

Jonathan S Mill

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

264
papers

29,640
citations

73
h-index

170
g-index

328
ext. papers

35,458
ext. citations

8.2
avg, IF

6.85
L-index

#	Paper	IF	Citations
264	DunedinPACE, a DNA methylation biomarker of the pace of aging.. <i>ELife</i> , 2022 , 11,	8.9	9
263	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS.. <i>Science Translational Medicine</i> , 2022 , 14, eabj0264	17.5	4
262	Methylome analysis of ALS patients and presymptomatic mutation carriers in blood cells.. <i>Neurobiology of Aging</i> , 2022 , 116, 16-24	5.6	0
261	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	36.3	19
260	Full-length transcript sequencing of human and mouse cerebral cortex identifies widespread isoform diversity and alternative splicing. <i>Cell Reports</i> , 2021 , 37, 110022	10.6	5
259	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	3.5	1
258	DNA methylation signatures of adolescent victimization: analysis of a longitudinal monozygotic twin sample. <i>Epigenetics</i> , 2021 , 16, 1169-1186	5.7	2
257	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , 2021 , 22, 90	18.3	6
256	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	6	11
255	The histone modification H3K4me3 is altered at the locus in Alzheimer's disease brain. <i>Future Science OA</i> , 2021 , 7, FSO665	2.7	5
254	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	17.4	8
253	DNA methylation-based sex classifier to predict sex and identify sex chromosome aneuploidy. <i>BMC Genomics</i> , 2021 , 22, 484	4.5	2
252	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	4.5	3
251	A central role for anterior cingulate cortex in the control of pathological aggression. <i>Current Biology</i> , 2021 , 31, 2321-2333.e5	6.3	6
250	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	4.5	3
249	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	15.1	7
248	DNA methylation meta-analysis reveals cellular alterations in psychosis and markers of treatment-resistant schizophrenia. <i>ELife</i> , 2021 , 10,	8.9	15

247	A machine learning case-control classifier for schizophrenia based on DNA methylation in blood. <i>Translational Psychiatry</i> , 2021 , 11, 412	8.6	3
246	The association of epigenetic clocks in brain tissue with brain pathologies and common aging phenotypes. <i>Neurobiology of Disease</i> , 2021 , 157, 105428	7.5	5
245	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021 , 12, 5618	17.4	6
244	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021 , 53, 1311-1321	36.3	27
243	Independent Methylome-Wide Association Studies of Schizophrenia Detect Consistent Case-Control Differences. <i>Schizophrenia Bulletin</i> , 2020 , 46, 319-327	1.3	3
242	Recalibrating the epigenetic clock: implications for assessing biological age in the human cortex. <i>Brain</i> , 2020 , 143, 3763-3775	11.2	32
241	Association of Neighborhood Disadvantage in Childhood With DNA Methylation in Young Adulthood. <i>JAMA Network Open</i> , 2020 , 3, e206095	10.4	20
240	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. <i>Npj Genomic Medicine</i> , 2020 , 5, 10	6.2	11
239	Epigenome-wide association study of attention-deficit/hyperactivity disorder in adults. <i>Translational Psychiatry</i> , 2020 , 10, 199	8.6	4
238	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	8.6	23
237	Genome-wide DNA methylation meta-analysis in the brains of suicide completers. <i>Translational Psychiatry</i> , 2020 , 10, 69	8.6	17
236	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	4.5	6
235	Major surgery induces acute changes in measured DNA methylation associated with immune response pathways. <i>Scientific Reports</i> , 2020 , 10, 5743	4.9	8
234	Genetic risk for Alzheimer's disease influences neuropathology via multiple biological pathways. <i>Brain Communications</i> , 2020 , 2, fcaa167	4.5	1
233	Quantification of the pace of biological aging in humans through a blood test, the DunedinPoAm DNA methylation algorithm. <i>ELife</i> , 2020 , 9,	8.9	85
232	Correlation between the Expression of Somatic ACE (190KDa) and of its Soluble N-Domain Isoforms (90KDa and 65KDa) with Different Nutritional Status and Cardiovascular Risk Profile. <i>FASEB Journal</i> , 2020 , 34, 1-1	0.9	
231	Transcriptional Signatures of Tau and Amyloid Neuropathology. <i>Cell Reports</i> , 2020 , 30, 2040-2054.e5	10.6	20
230	Clozapine-induced transcriptional changes in the zebrafish brain. <i>NPJ Schizophrenia</i> , 2020 , 6, 3	5.5	5

229	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	3.7	3
228	Psychosis-associated DNA methylomic variation in Alzheimer's disease cortex. <i>Neurobiology of Aging</i> , 2020 , 89, 83-88	5.6	4
227	Patterns of Reliability: Assessing the Reproducibility and Integrity of DNA Methylation Measurement. <i>Patterns</i> , 2020 , 1,	5.1	24
226	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	18	11
225	The molecular etiology of Alzheimer's disease. <i>Brain Pathology</i> , 2020 , 30, 964-965	6	6
224	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,	14.3	514
223	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	5.6	17
222	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	6	2
221	Integrative genomics identifies a convergent molecular subtype that links epigenomic with transcriptomic differences in autism. <i>Nature Communications</i> , 2020 , 11, 4873	17.4	23
220	Epigenetic studies of schizophrenia: current status and future directions. <i>Current Opinion in Behavioral Sciences</i> , 2019 , 25, 102-110	4	6
219	Growth disrupting mutations in epigenetic regulatory molecules are associated with abnormalities of epigenetic aging. <i>Genome Research</i> , 2019 , 29, 1057-1066	9.7	20
218	Methylation age acceleration does not predict mortality in schizophrenia. <i>Translational Psychiatry</i> , 2019 , 9, 157	8.6	9
217	Guidance for DNA methylation studies: statistical insights from the Illumina EPIC array. <i>BMC Genomics</i> , 2019 , 20, 366	4.5	87
216	20.3 DNA METHYLATION PROFILING MIGHT SHED LIGHT ON THE BIOLOGY OF CANNABIS ASSOCIATED PSYCHOSIS. <i>Schizophrenia Bulletin</i> , 2019 , 45, S122-S122	1.3	78
215	Parallel profiling of DNA methylation and hydroxymethylation highlights neuropathology-associated epigenetic variation in Alzheimer's disease. <i>Clinical Epigenetics</i> , 2019 , 11, 52	7.7	49
214	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	5.6	43
213	Genetics and the geography of health, behaviour and attainment. <i>Nature Human Behaviour</i> , 2019 , 3, 576-586	5.8	26
212	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	5.8	28

211	Evidence of causal effect of major depression on alcohol dependence: findings from the psychiatric genomics consortium. <i>Psychological Medicine</i> , 2019 , 49, 1218-1226	6.9	33
210	Genetic risk variants for brain disorders are enriched in cortical H3K27ac domains. <i>Molecular Brain</i> , 2019 , 12, 7	4.5	11
209	Longitudinal investigation of DNA methylation changes preceding adolescent psychotic experiences. <i>Translational Psychiatry</i> , 2019 , 9, 69	8.6	10
208	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. <i>Biological Psychiatry</i> , 2019 , 86, 599-607	7.9	24
207	Establishing a generalized polyepigenetic biomarker for tobacco smoking. <i>Translational Psychiatry</i> , 2019 , 9, 92	8.6	34
206	Systematic underestimation of the epigenetic clock and age acceleration in older subjects. <i>Genome Biology</i> , 2019 , 20, 283	18.3	41
205	RNA sequencing of identical twins discordant for autism reveals blood-based signatures implicating immune and transcriptional dysregulation. <i>Molecular Autism</i> , 2019 , 10, 38	6.5	8
204	Alzheimer's disease-associated (hydroxy)methylomic changes in the brain and blood. <i>Clinical Epigenetics</i> , 2019 , 11, 164	7.7	41
203	THE AUTHORS REPLY. <i>American Journal of Epidemiology</i> , 2019 , 188, 488-489	3.8	1
202	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	5.6	13
201	A cross-brain regions study of ANK1 DNA methylation in different neurodegenerative diseases. <i>Neurobiology of Aging</i> , 2019 , 74, 70-76	5.6	34
200	Bigmelon: tools for analysing large DNA methylation datasets. <i>Bioinformatics</i> , 2019 , 35, 981-986	7.2	20
199	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 & Integrative Physiology</i> , 2018 , 222, 16-25	2.6	14
198	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	11.9	83
197	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018 , 23, 2133-2144	15.1	46
196	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018 , 50, 668-681	36.3	1301
195	Peripheral DNA methylation, cognitive decline and brain aging: pilot findings from the Whitehall II imaging study. <i>Epigenomics</i> , 2018 , 10, 585-595	4.4	29
194	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	1.2	73

193	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	15.1	67
192	Genome-wide methylomic analysis in individuals with HNF1B intragenic mutation and 17q12 microdeletion. <i>Clinical Epigenetics</i> , 2018 , 10, 97	7.7	10
191	Socioeconomic Position and DNA Methylation Age Acceleration Across the Life Course. <i>American Journal of Epidemiology</i> , 2018 , 187, 2346-2354	3.8	49
190	Elevated polygenic burden for autism is associated with differential DNA methylation at birth. <i>Genome Medicine</i> , 2018 , 10, 19	14.4	58
189	Characterizing genetic and environmental influences on variable DNA methylation using monozygotic and dizygotic twins. <i>PLoS Genetics</i> , 2018 , 14, e1007544	6	92
188	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	8.6	21
187	Expression quantitative trait loci in the developing human brain and their enrichment in neuropsychiatric disorders. <i>Genome Biology</i> , 2018 , 19, 194	18.3	69
186	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	11	61
185	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	25.5	72
184	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. <i>Nature Communications</i> , 2018 , 9, 3738	17.4	12
183	DNA methylation and inflammation marker profiles associated with a history of depression. <i>Human Molecular Genetics</i> , 2018 , 27, 2840-2850	5.6	23
182	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	5.6	31
181	Epigenetic profiling of ADHD symptoms trajectories: a prospective, methylome-wide study. <i>Molecular Psychiatry</i> , 2017 , 22, 250-256	15.1	83
180	Advanced paternal age effects in neurodevelopmental disorders-review of potential underlying mechanisms. <i>Translational Psychiatry</i> , 2017 , 7, e1019	8.6	64
179	Is treatment-resistant schizophrenia categorically distinct from treatment-responsive schizophrenia? a systematic review. <i>BMC Psychiatry</i> , 2017 , 17, 12	4.2	124
178	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	11	61
177	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. <i>Nature Communications</i> , 2017 , 8, 15353	17.4	57
176	Paternal Age Alters Social Development in Offspring. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2017 , 56, 383-390	7.2	16

175	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	8.6	48
174	Genetic variation at 16q24.2 is associated with small vessel stroke. <i>Annals of Neurology</i> , 2017 , 81, 383-394	9.4	51
173	Profiling Regulatory Variation in the Brain: Methods for Exploring the Neuronal Epigenome. <i>Biological Psychiatry</i> , 2017 , 81, 90-91	7.9	2
172	5-hydroxymethylcytosine is highly dynamic across human fetal brain development. <i>BMC Genomics</i> , 2017 , 18, 738	4.5	43
171	Regional differences in mitochondrial DNA methylation in human post-mortem brain tissue. <i>Clinical Epigenetics</i> , 2017 , 9, 47	7.7	22
170	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	6.1	19
169	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	3.7	26
168	Schizophrenia-associated methylomic variation: molecular signatures of disease and polygenic risk burden across multiple brain regions. <i>Human Molecular Genetics</i> , 2017 , 26, 210-225	5.6	60
167	Erasure and reestablishment of random allelic expression imbalance after epigenetic reprogramming. <i>Rna</i> , 2016 , 22, 1620-30	5.8	9
166	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	18.3	189
165	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	5.6	60
164	Genome-wide DNA methylation levels and altered cortisol stress reactivity following childhood trauma in humans. <i>Nature Communications</i> , 2016 , 7, 10967	17.4	125
163	Histone Acetylome-wide Association Study of Autism Spectrum Disorder. <i>Cell</i> , 2016 , 167, 1385-1397.e1156.2	156.2	168
162	Mapping epigenetic changes to the host cell genome induced by Burkholderia pseudomallei reveals pathogen-specific and pathogen-generic signatures of infection. <i>Scientific Reports</i> , 2016 , 6, 30861	4.9	17
161	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	8.6	41
160	Elucidating novel dysfunctional pathways in Alzheimer's disease by integrating loci identified in genetic and epigenetic studies. <i>Neuroepigenetics</i> , 2016 , 6, 32-50		13
159	Variation in 5-hydroxymethylcytosine across human cortex and cerebellum. <i>Genome Biology</i> , 2016 , 17, 27	18.3	67
158	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, 152-60	7.9	66

157	Tissue-specific patterns of allelically-skewed DNA methylation. <i>Epigenetics</i> , 2016 , 11, 24-35	5.7	18
156	DNA Methylation Profiling in Inflammatory Bowel Disease Provides New Insights into Disease Pathogenesis. <i>Journal of Crohns and Colitis</i> , 2016 , 10, 77-86	1.5	80
155	Epigenetic regulation of mitochondrial function in neurodegenerative disease: New insights from advances in genomic technologies. <i>Neuroscience Letters</i> , 2016 , 625, 47-55	3.3	25
154	An epigenome-wide association meta-analysis of prenatal maternal stress in neonates: A model approach for replication. <i>Epigenetics</i> , 2016 , 11, 140-9	5.7	62
153	Age-associated changes in DNA methylation across multiple tissues in an inbred mouse model. <i>Mechanisms of Ageing and Development</i> , 2016 , 154, 20-3	5.6	27
152	Methylation QTLs in the developing brain and their enrichment in schizophrenia risk loci. <i>Nature Neuroscience</i> , 2016 , 19, 48-54	25.5	227
151	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. <i>Human Molecular Genetics</i> , 2016 , 25, 4339-4349	5.6	7
150	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016 , 7, 10561	17.4	55
149	Epigenetic Research in Neuropsychiatric Disorders: the "Tissue Issue". <i>Current Behavioral Neuroscience Reports</i> , 2016 , 3, 264-274	1.7	70
148	DNA methylation and substance-use risk: a prospective, genome-wide study spanning gestation to adolescence. <i>Translational Psychiatry</i> , 2016 , 6, e976	8.6	73
147	O2-06-05: Hydroxymethylomic Profiling Implicates Cortical Deregulation of ANK1 and APP in the Alzheimer's Disease Brain 2016 , 12, P240-P241		
146	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, 4830-5	11.5	74
145	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, 526-38	5.7	114
144	Epigenetic signatures of childhood abuse and neglect: Implications for psychiatric vulnerability. <i>Journal of Psychiatric Research</i> , 2016 , 83, 184-194	5.2	73
143	Methylomic trajectories across human fetal brain development. <i>Genome Research</i> , 2015 , 25, 338-52	9.7	188
142	Blood methylomic signatures of presymptomatic dementia in elderly subjects with type 2 diabetes mellitus. <i>Neurobiology of Aging</i> , 2015 , 36, 1600.e1-4	5.6	12
141	Methylomic analysis of monozygotic twins discordant for childhood psychotic symptoms. <i>Epigenetics</i> , 2015 , 10, 1014-23	5.7	36
140	Interindividual methylomic variation across blood, cortex, and cerebellum: implications for epigenetic studies of neurological and neuropsychiatric phenotypes. <i>Epigenetics</i> , 2015 , 10, 1024-32	5.7	272

139	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	2.7	
138	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015 , 18, 1707-12	25.5	226
137	Measuring adolescents' exposure to victimization: The Environmental Risk (E-Risk) Longitudinal Twin Study. <i>Development and Psychopathology</i> , 2015 , 27, 1399-416	4.3	74
136	Epigenome-Wide DNA Methylation Analysis of Monozygotic Twins Discordant for Diurnal Preference. <i>Twin Research and Human Genetics</i> , 2015 , 18, 662-9	2.2	11
135	A role for Ca1 and calcineurin signaling in depolarization-induced changes in neuronal DNA methylation. <i>Neuroepigenetics</i> , 2015 , 3, 1-6		2
134	Methylomic markers of persistent childhood asthma: a longitudinal study of asthma-discordant monozygotic twins. <i>Clinical Epigenetics</i> , 2015 , 7, 130	7.7	33
133	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, 241-2, 244-6	2.5	14
132	Effects of advanced paternal age on trajectories of social behavior in offspring. <i>Genes, Brain and Behavior</i> , 2015 , 14, 443-53	3.6	16
131	Association of Protein Phosphatase PPM1G With Alcohol Use Disorder and Brain Activity During Behavioral Control in a Genome-Wide Methylation Analysis. <i>American Journal of Psychiatry</i> , 2015 , 172, 543-52	11.9	49
130	O3-05-01: Systems-level evidence for epigenetic dysfunction in Alzheimer's disease 2015 , 11, P228-P228		
129	DNA modification study of major depressive disorder: beyond locus-by-locus comparisons. <i>Biological Psychiatry</i> , 2015 , 77, 246-255	7.9	49
128	Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015 , 6, 6363	17.4	67
127	Epigenetically regulated microRNAs in Alzheimer's disease. <i>Neurobiology of Aging</i> , 2014 , 35, 731-45	5.6	89
126	Environmental risk, Oxytocin Receptor Gene (OXTR) methylation and youth callous-unemotional traits: a 13-year longitudinal study. <i>Molecular Psychiatry</i> , 2014 , 19, 1071-7	15.1	161
125	Epigenetic regulation of adult neural stem cells: implications for Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2014 , 9, 25	19	46
124	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. <i>Nature Neuroscience</i> , 2014 , 17, 1156-63	25.5	579
123	Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. <i>Nature Neuroscience</i> , 2014 , 17, 1164-70	25.5	356
122	Cross-region reduction in 5-hydroxymethylcytosine in Alzheimer's disease brain. <i>Neurobiology of Aging</i> , 2014 , 35, 1850-4	5.6	96

121	Genome-wide methylomic analysis of monozygotic twins discordant for adolescent depression. <i>Biological Psychiatry</i> , 2014 , 76, 977-83	7.9	97
120	Epigenetics in health and disease: heralding the EWAS era. <i>Lancet, The</i> , 2014 , 383, 1952-4	4.0	55
119	O3-04-03: CROSS-TISSUE METHYLOMIC PROFILING IN ALZHEIMER'S DISEASE 2014 , 10, P215-P215		
118	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> , 2014 , 38, 165-70	4.3	39
117	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	3.7	4
116	Epigenomic and transcriptomic signatures of a Klinefelter syndrome (47,XXY) karyotype in the brain. <i>Epigenetics</i> , 2014 , 9, 587-99	5.7	37
115	The mitochondrial epigenome: a role in Alzheimer's disease?. <i>Epigenomics</i> , 2014 , 6, 665-75	4.4	30
114	Prenatal maternal immune activation causes epigenetic differences in adolescent mouse brain. <i>Translational Psychiatry</i> , 2014 , 4, e434	8.6	69
113	Differential methylation of the TRPA1 promoter in pain sensitivity. <i>Nature Communications</i> , 2014 , 5, 2978-7.4	7.4	107
112	Methylomic analysis of monozygotic twins discordant for autism spectrum disorder and related behavioural traits. <i>Molecular Psychiatry</i> , 2014 , 19, 495-503	15.1	236
111	Methylomic profiling of human brain tissue supports a neurodevelopmental origin for schizophrenia. <i>Genome Biology</i> , 2014 , 15, 483	18.3	114
110	Transcriptomic changes in the frontal cortex associated with paternal age. <i>Molecular Autism</i> , 2014 , 5, 24	6.5	8
109	Hypermethylation in the ZBTB20 gene is associated with major depressive disorder. <i>Genome Biology</i> , 2014 , 15, R56	18.3	73
108	Decreased methylation of the NK3 receptor coding gene (TACR3) after cocaine-induced place preference in marmoset monkeys. <i>Addiction Biology</i> , 2013 , 18, 452-4	4.6	27
107	From promises to practical strategies in epigenetic epidemiology. <i>Nature Reviews Genetics</i> , 2013 , 14, 585-94	30.1	270
106	A data-driven approach to preprocessing Illumina 450K methylation array data. <i>BMC Genomics</i> , 2013 , 14, 293	4.5	587
105	Protection from genetic diathesis in attention-deficit/hyperactivity disorder: possible complementary roles of exercise. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2013 , 52, 900-10	7.2	26
104	Epigenetic studies of schizophrenia: progress, predicaments, and promises for the future. <i>Schizophrenia Bulletin</i> , 2013 , 39, 11-6	1.3	59

103	Quantitative promoter DNA methylation analysis of four candidate genes in anorexia nervosa: a pilot study. <i>Journal of Psychiatric Research</i> , 2013 , 47, 280-2	5.2	19
102	P.1.a.017 S-Adenosyl-methionine impairs forced swimming-induced behavioural immobility by inhibiting gene expression in dentate gyrus neurons. <i>European Neuropsychopharmacology</i> , 2013 , 23, S169 ^{1,2}		
101	Genetic and epigenetic associations of MAOA and NR3C1 with depression and childhood adversities. <i>International Journal of Neuropsychopharmacology</i> , 2013 , 16, 1513-28	5.8	153
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12	A meta-analysis of epigenome-wide association studies in Alzheimer's disease highlights novel differentially methylated loci across cortex	8
11	Large-scale analysis of DNA methylation identifies cellular alterations in blood from psychosis patients and molecular biomarkers of treatment-resistant schizophrenia	1
10	Recalibrating the Epigenetic Clock: Implications for Assessing Biological Age in the Human Cortex	6
9	Assessing the co-variability of DNA methylation across peripheral cells and tissues: implications for the interpretation of findings in epigenetic epidemiology	2
8	Genomic and phenomic insights from an atlas of genetic effects on DNA methylation	7
7	Novel epigenetic clock for fetal brain development predicts prenatal age for cellular stem cell models and derived neurons	1
6	Properties of the epigenetic clock and age acceleration	4
5	Genome-wide DNA methylation profiling identifies convergent molecular signatures associated with idiopathic and syndromic forms of autism in post-mortem human brain tissue	1
4	Growth disrupting mutations in epigenetic regulatory molecules are associated with abnormalities of epigenetic aging	2
3	A histone acetylome-wide association study of Alzheimer's disease: neuropathology-associated regulatory variation in the human entorhinal cortex	1
2	Genome-wide study of DNA methylation in Amyotrophic Lateral Sclerosis identifies differentially methylated loci and implicates metabolic, inflammatory and cholesterol pathways	1
1	Quantification of the pace of biological aging in humans through a blood test: the DunedinPACE DNA methylation algorithm	3