

Jonathan S Mill

List of Publications by Citations

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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	Influence of life stress on depression: moderation by a polymorphism in the 5-HTT gene. <i>Science</i> , 2003 , 301, 386-9	33.3	6113
263	Role of genotype in the cycle of violence in maltreated children. <i>Science</i> , 2002 , 297, 851-4	33.3	3452
262	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
261	Transcriptomic analysis of autistic brain reveals convergent molecular pathology. <i>Nature</i> , 2011 , 474, 380-4	50.4	1281
260	Epigenomic profiling reveals DNA-methylation changes associated with major psychosis. <i>American Journal of Human Genetics</i> , 2008 , 82, 696-711	11	641
259	A data-driven approach to preprocessing Illumina 450K methylation array data. <i>BMC Genomics</i> , 2013 , 14, 293	4.5	587
258	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
257	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
256	Functional annotation of the human brain methylome identifies tissue-specific epigenetic variation across brain and blood. <i>Genome Biology</i> , 2012 , 13, R43	18.3	508
255	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	6	501
254	Disease-associated epigenetic changes in monozygotic twins discordant for schizophrenia and bipolar disorder. <i>Human Molecular Genetics</i> , 2011 , 20, 4786-96	5.6	364
253	Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. <i>Nature Neuroscience</i> , 2014 , 17, 1164-70	25.5	356
252	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, 576-81	15.1	333
251	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, 975-9		290
250	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
249	From promises to practical strategies in epigenetic epidemiology. <i>Nature Reviews Genetics</i> , 2013 , 14, 585-94	30.1	270
248	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	3.2	250

247	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, 74-81		248
246	A longitudinal study of epigenetic variation in twins. <i>Epigenetics</i> , 2010 , 5, 516-26	5.7	243
245	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
244	Molecular studies of major depressive disorder: the epigenetic perspective. <i>Molecular Psychiatry</i> , 2007 , 12, 799-814	15.1	232
243	Methylation QTLs in the developing brain and their enrichment in schizophrenia risk loci. <i>Nature Neuroscience</i> , 2016 , 19, 48-54	25.5	227
242	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015 , 18, 1707-12	25.5	226
241	Allelic skewing of DNA methylation is widespread across the genome. <i>American Journal of Human Genetics</i> , 2010 , 86, 196-212	11	211
240	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	3.7	193
239	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
238	Methylomic trajectories across human fetal brain development. <i>Genome Research</i> , 2015 , 25, 338-52	9.7	188
237	Dynamic changes in DNA methylation of stress-associated genes (OXTR, BDNF) after acute psychosocial stress. <i>Translational Psychiatry</i> , 2012 , 2, e150	8.6	180
236	Epigenetic mediation of environmental influences in major psychotic disorders. <i>Schizophrenia Bulletin</i> , 2009 , 35, 1045-56	1.3	175
235	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, 309-20	7	171
234	Histone Acetylome-wide Association Study of Autism Spectrum Disorder. <i>Cell</i> , 2016 , 167, 1385-1397.e1156.2		168
233	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
232	Pre- and peri-natal 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, 1020-30	7.9	160
231	Commentary: The seven plagues of epigenetic epidemiology. <i>International Journal of Epidemiology</i> , 2012 , 41, 74-8	7.8	158
230	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

229	Increased serotonin transporter gene (SERT) 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, 1813-23	6.9	151
228	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, 348-56	11	148
227	Association study of a dopamine transporter polymorphism and attention deficit hyperactivity disorder in UK and Turkish samples. <i>Molecular Psychiatry</i> , 2001 , 6, 425-8	15.1	130
226	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
225	Is treatment-resistant schizophrenia categorically distinct from treatment-responsive schizophrenia? a systematic review. <i>BMC Psychiatry</i> , 2017 , 17, 12	4.2	124
224	Methylomic profiling of human brain tissue supports a neurodevelopmental origin for schizophrenia. <i>Genome Biology</i> , 2014 , 15, 483	18.3	114
223	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
222	Allele-specific methylation in the human genome: implications for genetic studies of complex disease. <i>Epigenetics</i> , 2010 , 5, 578-82	5.7	110
221	Differential methylation of the TRPA1 promoter in pain sensitivity. <i>Nature Communications</i> , 2014 , 5, 2978	7.4	107
220	A multi-tissue analysis identifies HLA complex group 9 gene methylation differences in bipolar disorder. <i>Molecular Psychiatry</i> , 2012 , 17, 728-40	15.1	107
219	Haplotype analysis of SNAP-25 suggests a role in the aetiology of ADHD. <i>Molecular Psychiatry</i> , 2004 , 9, 801-10	15.1	107
218	Maternal separation is associated with strain-specific responses to stress and epigenetic alterations to Nr3c1, Avp, and Nr4a1 in mouse. <i>Brain and Behavior</i> , 2012 , 2, 455-67	3.4	105
217	The dopamine transporter gene is associated with attention deficit hyperactivity disorder in a Taiwanese sample. <i>Molecular Psychiatry</i> , 2003 , 8, 393-6	15.1	105
216	Drugs and addiction: an introduction to epigenetics. <i>Addiction</i> , 2011 , 106, 480-9	4.6	104
215	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, 421-5	3.5	104
214	Genome-wide methylomic analysis of monozygotic twins discordant for adolescent depression. <i>Biological Psychiatry</i> , 2014 , 76, 977-83	7.9	97
213	Cross-region reduction in 5-hydroxymethylcytosine in Alzheimer's disease brain. <i>Neurobiology of Aging</i> , 2014 , 35, 1850-4	5.6	96
212	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	95

211	Characterizing genetic and environmental influences on variable DNA methylation using monozygotic and dizygotic twins. <i>PLoS Genetics</i> , 2018 , 14, e1007544	6	92
210	Association of DRD4 in children with ADHD and comorbid conduct problems. <i>American Journal of Medical Genetics Part A</i> , 2002 , 114, 150-3		92
209	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 , 156B, 681-90	3.5	91
208	Epigenetically regulated microRNAs in Alzheimer's disease. <i>Neurobiology of Aging</i> , 2014 , 35, 731-45	5.6	89
207	Epigenetic studies of psychosis: current findings, methodological approaches, and implications for postmortem research. <i>Biological Psychiatry</i> , 2011 , 69, 146-56	7.9	89
206	Guidance for DNA methylation studies: statistical insights from the Illumina EPIC array. <i>BMC Genomics</i> , 2019 , 20, 366	4.5	87
205	Functional effects of a tandem duplication polymorphism in the 5'flanking region of the DRD4 gene. <i>Biological Psychiatry</i> , 2004 , 56, 691-7	7.9	87
204	Eating disorders, gene-environment interactions and epigenetics. <i>Neuroscience and Biobehavioral Reviews</i> , 2011 , 35, 784-93	9	85
203	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
202	Epigenetic profiling of ADHD symptoms trajectories: a prospective, methylome-wide study. <i>Molecular Psychiatry</i> , 2017 , 22, 250-256	15.1	83
201	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
200	Prediction of heterogeneity in intelligence and adult prognosis by genetic polymorphisms in the dopamine system among children with attention-deficit/hyperactivity disorder: evidence from 2 birth cohorts. <i>Archives of General Psychiatry</i> , 2006 , 63, 462-9		83
199	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
198	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
197	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
196	Association study of a SNAP-25 microsatellite and attention deficit hyperactivity disorder. <i>American Journal of Medical Genetics Part A</i> , 2002 , 114, 269-71		74
195	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
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	Hypermethylation in the ZBTB20 gene is associated with major depressive disorder. <i>Genome Biology</i> , 2014 , 15, R56	18.3	73
192	Schizophrenia is associated with dysregulation of a Cdk5 activator that regulates synaptic protein expression and cognition. <i>Brain</i> , 2011 , 134, 2408-21	11.2	73
191	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
190	Epigenetic signatures of childhood abuse and neglect: Implications for psychiatric vulnerability. <i>Journal of Psychiatric Research</i> , 2016 , 83, 184-194	5.2	73
189	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
188	Long-lasting regulation of hippocampal Bdnf gene transcription after contextual fear conditioning. <i>Genes, Brain and Behavior</i> , 2012 , 11, 651-9	3.6	70
187	Epigenetic Research in Neuropsychiatric Disorders: the "Tissue Issue". <i>Current Behavioral Neuroscience Reports</i> , 2016 , 3, 264-274	1.7	70
186	Prenatal maternal immune activation causes epigenetic differences in adolescent mouse brain. <i>Translational Psychiatry</i> , 2014 , 4, e434	8.6	69
185	Current status and future prospects for epigenetic psychopharmacology. <i>Epigenetics</i> , 2012 , 7, 20-8	5.7	69
184	Transient expression analysis of allelic variants of a VNTR in the dopamine transporter gene (DAT1). <i>BMC Genetics</i> , 2005 , 6, 3	2.6	69
183	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
182	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
181	Variation in 5-hydroxymethylcytosine across human cortex and cerebellum. <i>Genome Biology</i> , 2016 , 17, 27	18.3	67
180	Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015 , 6, 6363	17.4	67
179	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
178	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	3.7	65
177	Advanced paternal age effects in neurodevelopmental disorders-review of potential underlying mechanisms. <i>Translational Psychiatry</i> , 2017 , 7, e1019	8.6	64
176	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	3.5	64

175	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, 440-4	15.1	64
174	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
173	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
172	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
171	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
170	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
169	Epigenetic studies of schizophrenia: progress, predicaments, and promises for the future. <i>Schizophrenia Bulletin</i> , 2013 , 39, 11-6	1.3	59
168	Elevated polygenic burden for autism is associated with differential DNA methylation at birth. <i>Genome Medicine</i> , 2018 , 10, 19	14.4	58
167	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 , 162B, 789-99	3.5	58
166	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. <i>Nature Communications</i> , 2017 , 8, 15353	17.4	57
165	Epigenetics in health and disease: heralding the EWAS era. <i>Lancet, The</i> , 2014 , 383, 1952-4	40	55
164	DNA methylation in interleukin-11 predicts clinical response to antidepressants in GENDEP. <i>Translational Psychiatry</i> , 2013 , 3, e300	8.6	55
163	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, 850-6	7.9	55
162	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016 , 7, 10561	17.4	55
161	Genetic variation at 16q24.2 is associated with small vessel stroke. <i>Annals of Neurology</i> , 2017 , 81, 383-394	9.4	51
160	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, 83-6	3.5	50
159	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
158	Socioeconomic Position and DNA Methylation Age Acceleration Across the Life Course. <i>American Journal of Epidemiology</i> , 2018 , 187, 2346-2354	3.8	49

157	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
156	DNA modification study of major depressive disorder: beyond locus-by-locus comparisons. <i>Biological Psychiatry</i> , 2015 , 77, 246-255	7.9	49
155	SORL1 and SIRT1 mRNA expression and promoter methylation levels in aging and Alzheimer's Disease. <i>Neurochemistry International</i> , 2012 , 61, 973-5	4.4	49
154	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
153	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018 , 23, 2133-2144	15.1	46
152	Epigenetic regulation of adult neural stem cells: implications for Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2014 , 9, 25	19	46
151	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, 115-8	3.5	46
150	Stochastic choice of allelic expression in human neural stem cells. <i>Stem Cells</i> , 2012 , 30, 1938-47	5.8	45
149	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
148	5-hydroxymethylcytosine is highly dynamic across human fetal brain development. <i>BMC Genomics</i> , 2017 , 18, 738	4.5	43
147	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, 387-93		43
146	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
145	Systematic underestimation of the epigenetic clock and age acceleration in older subjects. <i>Genome Biology</i> , 2019 , 20, 283	18.3	41
144	Alzheimer's disease-associated (hydroxy)methylomic changes in the brain and blood. <i>Clinical Epigenetics</i> , 2019 , 11, 164	7.7	41
143	Bisulfite-based epityping on pooled genomic DNA provides an accurate estimate of average group DNA methylation. <i>Epigenetics and Chromatin</i> , 2009 , 2, 3	5.8	40
142	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
141	Epigenomic and transcriptomic signatures of a Klinefelter syndrome (47,XXY) karyotype in the brain. <i>Epigenetics</i> , 2014 , 9, 587-99	5.7	37
140	Analysis of SNAP25 mRNA expression and promoter DNA methylation in brain areas of Alzheimer's Disease patients. <i>Neuroscience</i> , 2012 , 220, 41-6	3.9	37

139	Polymorphisms in the dopamine D4 receptor gene and attention-deficit hyperactivity disorder. <i>NeuroReport</i> , 2003 , 14, 1463-6	1.7	37
138	Methylomic analysis of monozygotic twins discordant for childhood psychotic symptoms. <i>Epigenetics</i> , 2015 , 10, 1014-23	5.7	36
137	Sequence analysis of Drd2, Drd4, and Dat1 in SHR and WKY rat strains. <i>Behavioral and Brain Functions</i> , 2005 , 1, 24	4.1	36
136	Toward an integrated genetic and epigenetic approach to Alzheimer's disease. <i>Neurobiology of Aging</i> , 2011 , 32, 1188-91	5.6	34
135	DNA methylation profiling using bisulfite-based epityping of pooled genomic DNA. <i>Methods</i> , 2010 , 52, 255-8	4.6	34
134	Establishing a generalized polyepigenetic biomarker for tobacco smoking. <i>Translational Psychiatry</i> , 2019 , 9, 92	8.6	34
133	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
132	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
131	Methylomic markers of persistent childhood asthma: a longitudinal study of asthma-discordant monozygotic twins. <i>Clinical Epigenetics</i> , 2015 , 7, 130	7.7	33
130	Recalibrating the epigenetic clock: implications for assessing biological age in the human cortex. <i>Brain</i> , 2020 , 143, 3763-3775	11.2	32
129	A longitudinal twin study of skewed X chromosome-inactivation. <i>PLoS ONE</i> , 2011 , 6, e17873	3.7	32
128	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
127	A genetic association study of DNA methylation levels in the DRD4 gene region finds associations with nearby SNPs. <i>Behavioral and Brain Functions</i> , 2012 , 8, 31	4.1	31
126	The mitochondrial epigenome: a role in Alzheimer's disease?. <i>Epigenomics</i> , 2014 , 6, 665-75	4.4	30
125	Whole genome amplification of sodium bisulfite-treated DNA allows the accurate estimate of methylated cytosine density in limited DNA resources. <i>BioTechniques</i> , 2006 , 41, 603-7	2.5	30
124	Application of microarrays to the analysis of the inactivation status of human X-linked genes expressed in lymphocytes. <i>European Journal of Human Genetics</i> , 2004 , 12, 639-46	5.3	30
123	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
122	Epigenetic and genetic variation at the IGF2/H19 imprinting control region on 11p15.5 is associated with cerebellum weight. <i>Epigenetics</i> , 2012 , 7, 155-63	5.7	29

121	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
120	Brain weight in males is correlated with DNA methylation at IGF2. <i>Molecular Psychiatry</i> , 2010 , 15, 880-1	15.1	28
119	Epigenetics, genomic mutations and cognitive function. <i>Cognitive Neuropsychiatry</i> , 2009 , 14, 377-90	2	28
118	Association study of promoter polymorphisms at the dopamine transporter gene in Attention Deficit Hyperactivity Disorder. <i>BMC Psychiatry</i> , 2009 , 9, 3	4.2	28
117	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
116	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
115	Advanced paternal age is associated with altered DNA methylation at brain-expressed imprinted loci in inbred mice: implications for neuropsychiatric disease. <i>Molecular Psychiatry</i> , 2013 , 18, 635-6	15.1	27
114	Association study of the estrogen receptor alpha gene (ESR1) and childhood-onset mood disorders. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2008 , 147B, 1323-6	3.5	27
113	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021 , 53, 1311-1321	36.3	27
112	Genetics and the geography of health, behaviour and attainment. <i>Nature Human Behaviour</i> , 2019 , 3, 576-588	15.8	26
111	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
110	Family-based association study of serotonin transporter gene polymorphisms in attention deficit hyperactivity disorder: no evidence for association in UK and Taiwanese samples. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2005 , 139B, 11-3	3.5	26
109	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
108	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
107	Polymorphisms in the dopamine D5 receptor (DRD5) gene and ADHD. <i>American Journal of Medical Genetics Part A</i> , 2004 , 125B, 38-42		24
106	Patterns of Reliability: Assessing the Reproducibility and Integrity of DNA Methylation Measurement. <i>Patterns</i> , 2020 , 1,	5.1	24
105	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. <i>Biological Psychiatry</i> , 2019 , 86, 599-607	7.9	24
104	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

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