</i> , 2019, 29, S1116-S1117.	0.3	0
72	SA65DNA METHYLOME MARKS OF EXPOSURE TO PSYCHOSOCIAL STRESS DURING ADOLESCENCE: ANALYSIS OF A NOVEL LONGITUDINAL MZ DISCORDANT TWIN STUDY. <i>European Neuropsychopharmacology</i> , 2019, 29, S1223.	0.3	0

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73	Alzheimer's disease-associated (hydroxy)methylomic changes in the brain and blood. <i>Clinical Epigenetics</i> , 2019, 11, 164.	1.8	88
74	THE AUTHORS REPLY. <i>American Journal of Epidemiology</i> , 2019, 188, 488-489.	1.6	3
75	Association of NIPA1 repeat expansions with amyotrophic lateral sclerosis in a large international cohort. <i>Neurobiology of Aging</i> , 2019, 74, 234.e9-234.e15.	1.5	26
76	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
77	Bigmelon: tools for analysing large DNA methylation datasets. <i>Bioinformatics</i> , 2019, 35, 981-986.	1.8	49
78	Sex-specific transcription and DNA methylation profiles of reproductive and epigenetic associated genes in the gonads and livers of breeding zebrafish. <i>Comparative Biochemistry and Physiology Part A, Molecular &amp; Integrative Physiology</i> , 2018, 222, 16-25.	0.8	24
79	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
80	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018, 23, 2133-2144.	4.1	68
81	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
82	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
83	Elevated DNA methylation across a 48 kb region spanning the HOXA gene cluster is associated with Alzheimer's disease neuropathology. <i>Alzheimer's and Dementia</i> , 2018, 14, 1580-1588.	0.4	138
84	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
85	P8...Investigating epigenetic differences in response to shift work: findings from understanding society (UK longitudinal household survey). , 2018, , .		0
86	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
87	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
88	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
89	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
90	DNA methylation and inflammation marker profiles associated with a history of depression. <i>Human Molecular Genetics</i> , 2018, 27, 2840-2850.	1.4	46

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91	Genome-wide methylomic analysis in individuals with HNF1B intragenic mutation and 17q12 microdeletion. <i>Clinical Epigenetics</i> , 2018, 10, 97.	1.8	18
92	Socioeconomic Position and DNA Methylation Age Acceleration Across the Life Course. <i>American Journal of Epidemiology</i> , 2018, 187, 2346-2354.	1.6	81
93	Elevated polygenic burden for autism is associated with differential DNA methylation at birth. <i>Genome Medicine</i> , 2018, 10, 19.	3.6	88
94	Characterizing genetic and environmental influences on variable DNA methylation using monozygotic and dizygotic twins. <i>PLoS Genetics</i> , 2018, 14, e1007544.	1.5	153
95	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.	2.4	35
96	Schizophrenia-associated methylomic variation: molecular signatures of disease and polygenic risk burden across multiple brain regions. <i>Human Molecular Genetics</i> , 2017, 26, ddx373.	1.4	74
97	Rapid Down-Regulation of Glucocorticoid Receptor Gene Expression in the Dentate Gyrus after Acute Stress in vivo: Role of DNA Methylation and MicroRNA Activity. <i>Neuroendocrinology</i> , 2017, 104, 157-169.	1.2	37
98	Epigenetic profiling of ADHD symptoms trajectories: a prospective, methylome-wide study. <i>Molecular Psychiatry</i> , 2017, 22, 250-256.	4.1	124
99	Advanced paternal age effects in neurodevelopmental disorders—review of potential underlying mechanisms. <i>Translational Psychiatry</i> , 2017, 7, e1019-e1019.	2.4	94
100	Is treatment-resistant schizophrenia categorically distinct from treatment-responsive schizophrenia? a systematic review. <i>BMC Psychiatry</i> , 2017, 17, 12.	1.1	170
101	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
102	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. <i>Nature Communications</i> , 2017, 8, 15353.	5.8	92
103	Paternal Age Alters Social Development in Offspring. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2017, 56, 383-390.	0.3	20
104	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
105	Genetic variation at 16q24.2 is associated with small vessel stroke. <i>Annals of Neurology</i> , 2017, 81, 383-394.	2.8	73
106	Profiling Regulatory Variation in the Brain: Methods for Exploring the Neuronal Epigenome. <i>Biological Psychiatry</i> , 2017, 81, 90-91.	0.7	4
107	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
108	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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109	Targeted Genetic Screen in Amyotrophic Lateral Sclerosis Reveals Novel Genetic Variants with Synergistic Effect on Clinical Phenotype. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 370.	1.4	24
110	5-hydroxymethylcytosine is highly dynamic across human fetal brain development. <i>BMC Genomics</i> , 2017, 18, 738.	1.2	63
111	ANK1 is up-regulated in laser captured microglia in Alzheimer's brain; the importance of addressing cellular heterogeneity. <i>PLoS ONE</i> , 2017, 12, e0177814.	1.1	34
112	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. <i>Human Molecular Genetics</i> , 2016, 25, 4339-4349.	1.4	11
113	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016, 7, 10561.	5.8	69
114	Epigenetic Research in Neuropsychiatric Disorders: the "Tissue Issue". <i>Current Behavioral Neuroscience Reports</i> , 2016, 3, 264-274.	0.6	113
115	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
116	Hydroxymethylomic Profiling Implicates Cortical Deregulation of ANK1 and APP in the Alzheimer's Disease Brain. <i>Alzheimer's and Dementia</i> , 2016, 12, P240.	0.4	0
117	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
118	Bisphenol A causes reproductive toxicity, decreases dnmt1 transcription, and reduces global DNA methylation in breeding zebrafish ( <i>Danio rerio</i> ). <i>Epigenetics</i> , 2016, 11, 526-538.	1.3	149
119	Epigenetic signatures of childhood abuse and neglect: Implications for psychiatric vulnerability. <i>Journal of Psychiatric Research</i> , 2016, 83, 184-194.	1.5	99
120	Erasure and reestablishment of random allelic expression imbalance after epigenetic reprogramming. <i>Rna</i> , 2016, 22, 1620-1630.	1.6	10
121	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
122	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
123	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
124	Histone Acetylome-wide Association Study of Autism Spectrum Disorder. <i>Cell</i> , 2016, 167, 1385-1397.e11.	13.5	237
125	Mapping epigenetic changes to the host cell genome induced by <i>Burkholderia pseudomallei</i> reveals pathogen-specific and pathogen-generic signatures of infection. <i>Scientific Reports</i> , 2016, 6, 30861.	1.6	24
126	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



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127	Elucidating novel dysfunctional pathways in Alzheimer's disease by integrating loci identified in genetic and epigenetic studies. <i>Neuroepigenetics</i> , 2016, 6, 32-50.	2.8	17
128	Variation in 5-hydroxymethylcytosine across human cortex and cerebellum. <i>Genome Biology</i> , 2016, 17, 27.	3.8	83
129	Methylomic analysis of salivary <sc>DNA</sc> in childhood <sc>ADHD</sc> identifies altered <sc>DNA</sc> methylation in <i><sc>VIPR</sc>2</i>. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2016, 57, 152-160.	3.1	99
130	Tissue-specific patterns of allelically-skewed DNA methylation. <i>Epigenetics</i> , 2016, 11, 24-35.	1.3	32
131	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
132	Epigenetic regulation of mitochondrial function in neurodegenerative disease: New insights from advances in genomic technologies. <i>Neuroscience Letters</i> , 2016, 625, 47-55.	1.0	34
133	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
134	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
135	Methylation QTLs in the developing brain and their enrichment in schizophrenia risk loci. <i>Nature Neuroscience</i> , 2016, 19, 48-54.	7.1	306
136	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
137	Epigenome-Wide DNA Methylation Analysis of Monozygotic Twins Discordant for Diurnal Preference. <i>Twin Research and Human Genetics</i> , 2015, 18, 662-669.	0.3	16
138	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
139	Methylomic markers of persistent childhood asthma: a longitudinal study of asthma-discordant monozygotic twins. <i>Clinical Epigenetics</i> , 2015, 7, 130.	1.8	38
140	A comparison of mitochondrial DNA isolation methods in frozen post-mortem human brain tissue—applications for studies of mitochondrial genetics in brain disorders. <i>BioTechniques</i> , 2015, 59, 241-246.	0.8	17
141	Effects of advanced paternal age on trajectories of social behavior in offspring. <i>Genes, Brain and Behavior</i> , 2015, 14, 443-453.	1.1	22
142	Association of Protein Phosphatase<i>PPM1G</i>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
143	O3-05-01: Systems-level evidence for epigenetic dysfunction in Alzheimer's disease. , 2015, 11, P228-P228.		0
144	DNA Modification Study of Major Depressive Disorder: Beyond Locus-by-Locus Comparisons. <i>Biological Psychiatry</i> , 2015, 77, 246-255.	0.7	66

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145	Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015, 6, 6363.	5.8	91
146	Methylomic trajectories across human fetal brain development. <i>Genome Research</i> , 2015, 25, 338-352.	2.4	250
147	How Can Pharmacogenomics Biomarkers Be Translated into Patient Benefit. <i>European Psychiatry</i> , 2015, 30, 94.	0.1	2
148	Blood methylomic signatures of presymptomatic dementia in elderly subjects with type 2 diabetes mellitus. <i>Neurobiology of Aging</i> , 2015, 36, 1600.e1-1600.e4.	1.5	21
149	Methylomic analysis of monozygotic twins discordant for childhood psychotic symptoms. <i>Epigenetics</i> , 2015, 10, 1014-1023.	1.3	40
150	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
151	ISDN2014_0171: Dynamic and sex-specific changes in DNA methylation during human fetal brain development. <i>International Journal of Developmental Neuroscience</i> , 2015, 47, 50-51.	0.7	0
152	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712.	7.1	371
153	Long-Term Effects of Gestational Nicotine Exposure and Food-Restriction on Gene Expression in the Striatum of Adolescent Rats. <i>PLoS ONE</i> , 2014, 9, e88896.	1.1	5
154	Epigenomic and transcriptomic signatures of a Klinefelter syndrome (47,XXY) karyotype in the brain. <i>Epigenetics</i> , 2014, 9, 587-599.	1.3	53
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