Global Epigenomic Reconfiguration During Mammalian

Science 341, 1237905

DOI: 10.1126/science.1237905

Citation Report

#	Article	IF	CITATIONS
1	Cortical Evolution: Judge the Brain by Its Cover. Neuron, 2013, 80, 633-647.	8.1	444
2	Exposure to caregiver maltreatment alters expression levels of epigenetic regulators in the medial prefrontal cortex. International Journal of Developmental Neuroscience, 2013, 31, 804-810.	1.6	78
3	DNA Recognition of 5-Carboxylcytosine by a Zfp57 Mutant at an Atomic Resolution of 0.97 $\tilde{A}$ Biochemistry, 2013, 52, 9310-9317.	2.5	19
4	The Emerging Field of Neuroepigenetics. Neuron, 2013, 80, 624-632.	8.1	270
5	DNA methylation markers in the postnatal developing rat brain. Brain Research, 2013, 1533, 26-36.	2.2	53
6	DNA Modifications and Neurological Disorders. Neurotherapeutics, 2013, 10, 556-567.	4.4	40
7	DNA methylation, genotype and gene expression: who is driving and who is along for the ride?. Genome Biology, 2013, 14, 126.	9.6	48
8	DNA methylation: an identity card for brain cells. Genome Biology, 2013, 14, 131.	9.6	6
9	Twenty-Five Years of Progress: The View from NIMH and NINDS. Neuron, 2013, 80, 561-567.	8.1	73
10	5-hydroxymethylcytosine profiling as an indicator of cellular state. Epigenomics, 2013, 5, 655-669.	2.1	52
11	Function and Evolution of DNA Methylation in Nasonia vitripennis. PLoS Genetics, 2013, 9, e1003872.	3.5	162
12	TET Proteins and 5-Methylcytosine Oxidation in the Immune System. Cold Spring Harbor Symposia on Quantitative Biology, 2013, 78, 1-10.	1.1	28
13	The Maturing Brain Methylome. Science, 2013, 341, 626-627.	12.6	18
14	Big Brains, Meat, Tuberculosis, and the Nicotinamide Switches: Co-Evolutionary Relationships with Modern Repercussions?. International Journal of Tryptophan Research, 2013, 6, IJTR.S12838.	2.3	18
15	Reliability and Validity of the Korean Version of the Lifespan Sibling Relationship Scale. Experimental Neurobiology, 2013, 22, 330-336.	1.6	8
16	DNA methylation, a hand behind neurodegenerative diseases. Frontiers in Aging Neuroscience, 2013, 5, 85.	3.4	140
17	DNA methylation, microRNAs, and their crosstalk as potential biomarkers in hepatocellular carcinoma. World Journal of Gastroenterology, 2014, 20, 7894.	3.3	74
18	Homeostatic Maintenance of Allele-Specific p16 Methylation in Cancer Cells Accompanied by Dynamic Focal Methylation and Hydroxymethylation. PLoS ONE, 2014, 9, e97785.	2.5	13

#	Article	IF	CITATIONS
19	Epigenetic Genes and Emotional Reactivity to Daily Life Events: A Multi-Step Gene-Environment Interaction Study. PLoS ONE, 2014, 9, e100935.	2.5	27
20	Objective and Comprehensive Evaluation of Bisulfite Short Read Mapping Tools. Advances in Bioinformatics, 2014, 2014, 1-11.	5.7	52
21	Regulated DNA Methylation and the Circadian Clock: Implications in Cancer. Biology, 2014, 3, 560-577.	2.8	34
22	Sensing risk, fearing uncertainty: systems science approach to change. Frontiers in Computational Neuroscience, 2014, 8, 30.	2.1	1
23	Shaping the learning curve: epigenetic dynamics in neural plasticity. Frontiers in Integrative Neuroscience, 2014, 8, 55.	2.1	16
24	Mammalian Non-CpG Methylation: Stem Cells and Beyond. Biology, 2014, 3, 739-751.	2.8	81
25	Notch signaling genes. Epigenetics, 2014, 9, 842-850.	2.7	49
26	Decreased glutathione and elevated hair mercury levels are associated with nutritional deficiency-based autism in Oman. Experimental Biology and Medicine, 2014, 239, 697-706.	2.4	41
27	Genomics in Neurological Disorders. Genomics, Proteomics and Bioinformatics, 2014, 12, 156-163.	6.9	23
28	Epigenetic regulation of the placental HSD11B2 barrier and its role as a critical regulator of fetal development. Epigenetics, 2014, 9, 816-822.	2.7	79
29	Maternal choline modifies fetal liver copper, gene expression, DNA methylation, and neonatal growth in the tx-j mouse model of Wilson disease. Epigenetics, 2014, 9, 286-296.	2.7	54
30	Selective demethylation and altered gene expression are associated with ICF syndrome in human-induced pluripotent stem cells and mesenchymal stem cells. Human Molecular Genetics, 2014, 23, 6448-6457.	2.9	26
31	Epigenetics of Schizophrenia. International Review of Neurobiology, 2014, 115, 155-201.	2.0	18
32	Differences in DNA methylation between human neuronal and glial cells are concentrated in enhancers and non-CpG sites. Nucleic Acids Research, 2014, 42, 109-127.	14.5	187
33	Characterizing the strand-specific distribution of non-CpG methylation in human pluripotent cells. Nucleic Acids Research, 2014, 42, 3009-3016.	14.5	54
34	DNA methylation analysis of the autistic brain reveals multiple dysregulated biological pathways. Translational Psychiatry, 2014, 4, e433-e433.	4.8	203
35	Increased binding of MeCP2 to the GAD1 and RELN promoters may be mediated by an enrichment of 5-hmC in autism spectrum disorder (ASD) cerebellum. Translational Psychiatry, 2014, 4, e349-e349.	4.8	132
36	Brain somatic mutations: the dark matter of psychiatric genetics?. Molecular Psychiatry, 2014, 19, 156-158.	7.9	49

#	Article	IF	CITATIONS
37	A Role for Noncoding Variation in Schizophrenia. Cell Reports, 2014, 9, 1417-1429.	6.4	225
38	Dnmt3a Regulates Global Gene Expression in Olfactory Sensory Neurons and Enables Odorant-Induced Transcription. Neuron, 2014, 83, 823-838.	8.1	37
39	Hydroxymethylated Cytosines Are Associated with Elevated C to G Transversion Rates. PLoS Genetics, 2014, 10, e1004585.	3.5	31
40	Dynamic DNA methylation orchestrates cardiomyocyte development, maturation and disease. Nature Communications, 2014, 5, 5288.	12.8	272
41	Ontogeny, conservation and functional significance of maternally inherited DNA methylation at two classes of non-imprinted genes. Development (Cambridge), 2014, 141, 1313-1323.	2.5	19
42	Acute Depletion Redefines the Division of Labor among DNA Methyltransferases in Methylating the Human Genome. Cell Reports, 2014, 9, 1554-1566.	6.4	33
43	DNA cytosine methylation and hydroxymethylation at the borders. Epigenomics, 2014, 6, 563-566.	2.1	38
44	Epigenetic regulation: Basic concepts and relevance to neurologic disease. Neurology, 2014, 82, 1833-1840.	1.1	16
45	Assembly of telomeric chromatin to create ALTernative endings. Trends in Cell Biology, 2014, 24, 675-685.	7.9	54
46	Epigenetic regulation in neural crest development. Developmental Biology, 2014, 396, 159-168.	2.0	73
47	Integrating DNA methylation dynamics into a framework for understanding epigenetic codes. BioEssays, 2014, 36, 107-117.	2.5	37
48	The Future of Neuroepigenetics in the Human Brain. Progress in Molecular Biology and Translational Science, 2014, 128, 199-228.	1.7	14
49	Effects of negative stressors on DNA methylation in the brain: Implications for mood and anxiety disorders. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 541-554.	1.7	32
50	Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. Nature Communications, 2014, 5, 5442.	12.8	25
51	'Memory and molecular turnover,' 30Âyears after inception. Epigenetics and Chromatin, 2014, 7, 37.	3.9	17
52	Whole-genome analysis of 5-hydroxymethylcytosine and 5-methylcytosine at base resolution in the human brain. Genome Biology, 2014, 15, R49.	9.6	232
53	Non-coding RNAs and DNA methylation in plants. National Science Review, 2014, 1, 219-229.	9.5	23
54	Aberrant signature methylome by DNMT1 hot spot mutation in hereditary sensory and autonomic neuropathy 1E. Epigenetics, 2014, 9, 1184-1193.	2.7	55

#	Article	IF	Citations
55	Whole genome sequencing and methylome analysis of the wild guinea pig. BMC Genomics, 2014, 15, 1036.	2.8	14
56	The effects of perinatal testosterone exposure on the DNA methylome of the mouse brain are late-emerging. Biology of Sex Differences, 2014, 5, 8.	4.1	106
57	Distinct roles of the methylcytosine oxidases Tet1 and Tet2 in mouse embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1361-1366.	7.1	225
58	Process of cortical network formation and impact of early brain damage. Current Opinion in Neurology, 2014, 27, 133-141.	3.6	19
59	NGSmethDB: an updated genome resource for high quality, single-cytosine resolution methylomes. Nucleic Acids Research, 2014, 42, D53-D59.	14.5	22
60	Differential Methylation during Maize Leaf Growth Targets Developmentally Regulated Genes   Â. Plant Physiology, 2014, 164, 1350-1364.	4.8	84
61	Could monitoring methylation markers aid the management of schizophrenia?. Biomarkers in Medicine, 2014, 8, 607-611.	1.4	0
62	Enriched domain detector: a program for detection of wide genomic enrichment domains robust against local variations. Nucleic Acids Research, 2014, 42, e92-e92.	14.5	111
63	Epigenetic Function of Activation-Induced Cytidine Deaminase and Its Link to Lymphomagenesis. Frontiers in Immunology, 2014, 5, 642.	4.8	25
64	Epigenetic regulations through DNA methylation and hydroxymethylation: clues for early pregnancy in decidualization. Biomolecular Concepts, 2014, 5, 95-107.	2.2	23
65	A validated quantitative liquid chromatography–tandem quadrupole mass spectrometry method for monitoring isotopologues to evaluate global modified cytosine ratios in genomic DNA. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2014, 953-954, 38-47.	2.3	26
66	The nexus of vitamin homeostasis and DNA synthesis and modification in mammalian brain. Molecular Brain, 2014, 7, 3.	2.6	29
67	Genomic patterns and context specific interpretation of DNA methylation. Current Opinion in Genetics and Development, 2014, 25, 85-92.	3.3	135
68	Accessing epigenetic variation in the plant methylome. Briefings in Functional Genomics, 2014, 13, 318-327.	2.7	24
69	GeMes, Clusters of DNA Methylation under Genetic Control, Can Inform Genetic and Epigenetic Analysis of Disease. American Journal of Human Genetics, 2014, 94, 485-495.	6.2	93
70	The epigenome in pluripotency and differentiation. Epigenomics, 2014, 6, 121-137.	2.1	20
71	Epigenetic Analysis of Neurocognitive Development at 1Âyear of Age in a Community-Based Pregnancy Cohort. Behavior Genetics, 2014, 44, 113-125.	2.1	5
72	Epigenetic programming of reward function in offspring: a role for maternal diet. Mammalian Genome, 2014, 25, 41-48.	2.2	21

#	Article	IF	CITATIONS
73	What's wrong with epigenetics in Huntington's disease?. Neuropharmacology, 2014, 80, 103-114.	4.1	47
74	Epigenetic modifications in the nervous system and their impact upon cognitive impairments. Neuropharmacology, 2014, 80, 70-82.	4.1	95
75	Transcriptional and epigenetic regulation of Hebbian and non-Hebbian plasticity. Neuropharmacology, 2014, 80, 3-17.	4.1	68
76	X chromosome regulation: diverse patterns in development, tissues and disease. Nature Reviews Genetics, 2014, 15, 367-378.	16.3	261
77	Corticotropin releasing factor in neuroplasticity. Frontiers in Neuroendocrinology, 2014, 35, 171-179.	5.2	60
78	Patterns of DNA Methylation in Animals: An Ecotoxicological Perspective. Integrative and Comparative Biology, 2014, 54, 77-86.	2.0	97
79	A unique gene expression signature associated with serotonin 2C receptor RNA editing in the prefrontal cortex and altered in suicide. Human Molecular Genetics, 2014, 23, 4801-4813.	2.9	37
80	Programming and Inheritance of Parental DNA Methylomes in Mammals. Cell, 2014, 157, 979-991.	28.9	451
81	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. Nature, 2014, 510, 537-541.	27.8	378
82	Distribution, recognition and regulation of non-CpG methylation in the adult mammalian brain. Nature Neuroscience, 2014, 17, 215-222.	14.8	663
83	The genetics of cognitive epigenetics. Neuropharmacology, 2014, 80, 83-94.	4.1	78
84	Epigenetics and plant genome evolution. Current Opinion in Plant Biology, 2014, 18, 1-8.	7.1	90
85	Epigenetics and the regulation of stress vulnerability and resilience. Neuroscience, 2014, 264, 157-170.	2.3	165
86	Comprehensive DNA methylation and hydroxymethylation analysis in the human brain and its implication in mental disorders. Neuropharmacology, 2014, 80, 133-139.	4.1	84
87	Reversing DNA Methylation: Mechanisms, Genomics, and Biological Functions. Cell, 2014, 156, 45-68.	28.9	914
88	Single-base resolution analysis of active DNA demethylation using methylase-assisted bisulfite sequencing. Nature Biotechnology, 2014, 32, 1231-1240.	17.5	139
89	Early life adversity, genomic plasticity, and psychopathology. Lancet Psychiatry, the, 2014, 1, 461-466.	7.4	118
90	The Biological Basis of Human Sexual Orientation. Advances in Genetics, 2014, 86, 167-184.	1.8	60

#	Article	IF	CITATIONS
91	Analytical tools and current challenges in the modern era of neuroepigenomics. Nature Neuroscience, 2014, 17, 1476-1490.	14.8	100
92	DNA methylation: old dog, new tricks?. Nature Structural and Molecular Biology, 2014, 21, 949-954.	8.2	79
93	Methyl CpG Binding Domain Ultraâ€Sequencing: a novel method for identifying interâ€individual and cellâ€typeâ€specific variation in <scp>DNA</scp> methylation. Genes, Brain and Behavior, 2014, 13, 721-731.	2.2	26
94	The external–internal loop of interference: Two types of attention and their influence on the learning abilities of mice. Neurobiology of Learning and Memory, 2014, 116, 181-192.	1.9	49
95	The molecular bases of the suicidal brain. Nature Reviews Neuroscience, 2014, 15, 802-816.	10.2	219
96	Decoding neural transcriptomes and epigenomes via high-throughput sequencing. Nature Neuroscience, 2014, 17, 1463-1475.	14.8	49
97	TET enzymes and DNA hydroxymethylation in neural development and function — How critical are they?. Genomics, 2014, 104, 334-340.	2.9	87
98	Neocortical Tet3-mediated accumulation of 5-hydroxymethylcytosine promotes rapid behavioral adaptation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7120-7125.	7.1	165
99	Genomic distribution and possible functions of DNA hydroxymethylation in the brain. Genomics, 2014, 104, 341-346.	2.9	84
100	5-Methycytosine and 5-Hydroxymethylcytosine in Psychiatric Epigenetics. , 2014, , 209-240.		1
101	Epigenetic Mechanisms Underlying the Pathogenesis of Neurogenetic Diseases. Neurotherapeutics, 2014, 11, 708-720.	4.4	14
102	Human Endometrial DNA Methylome Is Cycle-Dependent and Is Associated With Gene Expression Regulation. Molecular Endocrinology, 2014, 28, 1118-1135.	3.7	68
103	Mental Disorders and Transgenerational Epigenetics. , 2014, , 343-354.		1
104	Neurobiological disease etiology and inheritance: an epigenetic perspective. Journal of Experimental Biology, 2014, 217, 94-101.	1.7	17
105	pENCODE: A Plant Encyclopedia of DNA Elements. Annual Review of Genetics, 2014, 48, 49-70.	7.6	38
106	Epigenetics in Child Psychiatry. , 2014, , 425-440.		1
107	Role of Epigenetics in the Brain., 2014, , 79-99.		1
108	Laboratory Techniques in Psychiatric Epigenetics. , 2014, , 129-162.		1

#	Article	IF	CITATIONS
109	An evolving view of epigenetic complexity in the brain. Philosophical Transactions of the Royal Society B: Biological Sciences, 2014, 369, 20130506.	4.0	23
110	5-Hydroxymethylcytosine: A stable or transient DNA modification?. Genomics, 2014, 104, 314-323.	2.9	114
111	Advances in the profiling of DNA modifications: cytosine methylation and beyond. Nature Reviews Genetics, 2014, 15, 647-661.	16.3	224
112	Connections between TET proteins and aberrant DNA modification in cancer. Trends in Genetics, 2014, 30, 464-474.	6.7	221
113	The Consequences of Earlyâ€Life Adversity: Neurobiological, Behavioural and Epigenetic Adaptations. Journal of Neuroendocrinology, 2014, 26, 707-723.	2.6	292
114	Transcriptomic Changes in Brain Development. International Review of Neurobiology, 2014, 116, 233-250.	2.0	9
115	Epigenetic Mechanisms in Autism Spectrum Disorder. International Review of Neurobiology, 2014, 115, 203-244.	2.0	41
116	Elevated 5-hydroxymethylcytosine in the Engrailed-2 (EN-2) promoter is associated with increased gene expression and decreased MeCP2 binding in autism cerebellum. Translational Psychiatry, 2014, 4, e460-e460.	4.8	61
117	Using beta-binomial regression for high-precision differential methylation analysis in multifactor whole-genome bisulfite sequencing experiments. BMC Bioinformatics, 2014, 15, 215.	2.6	156
118	DNA modifications in the mammalian brain. Philosophical Transactions of the Royal Society B: Biological Sciences, 2014, 369, 20130512.	4.0	29
119	Lithium reduces the effects of rotenone-induced complex I dysfunction on DNA methylation and hydroxymethylation in rat cortical primary neurons. Psychopharmacology, 2014, 231, 4189-4198.	3.1	33
120	The role of 5-hydroxymethylcytosine in human cancer. Cell and Tissue Research, 2014, 356, 631-641.	2.9	87
121	Epigenetic Mechanisms Affecting Regulation of Energy Balance: Many Questions, Few Answers. Annual Review of Nutrition, 2014, 34, 337-355.	10.1	76
122	The PEG13-DMR and brain-specific enhancers dictate imprinted expression within the 8q24 intellectual disability risk locus. Epigenetics and Chromatin, 2014, 7, 5.	3.9	46
123	Mechanism and Function of Oxidative Reversal of DNA and RNA Methylation. Annual Review of Biochemistry, 2014, 83, 585-614.	11.1	289
124	Early life epigenetic programming and transmission of stressâ€induced traits in mammals. BioEssays, 2014, 36, 491-502.	2.5	110
125	New concepts in DNA methylation. Trends in Biochemical Sciences, 2014, 39, 310-318.	7.5	361
126	Epigenetic Regulation of Pluripotency and Differentiation. Circulation Research, 2014, 115, 311-324.	4.5	205

#	ARTICLE	IF	Citations
127	The dynamics of DNA methylation fidelity during mouse embryonic stem cell self-renewal and differentiation. Genome Research, 2014, 24, 1296-1307.	5.5	72
128	Abnormalities in human pluripotent cells due to reprogramming mechanisms. Nature, 2014, 511, 177-183.	27.8	307
129	DNA methylation and gene deletion analysis of brain metastases in melanoma patients identifies mutually exclusive molecular alterations. Neuro-Oncology, 2014, 16, 1499-1509.	1.2	65
130	Major epigenetic development distinguishing neuronal and non-neuronal cells occurs postnatally in the murine hypothalamus. Human Molecular Genetics, 2014, 23, 1579-1590.	2.9	32
131	5-Hydroxymethylation marks a class of neuronal gene regulated by intragenic methylcytosine levels. Genomics, 2014, 104, 383-392.	2.9	27
132	DNA Methyltransferase Inhibitors and Psychiatric Disorders. , 2014, , 497-514.		2
133	From development to diseases: The role of 5hmC in brain. Genomics, 2014, 104, 347-351.	2.9	87
134	Integrating Early Life Experience, Gene Expression, Brain Development, and Emergent Phenotypes. Advances in Genetics, 2014, 86, 277-307.	1.8	52
135	The Social Environment and Epigenetics in Psychiatry. , 2014, , 547-562.		1
136	Epigenetic mechanisms in epilepsy. Progress in Brain Research, 2014, 213, 279-316.	1.4	54
137	Hydroxymethylation and DNA methylation profiles in the prefrontal cortex of the non-human primate rhesus macaque and the impact of maternal deprivation on hydroxymethylation. Neuroscience, 2014, 268, 139-148.	2.3	52
138	Minireview: Transgenerational Epigenetic Inheritance: Focus on Endocrine Disrupting Compounds. Endocrinology, 2014, 155, 2770-2780.	2.8	102
139	Role of methyl group vitamins in hypothalamic development of food intake regulation in Wistar rats. Applied Physiology, Nutrition and Metabolism, 2014, 39, 844-844.	1.9	3
140	Epigenomics and the control of fate, form and function in social insects. Current Opinion in Insect Science, 2014, 1, 31-38.	4.4	23
141	Transient Accumulation of 5-Carboxylcytosine Indicates Involvement of Active Demethylation in Lineage Specification of Neural Stem Cells. Cell Reports, 2014, 7, 1353-1361.	6.4	85
142	Diversity of two forms of DNA methylation in the brain. Frontiers in Genetics, 2014, 5, 46.	2.3	63
143	DNA Modifications: Function and Applications in Normal and Disease States. Biology, 2014, 3, 670-723.	2.8	129
144	Insights into DNA hydroxymethylation in the honeybee from in-depth analyses of TET dioxygenase. Open Biology, 2014, 4, 140110.	3.6	60

#	Article	IF	Citations
145	Age-Dependent Increment of Hydroxymethylation in the Brain Cortex in the Triple-Transgenic Mouse Model of Alzheimer's Disease. Journal of Alzheimer's Disease, 2014, 41, 845-854.	2.6	41
146	<i>Bdnf</i> DNA methylation modifications in the hippocampus and amygdala of male and female rats exposed to different caregiving environments outside the homecage. Developmental Psychobiology, 2014, 56, 1755-1763.	1.6	79
147	Summary: Cognition in 2014: Figure 1 Cold Spring Harbor Symposia on Quantitative Biology, 2014, 79, 237-241.	1.1	1
148	Impact of Early Environment on Children's Mental Health: Lessons From DNA Methylation Studies With Monozygotic Twins. Twin Research and Human Genetics, 2015, 18, 623-634.	0.6	16
149	Keystone Symposia on Neuroepigenetics—bridging the gap between genome and behavior. Neuroepigenetics, 2015, 2, 9-12.	2.8	2
150	A role for CaV1 and calcineurin signaling in depolarization-induced changes in neuronal DNA methylation. Neuroepigenetics, 2015, 3, 1-6.	2.8	4
151	Ageâ€Dependent Levels of 5â€Methylâ€, 5â€Hydroxymethylâ€, and 5â€Formylcytosine in Human and Mouse Brai Tissues. Angewandte Chemie - International Edition, 2015, 54, 12511-12514.	in 13.8	116
152	Multigenerational effects of parental prenatal exposure to famine on adult offspring cognitive function. Scientific Reports, 2015, 5, 13792.	3.3	36
155	AF9 promotes hESC neural differentiation through recruiting TET2 to neurodevelopmental gene loci for methylcytosine hydroxylation. Cell Discovery, 2015, 1, 15017.	6.7	20
156	Upcoming Meetings Related to Huntington's Disease. Journal of Huntington's Disease, 2015, 4, 107-107.	1.9	25
157	Epigenetics of Suicidal Behaviour. Advances in Biological Psychiatry, 0, , 75-87.	0.2	2
158	An integrative approach for efficient analysis of whole genome bisulfite sequencing data. BMC Genomics, 2015, 16, S14.	2.8	9
159	Adult porcine genome-wide DNA methylation patterns support pigs as a biomedical model. BMC Genomics, 2015, 16, 743.	2.8	96
160	Trans effects of chromosome aneuploidies on DNA methylation patterns in human Down syndrome and mouse models. Genome Biology, 2015, 16, 263.	8.8	68
161	Derivation of consensus inactivation status for X-linked genes from genome-wide studies. Biology of Sex Differences, 2015, 6, 35.	4.1	210
162	Astrocyte development: A Guide for the Perplexed. Glia, 2015, 63, 1320-1329.	4.9	230
163	Characterizing 5-hydroxymethylcytosine in human prefrontal cortex at single base resolution. BMC Genomics, 2015, 16, 672.	2.8	38
164	Epigenetic States of Nephron Progenitors and Epithelial Differentiation. Journal of Cellular Biochemistry, 2015, 116, 893-902.	2.6	15

#	ARTICLE	IF	CITATIONS
165	Epigenetics/Programming in the <scp>HPA</scp> Axis., 2015, 6, 87-110.		54
166	Epigenetic Mechanisms in the Pathophysiology of Psychotic Disorders. Harvard Review of Psychiatry, 2015, 23, 212-222.	2.1	7
167	Combined Whole Methylome and Genomewide Association Study Implicates <i>CNTN4 </i> Ion Alcohol Use. Alcoholism: Clinical and Experimental Research, 2015, 39, 1396-1405.	2.4	15
168	Epigenetic influences on the developing brain: effects of hormones and nutrition. Advances in Genomics and Genetics, 0, , 215.	0.8	3
170	Stress induced gene expression drives transient DNA methylation changes at adjacent repetitive elements. ELife, 2015, 4, .	6.0	285
171	Role of Mecp2 in Experience-Dependent Epigenetic Programming. Genes, 2015, 6, 60-86.	2.4	40
172	The State of Play with iPSCs and Spinal Cord Injury Models. Journal of Clinical Medicine, 2015, 4, 193-203.	2.4	9
173	At the frontier of epigenetics of brain sex differences. Frontiers in Behavioral Neuroscience, 2015, 9, 221.	2.0	112
174	Epigenetic Alterations in Alzheimer's Disease. Frontiers in Behavioral Neuroscience, 2015, 9, 347.	2.0	143
175	An epigenetic hypothesis for the genomic memory of pain. Frontiers in Cellular Neuroscience, 2015, 9, 88.	3.7	47
176	Dynamic DNA methylation in the brain: a new epigenetic mark for experience-dependent plasticity. Frontiers in Cellular Neuroscience, 2015, 9, 331.	3.7	67
177	Modular and coordinated expression of immune system regulatory and signaling components in the developing and adult nervous system. Frontiers in Cellular Neuroscience, 2015, 9, 337.	3.7	3
178	Turning over DNA methylation in the mind. Frontiers in Neuroscience, 2015, 9, 252.	2.8	49
179	Accurate Measurement of 5-Methylcytosine and 5-Hydroxymethylcytosine in Human Cerebellum DNA by Oxidative Bisulfite on an Array (OxBS-Array). PLoS ONE, 2015, 10, e0118202.	2.5	54
180	DNA Methylation: Insights into Human Evolution. PLoS Genetics, 2015, 11, e1005661.	3.5	90
181	PGCâ^'1α Promoter Methylation in Parkinson's Disease. PLoS ONE, 2015, 10, e0134087.	2.5	95
182	Base-resolution methylation patterns accurately predict transcription factor bindings in vivo. Nucleic Acids Research, 2015, 43, 2757-2766.	14.5	46
183	Exceptional epigenetics in the brain. Science, 2015, 348, 1094-1095.	12.6	11

#	Article	IF	CITATIONS
184	Association of Protein Phosphatase <i>PPM1G</i> With Alcohol Use Disorder and Brain Activity During Behavioral Control in a Genome-Wide Methylation Analysis. American Journal of Psychiatry, 2015, 172, 543-552.	7.2	68
185	Introduction to Data Types in Epigenomics. Translational Bioinformatics, 2015, , 3-34.	0.0	2
186	Epigenetic pathways through which experiences become linked with biology. Development and Psychopathology, 2015, 27, 637-648.	2.3	50
187	Adaptation of the targeted capture Methyl-Seq platform for the mouse genome identifies novel tissue-specific DNA methylation patterns of genes involved in neurodevelopment. Epigenetics, 2015, 10, 581-596.	2.7	18
188	Comprehensive DNA methylation analysis of hepatitis B virus genome in infected liver tissues. Scientific Reports, 2015, 5, 10478.	3.3	41
189	Cocaine shapes chromatin landscapes via Tet1. Nature Neuroscience, 2015, 18, 478-480.	14.8	2
190	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. Nature Genetics, 2015, 47, 746-756.	21.4	278
191	Can we observe epigenetic effects on human brain function?. Trends in Cognitive Sciences, 2015, 19, 366-373.	7.8	67
192	Molecular epigenetic switches in neurodevelopment in health and disease. Frontiers in Behavioral Neuroscience, 2015, 9, 120.	2.0	16
193	Human body epigenome maps reveal noncanonical DNA methylation variation. Nature, 2015, 523, 212-216.	27.8	605
194	Probing disorders of the nervous system using reprogramming approaches. EMBO Journal, 2015, 34, 1456-1477.	7.8	45
195	The Epigenome and Aging. Molecular and Integrative Toxicology, 2015, , 155-195.	0.5	0
196	Prospects for the development of epigenetic drugs for CNS conditions. Nature Reviews Drug Discovery, 2015, 14, 461-474.	46.4	83
197	<scp>DNA</scp> methylation and healthy human aging. Aging Cell, 2015, 14, 924-932.	6.7	665
198	AltersabhÃĦgige Level von 5â€Methylâ€, 5â€Hydroxymethyl―und 5â€Formylcytosin in Hirngeweben des Menschen und der Maus. Angewandte Chemie, 2015, 127, 12691-12695.	2.0	19
199	X-chromosome inactivation and escape. Journal of Genetics, 2015, 94, 591-599.	0.7	102
200	Tet1 oxidase regulates neuronal gene transcription, active DNA hydroxymethylation, object location memory, and threat recognition memory. Neuroepigenetics, 2015, 4, 12-27.	2.8	42
201	Evaluation of preprocessing, mapping and postprocessing algorithms for analyzing whole genome bisulfite sequencing data. Briefings in Bioinformatics, 2016, 17, bbv103.	6.5	20

#	ARTICLE	IF	CITATIONS
202	GADD45a physically and functionally interacts with TET1. Differentiation, 2015, 90, 59-68.	1.9	37
203	Embryonic transcription is controlled by maternally defined chromatin state. Nature Communications, 2015, 6, 10148.	12.8	103
204	Genome-Wide Epigenetic Studies in Human Disease: A Primer on -Omic Technologies. American Journal of Epidemiology, 2016, 183, kwv187.	3.4	23
205	DNA methylation pathways and their crosstalk with histone methylation. Nature Reviews Molecular Cell Biology, 2015, 16, 519-532.	37.0	779
206	High Precision DNA Modification Analysis of <i>HCG9</i> in Major Psychosis. Schizophrenia Bulletin, 2016, 42, sbv079.	4.3	16
207	Maternal immune activation induces <i>GAD1</i> and <i>GAD2</i> promoter remodeling in the offspring prefrontal cortex. Epigenetics, 2015, 10, 1143-1155.	2.7	102
208	Genomic Perspectives of Transcriptional Regulation in Forebrain Development. Neuron, 2015, 85, 27-47.	8.1	136
209	Development and the epigenome: the  synapse' of gene–environment interplay. Developmental Science, 2015, 18, 1-23.	2.4	110
210	The Dnmt3L ADD Domain Controls Cytosine Methylation Establishment during Spermatogenesis. Cell Reports, 2015, 10, 944-956.	6.4	39
211	MethylC-seq library preparation for base-resolution whole-genome bisulfite sequencing. Nature Protocols, 2015, 10, 475-483.	12.0	250
212	Neuroepigenomics: resources, obstacles, and opportunities. Neuroepigenetics, 2015, 1, 2-13.	2.8	16
213	Epigenetics of Reproduction. , 2015, , 2439-2501.		2
214	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	27.8	5,653
215	DNMT3A in haematological malignancies. Nature Reviews Cancer, 2015, 15, 152-165.	28.4	379
216	Semiconductor-based sequencing of genome-wide DNA methylation states. Epigenetics, 2015, 10, 153-166.	2.7	8
217	Function and information content of DNA methylation. Nature, 2015, 517, 321-326.	27.8	1,656
218	Differential DNA methylation profiles of coding and non-coding genes define hippocampal sclerosis in human temporal lobe epilepsy. Brain, 2015, 138, 616-631.	7.6	140
219	Nongenetic inheritance and transgenerational epigenetics. Trends in Molecular Medicine, 2015, 21, 134-144.	6.7	200

#	Article	IF	CITATIONS
220	Methylomic trajectories across human fetal brain development. Genome Research, 2015, 25, 338-352.	5.5	250
221	Targeting Epigenetics in the Development of New Diagnostic Applicationsâ€"Lessons from Autoimmune Diseases. , 2015, , 409-441.		0
222	Systematic discovery of regulated and conserved alternative exons in the mammalian brain reveals NMD modulating chromatin regulators. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3445-3450.	7.1	131
223	Rapid reprogramming of epigenetic and transcriptional profiles in mammalian culture systems. Genome Biology, 2015, 16, 11.	8.8	137
224	Nonparametric Bayesian clustering to detect bipolar methylated genomic loci. BMC Bioinformatics, 2015, 16, 11.	2.6	12
225	Chromatin methylation and cardiovascular aging. Journal of Molecular and Cellular Cardiology, 2015, 83, 21-31.	1.9	18
226	Regulation of Gene Expression and Pain States by Epigenetic Mechanisms. Progress in Molecular Biology and Translational Science, 2015, 131, 147-183.	1.7	35
227	Ballgown bridges the gap between transcriptome assembly and expression analysis. Nature Biotechnology, 2015, 33, 243-246.	17.5	716
228	Disruption of DNA-methylation-dependent long gene repression in Rett syndrome. Nature, 2015, 522, 89-93.	27.8	521
229	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. Neuron, 2015, 86, 1369-1384.	8.1	640
230	The Role of Epigenetic Change in Autism Spectrum Disorders. Frontiers in Neurology, 2015, 6, 107.	2.4	186
231	Neuronal DNA Methylation Profiling of Blast-Related Traumatic Brain Injury. Journal of Neurotrauma, 2015, 32, 1200-1209.	3.4	60
232	SMAP: a streamlined methylation analysis pipeline for bisulfite sequencing. GigaScience, 2015, 4, 29.	6.4	13
233	Transposable Elements and DNA Methylation Create in Embryonic Stem Cells Human-Specific Regulatory Sequences Associated with Distal Enhancers and Noncoding RNAs. Genome Biology and Evolution, 2015, 7, 1432-1454.	2.5	67
234	Post-conversion targeted capture of modified cytosines in mammalian and plant genomes. Nucleic Acids Research, 2015, 43, e81-e81.	14 <b>.</b> 5	62
235	Gadd45b and $\langle i \rangle N \langle  i \rangle$ -methyl- $\langle scp \rangle d \langle  scp \rangle$ -aspartate induced DNA demethylation in postmitotic neurons. Epigenomics, 2015, 7, 567-579.	2.1	25
236	DNA methylation fingerprint of neuroblastoma reveals new biological and clinical insights. Epigenomics, 2015, 7, 1137-1153.	2.1	40
237	Large-scale genomics unveil polygenic architecture of human cortical surface area. Nature Communications, 2015, 6, 7549.	12.8	30

#	Article	IF	CITATIONS
238	Animal Models in Biomedical Research. , 2015, , 1497-1534.		11
239	DNA Methylation in Basal Metazoans: Insights from Ctenophores. Integrative and Comparative Biology, 2015, 55, 1096-1110.	2.0	38
240	Epigenomic Landscapes Reflect Neuronal Diversity. Neuron, 2015, 86, 1319-1321.	8.1	1
241	Accurate CpG and non-CpG cytosine methylation analysis by high-throughput locus-specific pyrosequencing in plants. Plant Molecular Biology, 2015, 88, 471-485.	3.9	16
242	Non-CG Methylation in the Human Genome. Annual Review of Genomics and Human Genetics, 2015, 16, 55-77.	6.2	210
243	MBRidge: an accurate and cost-effective method for profiling DNA methylome at single-base resolution. Journal of Molecular Cell Biology, 2015, 7, 299-313.	3.3	5
244	Escape from X Inactivation Varies in Mouse Tissues. PLoS Genetics, 2015, 11, e1005079.	3.5	224
245	Rett syndrome: disruption of epigenetic control of postnatal neurological functions. Human Molecular Genetics, 2015, 24, R10-R16.	2.9	60
246	Role of 5-hydroxymethylcytosine in neurodegeneration. Gene, 2015, 570, 17-24.	2.2	72
247	Tet3 regulates synaptic transmission and homeostatic plasticity via DNA oxidation and repair. Nature Neuroscience, 2015, 18, 836-843.	14.8	164
248	A pooling-based approach to mapping genetic variants associated with DNA methylation. Genome Research, 2015, 25, 907-917.	5.5	30
249	Chromatin modifiers and histone modifications in bone formation, regeneration, and therapeutic intervention for bone-related disease. Bone, 2015, 81, 739-745.	2.9	66
250	Genetics and Brain Morphology. Neuropsychology Review, 2015, 25, 63-96.	4.9	49
252	DNA Methylation, Its Mediators and Genome Integrity. International Journal of Biological Sciences, 2015, 11, 604-617.	6.4	195
253	Concordant and discordant DNA methylation signatures of aging in human blood and brain. Epigenetics and Chromatin, 2015, 8, 19.	3.9	132
254	Germline-derived DNA methylation and early embryo epigenetic reprogramming: The selected survival of imprints. International Journal of Biochemistry and Cell Biology, 2015, 67, 128-138.	2.8	80
255	Postmitotic regulation of sensory area patterning in the mammalian neocortex by Lhx2. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6736-6741.	7.1	126
256	Rett syndrome: a complex disorder with simple roots. Nature Reviews Genetics, 2015, 16, 261-275.	16.3	277

#	Article	IF	CITATIONS
257	An alternative pluripotent state confers interspecies chimaeric competency. Nature, 2015, 521, 316-321.	27.8	215
258	Intrinsic regulations in neural fate commitment. Development Growth and Differentiation, 2015, 57, 109-120.	1.5	24
259	Brain feminization requires active repression of masculinization via DNA methylation. Nature Neuroscience, 2015, 18, 690-697.	14.8	339
260	Crop Epigenomics: Identifying, Unlocking, and Harnessing Cryptic Variation in Crop Genomes. Molecular Plant, 2015, 8, 860-870.	8.3	44
261	Reading the unique DNA methylation landscape of the brain: Non-CpG methylation, hydroxymethylation, and MeCP2. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6800-6806.	7.1	205
262	The interaction of mycobacterial protein Rv2966c with host chromatin is mediated through non-CpG methylation and histone H3/H4 binding. Nucleic Acids Research, 2015, 43, 3922-3937.	14.5	91
263	Profiling DNA methylome landscapes of mammalian cells with single-cell reduced-representation bisulfite sequencing. Nature Protocols, 2015, 10, 645-659.	12.0	152
264	DNA Methylation in Memory Formation. Neuroscientist, 2015, 21, 475-489.	3.5	71
265	MeCP2 binds to non-CG methylated DNA as neurons mature, influencing transcription and the timing of onset for Rett syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5509-5514.	7.1	256
266	Somatic mutation in single human neurons tracks developmental and transcriptional history. Science, 2015, 350, 94-98.	12.6	486
267	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. Genome Research, 2015, 25, 1801-1811.	5.5	195
268	GC skew is a conserved property of unmethylated CpG island promoters across vertebrates. Nucleic Acids Research, 2015, 43, gkv811.	14.5	45
269	Histone modifications controlling native and induced neural stem cell identity. Current Opinion in Genetics and Development, 2015, 34, 95-101.	3.3	9
270	Epigenetics and therapeutic targets mediating neuroprotection. Brain Research, 2015, 1628, 265-272.	2.2	10
271	Epigenetic regulatory functions of DNA modifications: $5$ -methylcytosine and beyond. Epigenetics and Chromatin, $2015$ , $8$ , $24$ .	3.9	249
272	Epigenetics and Epilepsy. Cold Spring Harbor Perspectives in Medicine, 2015, 5, a022731.	6.2	68
273	Genomic Views of Transcriptional Enhancers: Essential Determinants of Cellular Identity and Activity-Dependent Responses in the CNS. Journal of Neuroscience, 2015, 35, 13819-13826.	3.6	33
274	The Mechanisms of Generation, Recognition, and Erasure of DNA 5-Methylcytosine and Thymine Oxidations. Journal of Biological Chemistry, 2015, 290, 20723-20733.	3.4	35

#	ARTICLE	IF	CITATIONS
275	Epigenetic regulation of ageing: linking environmental inputs to genomic stability. Nature Reviews Molecular Cell Biology, 2015, 16, 593-610.	37.0	515
276	Charting oxidized methylcytosines at base resolution. Nature Structural and Molecular Biology, 2015, 22, 656-661.	8.2	62
277	Epigenetic mechanisms in diurnal cycles of metabolism and neurodevelopment. Human Molecular Genetics, 2015, 24, R1-R9.	2.9	32
278	Dynamics and function of distal regulatory elements during neurogenesis and neuroplasticity. Genome Research, 2015, 25, 1309-1324.	5.5	46
279	TET proteins in cancer: Current â€~state of the art'. Critical Reviews in Oncology/Hematology, 2015, 96, 425-436.	4.4	30
280	EDC-2: The Endocrine Society's Second Scientific Statement on Endocrine-Disrupting Chemicals. Endocrine Reviews, 2015, 36, E1-E150.	20.1	1,508
281	Adversity in childhood and depression: linked through SIRT1. Translational Psychiatry, 2015, 5, e629-e629.	4.8	44
282	Structure and mutagenesis of the DNA modification-dependent restriction endonuclease AspBHI. Scientific Reports, 2015, 4, 4246.	3.3	14
283	The Breadth and Type of Systemic Inflammation and the Risk of Adverse Neurological Outcomes in Extremely Low Gestation Newborns. Pediatric Neurology, 2015, 52, 42-48.	2.1	82
284	DNA Methylation and Its Implications and Accessibility for Neuropsychiatric Therapeutics. Annual Review of Pharmacology and Toxicology, 2015, 55, 591-611.	9.4	63
285	Stress-induced perinatal and transgenerational epigenetic programming of brain development and mental health. Neuroscience and Biobehavioral Reviews, 2015, 48, 70-91.	6.1	414
286	Alterations in Gene Expression and DNA Methylation during Murine and Human Lung Alveolar Septation. American Journal of Respiratory Cell and Molecular Biology, 2015, 53, 60-73.	2.9	49
287	Methodological aspects of whole-genome bisulfite sequencing analysis. Briefings in Bioinformatics, 2015, 16, 369-379.	6.5	63
288	SMN is required for the maintenance of embryonic stem cells and neuronal differentiation in mice. Brain Structure and Function, 2015, 220, 1539-1553.	2.3	14
289	Epigenetic regulation of persistent pain. Translational Research, 2015, 165, 177-199.	5.0	59
290	DNA Methylation in Social Insects: How Epigenetics Can Control Behavior and Longevity. Annual Review of Entomology, 2015, 60, 435-452.	11.8	156
291	Characterization of brain cell nuclei with decondensed chromatin. Developmental Neurobiology, 2015, 75, 738-756.	3.0	20
292	Notes on the role of dynamic DNA methylation in mammalian development. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6796-6799.	7.1	200

#	Article	IF	CITATIONS
293	The DNA methylation signature of human TCRÎ $\pm$ Î $^2$ +CD4â $^2$ CD8â $^2$ double negative T cells reveals CG demethylation and a unique epigenetic architecture permissive to a broad stimulatory immune response. Clinical Immunology, 2015, 156, 19-27.	3.2	25
294	Evolving insights on how cytosine methylation affects protein-DNA binding. Briefings in Functional Genomics, 2015, 14, 61-73.	2.7	122
295	Epigenetic mechanisms of neuroplasticity and the implications for stroke recovery. Experimental Neurology, 2015, 268, 37-45.	4.1	88
296	Do ageâ€associated DNA methylation changes increase the risk of malignant transformation?. BioEssays, 2015, 37, 20-24.	2.5	22
297	Effects of quetiapine on DNA methylation in neuroblastoma cells. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2015, 56, 117-121.	4.8	26
298	oxBS-450K: A method for analysing hydroxymethylation using 450K BeadChips. Methods, 2015, 72, 9-15.	3.8	83
299	H3K4me1 marks DNA regions hypomethylated during aging in human stem and differentiated cells. Genome Research, 2015, 25, 27-40.	5.5	119
300	<scp>DNA</scp> demethylation and invasive cancer: implications for therapeutics. British Journal of Pharmacology, 2015, 172, 2705-2715.	5.4	68
301	The neurobiological effects of stress as contributors to psychiatric disorders: focus on epigenetics. Current Opinion in Neurobiology, 2015, 30, 31-37.	4.2	55
302	DNA Methylation Biomarkers in Lung Cancer. , 2016, , 259-273.		1
303	Sexual Dimorphism and DOHaD through the Lens of Epigenetics. , 2016, , 389-424.		1
304	Early experiences can alter the size of cortical fields in prairie voles ( <i>Microtus ochrogaster</i> ). Environmental Epigenetics, 2016, 2, dvw019.	1.8	20
305	Epigenetic Approaches to Define the Molecular and Genetic Risk Architectures of Schizophrenia. , 2016, , 61-82.		1
306	Reduced representation bisulphite sequencing of ten bovine somatic tissues reveals DNA methylation patterns and their impacts on gene expression. BMC Genomics, 2016, 17, 779.	2.8	30
307	Epigenetics of Psychiatric Disorders. , 2016, , 335-350.		2
308	Detection of Modified Forms of Cytosine Using Sensitive Immunohistochemistry. Journal of Visualized Experiments, 2016, , .	0.3	8
309	Maternal Prenatal Stress and the Developmental Origins of Mental Health. , 2016, , 103-126.		4
310	Recent advances in understanding neuropathic pain: glia, sex differences, and epigenetics. F1000Research, 2016, 5, 2743.	1.6	40

#	Article	IF	CITATIONS
311	Huntington's disease accelerates epigenetic aging of human brain and disrupts DNA methylation levels. Aging, 2016, 8, 1485-1512.	3.1	192
312	META2: Intercellular DNA Methylation Pairwise Annotation and Integrative Analysis. BioMed Research International, 2016, 2016, 1-10.	1.9	0
313	Where Environment Meets Cognition: A Focus on Two Developmental Intellectual Disability Disorders. Neural Plasticity, 2016, 2016, 1-20.	2.2	18
314	Epigenetic Research of Neurodegenerative Disorders Using Patient iPSC-Based Models. Stem Cells International, 2016, 2016, 1-16.	2.5	13
315	Epigenetics in Schistosomes: What We Know and What We Need Know. Frontiers in Cellular and Infection Microbiology, 2016, 6, 149.	3.9	15
316	Emerging Molecular and Biological Functions of MBD2, a Reader of DNA Methylation. Frontiers in Genetics, 2016, 7, 93.	2.3	61
317	Global and Site-Specific Changes in 5-Methylcytosine and 5-Hydroxymethylcytosine after Extended Post-mortem Interval. Frontiers in Genetics, 2016, 7, 120.	2.3	5
318	The Future is The Past: Methylation QTLs in Schizophrenia. Genes, 2016, 7, 104.	2.4	26
319	Cord Blood DNA Methylation Biomarkers for Predicting Neurodevelopmental Outcomes. Genes, 2016, 7, 117.	2.4	27
321	DNA methylation analysis of paediatric low-grade astrocytomas identifies a tumour-specific hypomethylation signature in pilocytic astrocytomas. Acta Neuropathologica Communications, 2016, 4, 54.	5.2	17
322	Misregulation of Alternative Splicing in a Mouse Model of Rett Syndrome. PLoS Genetics, 2016, 12, e1006129.	3.5	57
323	Trisomy 21 Alters DNA Methylation in Parent-of-Origin-Dependent and -Independent Manners. PLoS ONE, 2016, 11, e0154108.	2.5	52
324	Characterisation of CDKL5 Transcript Isoforms in Human and Mouse. PLoS ONE, 2016, 11, e0157758.	2.5	53
325	5'-Hydroxymethylcytosine Precedes Loss of CpG Methylation in Enhancers and Genes Undergoing Activation in Cardiomyocyte Maturation. PLoS ONE, 2016, 11, e0166575.	2.5	13
326	DNA Methylation in Neurodegenerative Diseases. , 2016, , 401-415.		6
327	Alcohol Metabolism and Epigenetic Methylation and Acetylation. , 2016, , 287-303.		0
328	Epigenetic determinants of cardiovascular gene expression: vascular endothelium. Epigenomics, 2016, 8, 959-979.	2.1	13
329	Epigenetic Biomarkers for Early-Life Adversity. Epigenetics and Human Health, 2016, , 159-175.	0.2	1

#	Article	IF	CITATIONS
330	Liganded Thyroid Hormone Receptors Transactivate the DNA Methyltransferase 3a Gene in Mouse Neuronal Cells. Endocrinology, 2016, 157, 3647-3657.	2.8	36
331	<i>FASTmC</i> : A Suite of Predictive Models for Nonreference-Based Estimations of DNA Methylation. G3: Genes, Genomes, Genetics, 2016, 6, 447-452.	1.8	18
332	Why we should consider sex (and study sex differences) in addiction research. Addiction Biology, 2016, 21, 995-1006.	2.6	70
333	Sculpting infant soothability: the role of prenatal SSRI antidepressant exposure and neonatal <i>SLC6A4</i> methylation status. Developmental Psychobiology, 2016, 58, 745-758.	1.6	16
334	Impact of neonatal iron deficiency on hippocampal DNA methylation and gene transcription in a porcine biomedical model of cognitive development. BMC Genomics, 2016, 17, 856.	2.8	44
335	A genome-wide search for epigenetically regulated genes in zebra finch using MethylCap-seq and RNA-seq. Scientific Reports, 2016, 6, 20957.	3.3	9
336	Epigenome Dynamics and Reader Proteins in Cardiomyocyte Development and Heart Failure. Cardiac and Vascular Biology, 2016, , 37-51.	0.2	0
337	Extra-coding RNAs regulate neuronal DNA methylation dynamics. Nature Communications, 2016, 7, 12091.	12.8	57
338	Investigating epigenetic consequences of early-life adversity: some methodological considerations. Högre Utbildning, 2016, 7, 31593.	3.0	17
339	Genetics of Schizophrenia. Advances in Genetics, 2016, 96, 99-141.	1.8	46
340	Cerebral Organoids Recapitulate Epigenomic Signatures of the Human Fetal Brain. Cell Reports, 2016, 17, 3369-3384.	6.4	296
341	Genome-wide DNA methylation profiles changes associated with constant heat stress in pigs as measured by bisulfite sequencing. Scientific Reports, 2016, 6, 27507.	3.3	80
342	Cumulative Impact of Polychlorinated Biphenyl and Large Chromosomal Duplications on DNA Methylation, Chromatin, and Expression of Autism Candidate Genes. Cell Reports, 2016, 17, 3035-3048.	6.4	69
343	DNA methylation in the gene body influences MeCP2-mediated gene repression. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 15114-15119.	7.1	100
344	Developmental and Thyroid Hormone Regulation of the DNA Methyltransferase 3a Gene in Xenopus Tadpoles. Endocrinology, 2016, 157, 4961-4972.	2.8	18
345	The effects of cytosine methylation on general transcription factors. Scientific Reports, 2016, 6, 29119.	3.3	38
346	LuxGLM: a probabilistic covariate model for quantification of DNA methylation modifications with complex experimental designs. Bioinformatics, 2016, 32, i511-i519.	4.1	15
347	Variations in 5-methylcytosine and 5-hydroxymethylcytosine among human brain, blood, and saliva using oxBS and the Infinium MethylationEPIC array. Biology Methods and Protocols, 2016, 1, 1-8.	2.2	10

#	Article	IF	Citations
348	Merging data from genetic and epigenetic approaches to better understand autistic spectrum disorder. Epigenomics, 2016, 8, 85-104.	2.1	38
349	Role of TET enzymes in DNA methylation, development, and cancer. Genes and Development, 2016, 30, 733-750.	5.9	781
350	Epigenetic regulation of G protein coupled receptor signaling and its implications in psychiatric disorders. International Journal of Biochemistry and Cell Biology, 2016, 77, 226-239.	2.8	14
351	The Complete Genome Sequences, Unique Mutational Spectra, and Developmental Potency of Adult Neurons Revealed by Cloning. Neuron, 2016, 89, 1223-1236.	8.1	85
352	Alterations in DNA Methylation and Hydroxymethylation Due to Parental Care in Rhesus Macaques. Epigenetics and Human Health, 2016, , 165-190.	0.2	1
353	Comparative epigenomics: a powerful tool to understand the evolution of <scp>DNA</scp> methylation. New Phytologist, 2016, 210, 76-80.	<b>7.</b> 3	48
354	The molecular basis of variable phenotypic severity among common missense mutations causing Rett syndrome. Human Molecular Genetics, 2016, 25, 558-570.	2.9	76
355	Tagging methyl-CpG-binding domain proteins reveals different spatiotemporal expression and supports distinct functions. Epigenomics, 2016, 8, 455-473.	2.1	25
356	Non-random distribution of methyl-CpG sites and non-CpG methylation in the human rDNA promoter identified by next generation bisulfite sequencing. Gene, 2016, 585, 35-43.	2.2	16
357	Substantial DNA methylation differences between two major neuronal subtypes in human brain. Nucleic Acids Research, 2016, 44, 2593-2612.	14.5	97
358	Hydroxymethylation is uniquely distributed within term placenta, and is associated with gene expression. FASEB Journal, 2016, 30, 2874-2884.	0.5	38
359	Single base resolution analysis of 5-hydroxymethylcytosine in 188 human genes: implications for hepatic gene expression. Nucleic Acids Research, 2016, 44, 6756-6769.	14.5	15
360	The landscape of DNA methylation amid a perfect storm of autism aetiologies. Nature Reviews Neuroscience, 2016, 17, 411-423.	10.2	139
361	Escape Artists of the X Chromosome. Trends in Genetics, 2016, 32, 348-359.	6.7	144
362	New Perspectives on Genomic Imprinting, an Essential and Multifaceted Mode of Epigenetic Control in the Developing and Adult Brain. Annual Review of Neuroscience, 2016, 39, 347-384.	10.7	86
363	Base-resolution profiling of active DNA demethylation using MAB-seq and caMAB-seq. Nature Protocols, 2016, 11, 1081-1100.	12.0	30
364	DNA cytosine hydroxymethylation levels are distinct among non-overlapping classes of peripheral blood leukocytes. Journal of Immunological Methods, 2016, 436, 1-15.	1.4	5
365	The FMR1 promoter is selectively hydroxymethylated in primary neurons of fragile X syndrome patients. Human Molecular Genetics, 2016, 25, ddw311.	2.9	18

#	ARTICLE	IF	CITATIONS
366	Characterization of How DNA Modifications Affect DNA Binding by C2H2 Zinc Finger Proteins. Methods in Enzymology, 2016, 573, 387-401.	1.0	31
367	Ethanol-induced changes in poly (ADP ribose) polymerase and neuronal developmental gene expression. Neuropharmacology, 2016, 110, 287-296.	4.1	8
368	A Slice of the Suicidal Brain: What Have Postmortem Molecular Studies Taught Us?. Current Psychiatry Reports, 2016, 18, 98.	4.5	29
369	The role of the mtDNA set point in differentiation, development and tumorigenesis. Biochemical Journal, 2016, 473, 2955-2971.	3.7	40
370	MeCP2… Nature's Wonder Protein or Medicine's Most Feared One?. Current Genetic Medicine Reports, 2016, 4, 180-194.	1.9	5
371	Transcription factors as readers and effectors of DNA methylation. Nature Reviews Genetics, 2016, 17, 551-565.	16.3	482
372	5-Hydroxymethylcytosine in E-box motifs ACAT   GTG and ACAC   GTG increases DNA-binding of the B-HLH transcription factor TCF4. Integrative Biology (United Kingdom), 2016, 8, 936-945.	1.3	21
373	5-Hydroxymethylcytosine Expression in Proliferative Nodules Arising within Congenital Nevi Allows Differentiation from Malignant Melanoma. Journal of Investigative Dermatology, 2016, 136, 2453-2461.	0.7	22
374	Detection of differentially methylated regions in whole genome bisulfite sequencing data using local Getis-Ord statistics. Bioinformatics, 2016, 32, 3396-3404.	4.1	27
375	DNA methylation dynamics: identification and functional annotation. Briefings in Functional Genomics, 2016, 15, elw029.	2.7	13
376	Cell typeâ€specific epigenome profiling using affinityâ€purified nuclei. Genesis, 2016, 54, 160-169.	1.6	4
377	Scp>DNA methylation in Parkinson's disease. Journal of Neurochemistry, 2016, 139, 108-120.	3.9	78
378	Impact of DNMT1 and DNMT3a forebrain knockout on depressive- and anxiety like behavior in mice. Neurobiology of Learning and Memory, 2016, 135, 139-145.	1.9	50
379	Epigenetic mechanisms involved in the effects of stress exposure: focus on 5-hydroxymethylcytosine: Table 1:. Environmental Epigenetics, 2016, 2, dvw016.	1.8	16
380	The epigenome in Alzheimer's disease: current state and approaches for a new path to gene discovery and understanding disease mechanism. Acta Neuropathologica, 2016, 132, 503-514.	7.7	44
381	Features of the interactions between the methyl-CpG motif and the arginine residues on the surface of MBD proteins. Structural Chemistry, 2016, 27, 1317-1326.	2.0	5
382	Genome-Wide Techniques for the Study of Clinical Epigenetic Biomarkers. , 2016, , 119-135.		O
383	Chromatin Landscape and Epigenetic Signatures in Neurological Disorders. , 2016, , 519-537.		1

#	Article	IF	CITATIONS
384	Epigenetic regulation of cognition: A circumscribed review of the field. Development and Psychopathology, 2016, 28, 1285-1304.	2.3	33
385	Sex-Specific Effects of Testosterone on the Sexually Dimorphic Transcriptome and Epigenome of Embryonic Neural Stem/Progenitor Cells. Scientific Reports, 2016, 6, 36916.	3.3	41
386	Distinctive Klf4 mutants determine preference for DNA methylation status. Nucleic Acids Research, 2016, 44, gkw774.	14.5	19
387	Editing DNA Methylation in the Mammalian Genome. Cell, 2016, 167, 233-247.e17.	28.9	932
388	Allosteric control of mammalian DNA methyltransferases – a new regulatory paradigm. Nucleic Acids Research, 2016, 44, 8556-8575.	14.5	156
389	Neonatal maternal separation stress elicits lasting <scp>DNA</scp> methylation changes in the hippocampus of stressâ€reactive Wistar Kyoto rats. European Journal of Neuroscience, 2016, 44, 2829-2845.	2.6	41
390	Uncovering the Role of the Methylome in Dementia and Neurodegeneration. Trends in Molecular Medicine, 2016, 22, 687-700.	6.7	25
391	Epigenetic and gene expression changes in the adolescent brain: What have we learned from animal models?. Neuroscience and Biobehavioral Reviews, 2016, 70, 189-197.	6.1	43
393	Single neuron transcriptome analysis can reveal more than cell type classification. BioEssays, 2016, 38, 157-161.	2.5	14
394	Locus- and cell type-specific epigenetic switching during cellular differentiation in mammals. Frontiers in Biology, 2016, 11, 311-322.	0.7	6
395	Neuroepigenomics and Human Disease., 2016,, 73-91.		0
396	The Molecular Landscape of the Developing Human Central Nervous System. , 2016, , 203-220.		1
397	Epigenetics and developmental programming of welfare and production traits in farm animals. Reproduction, Fertility and Development, 2016, 28, 1443.	0.4	78
399	Absence of genomic hypomethylation or regulation of cytosine-modifying enzymes with aging in male and female mice. Epigenetics and Chromatin, 2016, 9, 30.	3.9	45
400	The elusive role of 5′-hydroxymethylcytosine. Epigenomics, 2016, 8, 1539-1551.	2.1	28
401	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. Cell Reports, 2016, 17, 2101-2111.	6.4	54
402	DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. Cell Stem Cell, 2016, 19, 808-822.	11.1	216
403	5-Methylcytosine (5mC) and 5-Hydroxymethylcytosine (5hmC) Enhance the DNA Binding of CREB1 to the C/EBP Half-Site Tetranucleotide GCAA. Biochemistry, 2016, 55, 6940-6948.	2.5	21

#	Article	IF	CITATIONS
404	Rewriting DNA Methylation Signatures at Will: The Curable Genome Within Reach?. Advances in Experimental Medicine and Biology, 2016, 945, 475-490.	1.6	8
405	Enzymology of Mammalian DNA Methyltransferases. Advances in Experimental Medicine and Biology, 2016, 945, 87-122.	1.6	49
406	DNA Methylation and Gene Regulation in Honeybees: From Genome-Wide Analyses to Obligatory Epialleles. Advances in Experimental Medicine and Biology, 2016, 945, 193-211.	1.6	19
407	The Role of Epigenetic Mechanisms in the Regulation of Gene Expression in the Nervous System. Journal of Neuroscience, 2016, 36, 11427-11434.	3.6	109
408	Epigenetics in Development, Differentiation and Reprogramming. , 2016, , 421-448.		0
409	DNA hydroxymethylation controls cardiomyocyte gene expression in development and hypertrophy. Nature Communications, 2016, 7, 12418.	12.8	127
410	Epigenetics and Genome Evolution. , 2016, , 6-12.		0
412	Quantifying mammalian genomic DNA hydroxymethylcytosine content using solid-state nanopores. Scientific Reports, 2016, 6, 29565.	3.3	32
413	Gene regulation and genetics in neurochemistry, past to future. Journal of Neurochemistry, 2016, 139, 24-57.	3.9	4
414	Mammalian non-CG methylations are conserved and cell-type specific and may have been involved in the evolution of transposon elements. Scientific Reports, 2016, 6, 32207.	3.3	8
415	DISMISS: detection of stranded methylation in MeDIP-Seq data. BMC Bioinformatics, 2016, 17, 295.	2.6	16
416	Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and Biology Insights, 2016, 10, BBI.S38427.	2.0	22
417	Sequence features accurately predict genome-wide MeCP2 binding in vivo. Nature Communications, 2016, 7, 11025.	12.8	46
418	Genome-wide methylation analysis identifies genes silenced in non-seminoma cell lines. Npj Genomic Medicine, 2016, 1, 15009.	3.8	6
419	Assessing Cell-to-Cell DNA Methylation Variability on Individual Long Reads. Scientific Reports, 2016, 6, 21317.	3.3	11
420	Mammalian Brain Development is Accompanied by a Dramatic Increase in Bipolar DNA Methylation. Scientific Reports, 2016, 6, 32298.	3.3	13
421	Modular reorganization of the global network of gene regulatory interactions during perinatal human brain development. BMC Developmental Biology, 2016, 16, 13.	2.1	5
422	Genome-wide redistribution of MeCP2 in dorsal root ganglia after peripheral nerve injury. Epigenetics and Chromatin, 2016, 9, 23.	3.9	22

#	Article	IF	CITATIONS
423	Genome-wide alteration of 5-hydroxymenthylcytosine in a mouse model of Alzheimer's disease. BMC Genomics, 2016, 17, 381.	2.8	48
424	Developmental and adult expression patterns of the Gâ€proteinâ€coupled receptor GPR88 in the rat: Establishment of a dual nuclear–cytoplasmic localization. Journal of Comparative Neurology, 2016, 524, 2776-2802.	1.6	17
425	Annual Research Review: Discovery science strategies in studies of the pathophysiology of child and adolescent psychiatric disorders ―promises and limitations. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2016, 57, 421-439.	5.2	58
426	The High-Throughput Sequencing Technologies Triple-W Discussion: Why Use HTS, What Is the Optimal HTS Method to Use, and Which Data Analysis Workflow to Follow. , 2016, , 1-12.		2
427	Genome-Wide Analysis of DNA Methylation Patterns by High-Throughput Sequencing., 2016,, 197-221.		5
428	The interplay between DNA methylation, folate and neurocognitive development. Epigenomics, 2016, 8, 863-879.	2.1	64
429	Epigenetic mechanisms in neurogenesis. Nature Reviews Neuroscience, 2016, 17, 537-549.	10.2	299
430	The dynamic changes of DNA methylation in primordial germ cell differentiation. Gene, 2016, 591, 305-312.	2.2	12
431	Differential patterns of histone methylase EHMT2 and its catalyzed histone modifications H3K9me1 and H3K9me2 during maturation of central auditory system. Cell and Tissue Research, 2016, 365, 247-264.	2.9	13
432	Neurofilament-labeled pyramidal neurons and astrocytes are deficient in DNA methylation marks in Alzheimer's disease. Neurobiology of Aging, 2016, 45, 30-42.	3.1	40
433	Developmental and behavioral consequences of early life maternal separation stress in a mouse model of fetal alcohol spectrum disorder. Behavioural Brain Research, 2016, 308, 94-103.	2.2	24
434	Functional Characterization of DNA Methylation in the Oligodendrocyte Lineage. Cell Reports, 2016, 15, 748-760.	6.4	81
435	Gene and transposable element methylation in great tit (Parus major) brain and blood. BMC Genomics, 2016, 17, 332.	2.8	66
436	A probabilistic generative model for quantification of DNA modifications enables analysis of demethylation pathways. Genome Biology, 2016, 17, 49.	8.8	16
437	DNA methylation dynamics in cellular commitment and differentiation. Briefings in Functional Genomics, 2016, 15, elw017.	2.7	66
438	DNA methylation in adult diffuse gliomas. Briefings in Functional Genomics, 2016, 15, elw019.	2.7	11
439	OGG1 is essential in oxidative stress induced DNA demethylation. Cellular Signalling, 2016, 28, 1163-1171.	3.6	72
440	MECP2, a multi-talented modulator of chromatin architecture. Briefings in Functional Genomics, 2016, 15, elw023.	2.7	59

#	Article	IF	CITATIONS
441	Bridging the Gap between DNA Methylation, DNA Methylation Readers, and Neurodevelopmental Disorders. Journal of Neuroscience, 2016, 36, 6851-6853.	3.6	1
442	Human DNA methylomes of neurodegenerative diseases show common epigenomic patterns. Translational Psychiatry, 2016, 6, e718-e718.	4.8	137
443	Obesity Weighs down Memory through a Mechanism Involving the Neuroepigenetic Dysregulation of Sirt1. Journal of Neuroscience, 2016, 36, 1324-1335.	3.6	69
444	The Cellular and Molecular Landscapes of the Developing Human Central Nervous System. Neuron, 2016, 89, 248-268.	8.1	571
445	Tissue-specific patterns of allelically-skewed DNA methylation. Epigenetics, 2016, 11, 24-35.	2.7	32
446	Validation of a DNA methylation microarray for 850,000 CpG sites of the human genome enriched in enhancer sequences. Epigenomics, 2016, 8, 389-399.	2.1	529
447	Epigenetic regulation of early neural fate commitment. Cellular and Molecular Life Sciences, 2016, 73, 1399-1411.	5.4	13
448	Resetting the epigenome for heart regeneration Seminars in Cell and Developmental Biology, 2016, 58, 2-13.	5.0	18
449	DNA methylation analysis in constitutional disorders: Clinical implications of the epigenome. Critical Reviews in Clinical Laboratory Sciences, 2016, 53, 147-165.	6.1	28
450	CpG methylation differences between neurons and glia are highly conserved from mouse to human. Human Molecular Genetics, 2016, 25, 223-232.	2.9	16
451	Neurodevelopmental origins of bipolar disorder: iPSC models. Molecular and Cellular Neurosciences, 2016, 73, 63-83.	2.2	90
452	DNA methylation in human epigenomes depends on local topology of CpG sites. Nucleic Acids Research, 2016, 44, 5123-5132.	14.5	153
453	Mapping of Variable DNA Methylation Across Multiple Cell Types Defines a Dynamic Regulatory Landscape of the Human Genome. G3: Genes, Genomes, Genetics, 2016, 6, 973-986.	1.8	41
454	Decoding the nonâ€coding genome: elucidating genetic risk outside the coding genome. Genes, Brain and Behavior, 2016, 15, 187-204.	2.2	32
455	DNA Methylation Signatures of Early Childhood Malnutrition Associated With Impairments in Attention and Cognition. Biological Psychiatry, 2016, 80, 765-774.	1.3	124
456	Regulation of nucleus accumbens transcript levels in mice by early-life social stress and cocaine. Neuropharmacology, 2016, 103, 183-194.	4.1	27
457	Principles Governing DNA Methylation during Neuronal Lineage and Subtype Specification. Journal of Neuroscience, 2016, 36, 1711-1722.	3.6	50
458	Epigenetic mechanisms in sexual differentiation of the brain and behaviour. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150114.	4.0	63

#	Article	IF	Citations
459	Single-locus enrichment without amplification for sequencing and direct detection of epigenetic modifications. Molecular Genetics and Genomics, 2016, 291, 1491-1504.	2.1	16
460	Understanding the genetic liability to schizophrenia through the neuroepigenome. Schizophrenia Research, 2016, 177, 115-124.	2.0	22
461	Single-base resolution analysis of DNA epigenome via high-throughput sequencing. Science China Life Sciences, 2016, 59, 219-226.	4.9	9
462	Active DNA demethylation at enhancers during the vertebrate phylotypic period. Nature Genetics, 2016, 48, 417-426.	21.4	210
463	DNA methylation profiling in human Huntington's disease brain. Human Molecular Genetics, 2016, 25, 2013-2030.	2.9	56
464	DNA methylation dynamics in neurogenesis. Epigenomics, 2016, 8, 401-414.	2.1	52
465	Role of Tet1/3 Genes and Chromatin Remodeling Genes in Cerebellar Circuit Formation. Neuron, 2016, 89, 100-112.	8.1	72
466	A Loss-of-Function Variant in a Minor Isoform of ANK3 Protects Against Bipolar Disorder and Schizophrenia. Biological Psychiatry, 2016, 80, 323-330.	1.3	31
467	Back to the past in schizophrenia genomics. Nature Neuroscience, 2016, 19, 1-2.	14.8	49
468	Mapping DNA methylation across development, genotype and schizophrenia in the human frontal cortex. Nature Neuroscience, 2016, 19, 40-47.	14.8	417
469	Recent Developments in Understanding Brain Aging: Implications for Alzheimer's Disease and Vascular Cognitive Impairment. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2016, 71, 13-20.	3.6	42
470	Whole-genome bisulfite sequencing maps from multiple human tissues reveal novel CpG islands associated with tissue-specific regulation. Human Molecular Genetics, 2016, 25, 69-82.	2.9	44
471	Immunohistochemical Detection of Oxidized Forms of 5-Methylcytosine in Embryonic and Adult Brain Tissue. Neuromethods, 2016, , 125-137.	0.3	2
472	Epigenetic Basis of Mental Illness. Neuroscientist, 2016, 22, 447-463.	3.5	236
473	Cell Type-Specific DNA Methylation Analysis in Neurons and Glia. Neuromethods, 2016, , 115-123.	0.3	2
474	DNA Methylation and Hydroxymethylation Levels in Relation to Two Weight Loss Strategies: Energy-Restricted Diet or Bariatric Surgery. Obesity Surgery, 2016, 26, 603-611.	2.1	71
475	Integrative Single-Cell Transcriptomics Reveals Molecular Networks Defining Neuronal Maturation During Postnatal Neurogenesis. Cerebral Cortex, 2017, 27, 2064-2077.	2.9	28
476	Practical Guidelines for High-Resolution Epigenomic Profiling of Nucleosomal Histones in Postmortem Human Brain Tissue. Biological Psychiatry, 2017, 81, 162-170.	1.3	48

#	Article	IF	Citations
477	Molecular mechanisms underlying noncoding risk variations in psychiatric genetic studies. Molecular Psychiatry, 2017, 22, 497-511.	7.9	43
478	The OPRM1 A118G polymorphism modulates the descending pain modulatory system for individual pain experience in young women with primary dysmenorrhea. Scientific Reports, 2017, 7, 39906.	3.3	31
479	<scp>DNA</scp> sequence properties that predict susceptibility to epiallelic switching. EMBO Journal, 2017, 36, 617-628.	7.8	56
480	Whole genome grey and white matter DNA methylation profiles in dorsolateral prefrontal cortex. Synapse, 2017, 71, e21959.	1.2	13
481	The 5-Hydroxymethylcytosine (5hmC) Reader UHRF2 Is Required for Normal Levels of 5hmC in Mouse Adult Brain and Spatial Learning and Memory. Journal of Biological Chemistry, 2017, 292, 4533-4543.	3.4	39
482	Recent Progress in Functional Genomic Studies of Depression and Suicide. Current Genetic Medicine Reports, 2017, 5, 22-34.	1.9	1
483	Epigenetics studies of fetal alcohol spectrum disorder: where are we now?. Epigenomics, 2017, 9, 291-311.	2.1	84
484	Epigenetic Mistakes in Neurodevelopmental Disorders. Journal of Molecular Neuroscience, 2017, 61, 590-602.	2.3	29
485	In utero exposure to maternal smoking is associated with DNA methylation alterations and reduced neuronal content in the developing fetal brain. Epigenetics and Chromatin, 2017, 10, 4.	3.9	74
486	Multi-tissue DNA methylation age predictor in mouse. Genome Biology, 2017, 18, 68.	8.8	341
487	An Intrinsic Epigenetic Barrier for Functional Axon Regeneration. Neuron, 2017, 94, 337-346.e6.	8.1	130
488	Transcribing the connectome: roles for transcription factors and chromatin regulators in activity-dependent synapse development. Journal of Neurophysiology, 2017, 118, 755-770.	1.8	26
490	DNA methylome analysis reveals distinct epigenetic patterns of ascending aortic dissection and bicuspid aortic valve. Cardiovascular Research, 2017, 113, 692-704.	3.8	33
491	Using Epigenetic Reprogramming to Treat Pediatric Brain Cancer. Cancer Cell, 2017, 31, 609-611.	16.8	5
492	The role of 5-hydroxymethylcytosine in development, aging and age-related diseases. Ageing Research Reviews, 2017, 37, 28-38.	10.9	69
493	Methylation of $\langle i \rangle$ avpr $1a \langle i \rangle$ in the cortex of wild prairie voles: effects of CpG position and polymorphism. Royal Society Open Science, 2017, 4, 160646.	2.4	16
494	DNA methylation regulated gene expression in organ fibrosis. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2017, 1863, 2389-2397.	3.8	37
495	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. Neuron, 2017, 94, 550-568.e10.	8.1	222

#	Article	IF	CITATIONS
496	Comprehensive evaluation of genome-wide 5-hydroxymethylcytosine profiling approaches in human DNA. Epigenetics and Chromatin, 2017, 10, 16.	3.9	68
497	Integration of CpG-free DNA induces de novo methylation of CpG islands in pluripotent stem cells. Science, 2017, 356, 503-508.	12.6	68
498	Enrichment methods provide a feasible approach to comprehensive and adequately powered investigations of the brain methylome. Nucleic Acids Research, 2017, 45, e97-e97.	14.5	32
499	Neurobiological basis for pain vulnerability: why me?. Pain, 2017, 158, S108-S114.	4.2	26
500	Caregiver maltreatment causes altered neuronal DNA methylation in female rodents. Development and Psychopathology, 2017, 29, 477-489.	2.3	39
501	Structural Basis of MeCP2 Distribution on Non-CpG Methylated and Hydroxymethylated DNA. Journal of Molecular Biology, 2017, 429, 1581-1594.	4.2	43
502	Prospects for Medications to Reverse Causative Epigenetic Processes in Neuropsychiatry Disorders. Neuropsychopharmacology, 2017, 42, 367-368.	5.4	3
503	Association of 5-hydroxymethylation and 5-methylation of DNA cytosine with tissue-specific gene expression. Epigenetics, 2017, 12, 123-138.	2.7	61
504	Epigenetics of cell fate reprogramming and its implications for neurological disorders modelling. Neurobiology of Disease, 2017, 99, 84-120.	4.4	11
505	Epigenetics and the Biology of Gene $ ilde{A}-$ Environment Interactions. , 2017, , 59-94.		8
506	L1 retrotransposition is activated by Ten-eleven-translocation protein 1 and repressed by methyl-CpG binding proteins. Nucleus, 2017, 8, 548-562.	2.2	19
507	DNA methylation and transcription onset in the brain. Epigenomics, 2017, 9, 797-809.	2.1	12
508	Epigenetics of Autism Spectrum Disorder. Advances in Experimental Medicine and Biology, 2017, 978, 63-90.	1.6	96
509	MeCP2, A Modulator of Neuronal Chromatin Organization Involved in Rett Syndrome. Advances in Experimental Medicine and Biology, 2017, 978, 3-21.	1.6	13
510	Gene-body 5-hydroxymethylation is associated with gene expression changes in the prefrontal cortex of depressed individuals. Translational Psychiatry, 2017, 7, e1119-e1119.	4.8	63
511	Non-CpG methylation by DNMT3B facilitates REST binding and gene silencing in developing mouse hearts. Nucleic Acids Research, 2017, 45, 3102-3115.	14.5	45
512	TET-mediated active DNA demethylation: mechanism, function and beyond. Nature Reviews Genetics, 2017, 18, 517-534.	16.3	1,109
513	History and Modern View on DNA Modifications in the Brain. , 2017, , 1-25.		O

#	Article	IF	CITATIONS
514	Allele-specific non-CG DNA methylation marks domains of active chromatin in female mouse brain. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2882-E2890.	7.1	45
515	The Transitional Age Brain. Child and Adolescent Psychiatric Clinics of North America, 2017, 26, 157-175.	1.9	46
516	Combinatorial DNA methylation codes at repetitive elements. Genome Research, 2017, 27, 934-946.	5.5	44
517	Genome-wide DNA methylation profiles reveal novel candidate genes associated with meat quality at different age stages in hens. Scientific Reports, 2017, 7, 45564.	3.3	61
518	DNA Methylation Divergence and Tissue Specialization in the Developing Mouse Placenta. Molecular Biology and Evolution, 2017, 34, 1702-1712.	8.9	39
519	A methylome-wide mQTL analysis reveals associations of methylation sites with GAD1 and HDAC3 SNPs and a general psychiatric risk score. Translational Psychiatry, 2017, 7, e1002-e1002.	4.8	29
520	Microfluidics for genome-wide studies involving next generation sequencing. Biomicrofluidics, 2017, 11, 021501.	2.4	29
521	Global DNA methylation profiling of manganese-exposed human neuroblastoma SH-SY5Y cells reveals epigenetic alterations in Parkinson's disease-associated genes. Archives of Toxicology, 2017, 91, 2629-2641.	4.2	41
522	Comprehensive mapping of 5-hydroxymethylcytosine epigenetic dynamics in axon regeneration. Epigenetics, 2017, 12, 77-92.	2.7	44
523	Opening up the DNA methylome of dementia. Molecular Psychiatry, 2017, 22, 485-496.	7.9	59
524	Distinct cellular and molecular environments support aging-related DNA methylation changes in the substantia nigra. Epigenomics, 2017, 9, 21-31.	2.1	16
525	Epigenetic Biomarkers for Parkinson's Disease: From Diagnostics to Therapeutics. Journal of Parkinson's Disease, 2017, 7, 1-12.	2.8	43
526	The Epstein-Barr Virus B-ZIP Protein Zta Recognizes Specific DNA Sequences Containing 5-Methylcytosine and 5-Hydroxymethylcytosine. Biochemistry, 2017, 56, 6200-6210.	2.5	17
527	Dysregulation of Cortical Neuron DNA Methylation Profile in Autism Spectrum Disorder. Cerebral Cortex, 2017, 27, 5739-5754.	2.9	118
528	Sexually Dimorphic Epigenetic Regulation of Brain-Derived Neurotrophic Factor in Fetal Brain in the Valproic Acid Model of Autism Spectrum Disorder. Developmental Neuroscience, 2017, 39, 507-518.	2.0	19
529	The BRAIN Initiative Cell Census Consortium: Lessons Learned toward Generating a Comprehensive Brain Cell Atlas. Neuron, 2017, 96, 542-557.	8.1	235
530	Maternal Nutrition and Cognition. , 2017, , 29-42.		0
531	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	27.8	764

#	Article	IF	CITATIONS
532	Mouse olfactory bulb methylome and hydroxymethylome maps reveal noncanonical active turnover of DNA methylation. Epigenetics, 2017, 12, 708-714.	2.7	7
533	When the Lyon(ized chromosome) roars: ongoing expression from an inactive X chromosome. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160355.	4.0	71
534	Sexually divergent <scp>DNA</scp> methylation patterns with hippocampal aging. Aging Cell, 2017, 16, 1342-1352.	6.7	67
535	<scp>RNA</scp> polymerase <scp>II</scp> primes Polycombâ€repressed developmental genes throughout terminal neuronal differentiation. Molecular Systems Biology, 2017, 13, 946.	7.2	44
536	Neuron-specific methylome analysis reveals epigenetic regulation and tau-related dysfunction of BRCA1 in Alzheimer's disease. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9645-E9654.	7.1	72
537	Early-Life Gene Expression in Neurons Modulates Lasting Epigenetic States. Cell, 2017, 171, 1151-1164.e16.	28.9	167
538	Bi-directional and shared epigenomic signatures following proton and 56Fe irradiation. Scientific Reports, 2017, 7, 10227.	3.3	36
539	Detecting rare asymmetrically methylated cytosines and decoding methylation patterns in the honeybee genome. Royal Society Open Science, 2017, 4, 170248.	2.4	11
540	Functional impacts of 5-hydroxymethylcytosine, 5-formylcytosine, and 5-carboxycytosine at a single hemi-modified CpG dinucleotide in a gene promoter. Nucleic Acids Research, 2017, 45, 11033-11042.	14.5	33
541	Strategies for analyzing bisulfite sequencing data. Journal of Biotechnology, 2017, 261, 105-115.	3.8	113
542	5-hydroxymethylcytosine accumulation in postmitotic neurons results in functional demethylation of expressed genes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7812-E7821.	7.1	122
543	Misregulation of DNA Methylation Regulators in Cancer. Cancer Drug Discovery and Development, 2017, , 97-124.	0.4	2
544	UBE3A-mediated regulation of imprinted genes and epigenome-wide marks in human neurons. Epigenetics, 2017, 12, 982-990.	2.7	18
545	Differential landscape of non-CpG methylation in embryonic stem cells and neurons caused by DNMT3s. Scientific Reports, 2017, 7, 11295.	3.3	59
546	MicroRNAs Induce a Permissive Chromatin Environment that Enables Neuronal Subtype-Specific Reprogramming of Adult Human Fibroblasts. Cell Stem Cell, 2017, 21, 332-348.e9.	11.1	112
547	Evolution of the Human Nervous System Function, Structure, and Development. Cell, 2017, 170, 226-247.	28.9	316
548	Epigenetic research in multiple sclerosis: progress, challenges, and opportunities. Physiological Genomics, 2017, 49, 447-461.	2.3	30
549	Associating transcription factors and conserved RNA structures with gene regulation in the human brain. Scientific Reports, 2017, 7, 5776.	3.3	12

#	Article	IF	CITATIONS
550	Genomic plasticity between human and mycobacterial DNA: A review. Tuberculosis, 2017, 107, 38-47.	1.9	11
551	Genomewide <scp>DNA</scp> methylation analysis in combat veterans reveals a novel locus for <scp>PTSD</scp> . Acta Psychiatrica Scandinavica, 2017, 136, 493-505.	4.5	53
552	Single-cell methylomes identify neuronal subtypes and regulatory elements in mammalian cortex. Science, 2017, 357, 600-604.	12.6	445
553	MeCP2 and CTCF: enhancing the cross-talk of silencers. Biochemistry and Cell Biology, 2017, 95, 593-608.	2.0	7
554	Genome-wide DNA methylation changes associated with olfactory learning and memory in Apis mellifera. Scientific Reports, 2017, 7, 17017.	3.3	20
555	Dissecting Cell-Type Composition and Activity-Dependent Transcriptional State in Mammalian Brains by Massively Parallel Single-Nucleus RNA-Seq. Molecular Cell, 2017, 68, 1006-1015.e7.	9.7	143
556	DNA methylation signatures follow preformed chromatin compartments in cardiac myocytes. Nature Communications, 2017, 8, 1667.	12.8	76
557	Epigenetic Etiology of Intellectual Disability. Journal of Neuroscience, 2017, 37, 10773-10782.	3.6	113
558	Neuropathology of suicide: recent findings and future directions. Molecular Psychiatry, 2017, 22, 1395-1412.	7.9	111
559	Genome-wide, Single-Cell DNA Methylomics Reveals Increased Non-CpG Methylation during Human Oocyte Maturation. Stem Cell Reports, 2017, 9, 397-407.	4.8	77
560	Integration of DNA methylation and gene transcription across nineteen cell types reveals cell type-specific and genomic region-dependent regulatory patterns. Scientific Reports, 2017, 7, 3626.	3.3	21
561	Genome-wide DNA methylation analysis of the porcine hypothalamus-pituitary-ovary axis. Scientific Reports, 2017, 7, 4277.	3.3	25
562	Epigenetic mechanisms during ageing and neurogenesis as novel therapeutic avenues in human brain disorders. Clinical Epigenetics, 2017, 9, 67.	4.1	108
563	P-Hint-Hunt: a deep parallelized whole genome DNA methylation detection tool. BMC Genomics, 2017, 18, 134.	2.8	2
564	Single-base resolution methylomes of upland cotton (Gossypium hirsutum L.) reveal epigenome modifications in response to drought stress. BMC Genomics, 2017, 18, 297.	2.8	58
565	Exaggerated CpH methylation in the autism-affected brain. Molecular Autism, 2017, 8, 6.	4.9	31
566	Ten-eleven translocation 2 interacts with forkhead box O3 and regulates adult neurogenesis. Nature Communications, 2017, 8, 15903.	12.8	82
567	Tracking the evolution of epialleles during neural differentiation and brain development: <i>D-Aspartate oxidase</i> as a model gene. Epigenetics, 2017, 12, 41-54.	2.7	21

#	Article	IF	CITATIONS
568	Dynamic and rapid changes in the transcriptome and epigenome during germination and in developing rice ( <i>Oryza sativa</i> ) coleoptiles under anoxia and reâ€oxygenation. Plant Journal, 2017, 89, 805-824.	5.7	63
569	Inhibition of <scp>DNA</scp> methyltransferases regulates cocaine selfâ€administration by rats: a genomeâ€wide <scp>DNA</scp> methylation study. Genes, Brain and Behavior, 2017, 16, 313-327.	2.2	28
570	Social threat exposure in juvenile mice promotes cocaineâ€seeking by altering blood clotting and brain vasculature. Addiction Biology, 2017, 22, 911-922.	2.6	13
571	It's All in the Brain: A Review of Available Functional Genomic Annotations. Biological Psychiatry, 2017, 81, 478-483.	1.3	14
572	Neurons versus Networks: The Interplay between Individual Neurons and Neural Networks in Cognitive Functions. Neuroscientist, 2017, 23, 341-355.	<b>3.</b> 5	20
573	A pre-neoplastic epigenetic field defect in HCV-infected liver at transcription factor binding sites and polycomb targets. Oncogene, 2017, 36, 2030-2044.	5.9	43
574	Multiregional analysis of global 5â€methylcytosine and 5â€hydroxymethylcytosine throughout the progression of Alzheimer's disease. Journal of Neurochemistry, 2017, 140, 383-394.	3.9	42
575	Linking Telomere Regulation to Stem Cell Pluripotency. Trends in Genetics, 2017, 33, 16-33.	6.7	50
576	Oxidatively generated base modifications in DNA: Not only carcinogenic risk factor but also regulatory mark? Free Radical Biology and Medicine, 2017, 107, 258-265.	2.9	60
577	Chromatin remodeling during in vivo neural stem cells differentiating to neurons in early Drosophila embryos. Cell Death and Differentiation, 2017, 24, 409-420.	11.2	24
578	DNA Demethylation Agents in Clinical Medicine. , 2017, , 595-603.		1
579	Methyl-dependent and spatial-specific DNA recognition by the orthologous transcription factors human AP-1 and Epstein-Barr virus Zta. Nucleic Acids Research, 2017, 45, 2503-2515.	14.5	38
580	DNA Methylation and Adult Neurogenesis. Brain Plasticity, 2017, 3, 5-26.	3.5	56
581	Potential Benefits of Ameliorating Metabolic and Nutritional Abnormalities in People With Profound Developmental Disabilities. Nutrition and Metabolic Insights, 2017, 10, 117863881771645.	1.9	0
582	Tissue-specific DNA methylation is conserved across human, mouse, and rat, and driven by primary sequence conservation. BMC Genomics, 2017, 18, 724.	2.8	71
583	Genome-wide comparative analysis of DNA methylation between soybean cytoplasmic male-sterile line NJCMS5A and its maintainer NJCMS5B. BMC Genomics, 2017, 18, 596.	2.8	34
584	Epigenetics of Rheumatic Diseases. , 2017, , 344-354.		0
585	Epigenetics of Brain Disorders. , 2017, , 553-568.		0

#	Article	IF	Citations
586	CpG and Non-CpG Methylation in Epigenetic Gene Regulation and Brain Function. Genes, 2017, 8, 148.	2.4	269
587	Epigenomics of Major Depressive Disorders and Schizophrenia: Early Life Decides. International Journal of Molecular Sciences, 2017, 18, 1711.	4.1	49
588	Alpha-Lipoic Acid Downregulates IL- $1\hat{l}^2$ and IL-6 by DNA Hypermethylation in SK-N-BE Neuroblastoma Cells. Antioxidants, 2017, 6, 74.	5.1	29
589	Driver or Passenger: Epigenomes in Alzheimer's Disease. Epigenomes, 2017, 1, 5.	1.8	2
590	Chromatin Switches during Neural Cell Differentiation and Their Dysregulation by Prenatal Alcohol Exposure. Genes, 2017, 8, 137.	2.4	17
591	DNA Methylation Dynamics and Cocaine in the Brain: Progress and Prospects. Genes, 2017, 8, 138.	2.4	37
592	The Crucial Role of DNA Methylation and MeCP2 in Neuronal Function. Genes, 2017, 8, 141.	2.4	60
593	DNA Methylation Profiling of Human Prefrontal Cortex Neurons in Heroin Users Shows Significant Difference between Genomic Contexts of Hyper- and Hypomethylation and a Younger Epigenetic Age. Genes, 2017, 8, 152.	2.4	66
594	DNA Methylation of Synaptic Genes in the Prefrontal Cortex Is Associated with Aging and Age-Related Cognitive Impairment. Frontiers in Aging Neuroscience, 2017, 9, 249.	3.4	51
595	Epigenome-Wide Association Study of Cognitive Functioning in Middle-Aged Monozygotic Twins. Frontiers in Aging Neuroscience, 2017, 9, 413.	3.4	52
596	Stress and the Emerging Roles of Chromatin Remodeling in Signal Integration and Stable Transmission of Reversible Phenotypes. Frontiers in Behavioral Neuroscience, 2017, 11, 41.	2.0	57
597	Individual Differences in Social Behavior and Cortical Vasopressin Receptor: Genetics, Epigenetics, and Evolution. Frontiers in Neuroscience, 2017, 11, 537.	2.8	19
598	Assessing Relevance of External Cognitive Measures. Frontiers in Integrative Neuroscience, 2017, 11, 3.	2.1	2
599	Implications of DNA Methylation in Parkinson's Disease. Frontiers in Molecular Neuroscience, 2017, 10, 225.	2.9	71
600	Cocaine and Epigenetics. , 2017, , 81-88.		0
601	Epigenetics in Chronic Pain. , 2017, , 185-226.		1
602	Neurodevelopmental Disorders and Environmental Toxicants: Epigenetics as an Underlying Mechanism. International Journal of Genomics, 2017, 2017, 1-23.	1.6	102
603	TET and 5hmC in Neurodevelopment and the Adult Brain. , 2017, , 61-79.		2

#	Article	IF	CITATIONS
604	Body-hypomethylated human genes harbor extensive intragenic transcriptional activity and are prone to cancer-associated dysregulation. Nucleic Acids Research, 2017, 45, gkx020.	14.5	34
605	5-hydroxymethylcytosine is highly dynamic across human fetal brain development. BMC Genomics, 2017, 18, 738.	2.8	63
606	Epigenetic Advances in Behavioral and Brain Sciences Have Relevance for Public Policy. Policy Insights From the Behavioral and Brain Sciences, 2017, 4, 202-209.	2.4	2
607	DNA epigenome editing using CRISPR-Cas SunTag-directed DNMT3A. Genome Biology, 2017, 18, 176.	8.8	153
608	Neuroepigenetic mechanisms in disease. Epigenetics and Chromatin, 2017, 10, 47.	3.9	52
609	Early Adversity and Epigenetics: Implications for Early Care and Educational Policy. , 0, , 86-106.		0
610	Whole genome DNA methylation: beyond genes silencing. Oncotarget, 2017, 8, 5629-5637.	1.8	105
611	What Does the Future Hold for the Study of Nucleic Acid Modifications in the Brain?., 2017, , 149-159.		0
612	Environmental factors and epigenetics of neuropsychiatric disorders., 2017,, 9-33.		0
613	Beyond mCG., 2017,, 81-94.		0
614	DNA Modifications and Memory. , 2017, , 95-111.		2
615	The Epigenetic Link between Prenatal Adverse Environments and Neurodevelopmental Disorders. Genes, 2017, 8, 104.	2.4	134
616	Approaches to Detecting DNA Base Modification in the Brain. , 2017, , 27-41.		0
617	Natural Epigenomic Variations in <i>Arabidopsis thaliana</i> . Kagaku To Seibutsu, 2017, 55, 810-816.	0.0	0
618	Cell-type-specific brain methylomes profiled via ultralow-input microfluidics. Nature Biomedical Engineering, 2018, 2, 183-194.	22.5	29
619	Considering Epigenetics in Adverse Outcome Pathways. , 2018, , 219-234.		2
620	Chromatin Regulation of Neuronal Maturation and Plasticity. Trends in Neurosciences, 2018, 41, 311-324.	8.6	77
621	Developmentally linked human DNA hypermethylation is associated with down-modulation, repression, and upregulation of transcription. Epigenetics, 2018, 13, 275-289.	2.7	31

#	Article	IF	CITATIONS
622	Genic C-Methylation in Soybean Is Associated with Gene Paralogs Relocated to Transposable Element-Rich Pericentromeres. Molecular Plant, 2018, 11, 485-495.	8.3	19
623	Experience-dependent neuroplasticity of the developing hypothalamus: integrative epigenomic approaches. Epigenetics, 2018, 13, 318-330.	2.7	21
624	De Novo DNA Methylation: Marking the Path from Stem Cell to Neural Fate. Cell Stem Cell, 2018, 22, 469-471.	11.1	2
625	Highly scalable generation of DNA methylation profiles in single cells. Nature Biotechnology, 2018, 36, 428-431.	17.5	215
626	Caloric restriction mitigates age-associated hippocampal differential CG and non-CG methylation. Neurobiology of Aging, 2018, 67, 53-66.	3.1	45
627	Comparative whole genome DNA methylation profiling of cattle sperm and somatic tissues reveals striking hypomethylated patterns in sperm. GigaScience, 2018, 7, .	6.4	60
628	Decoding the dynamic DNA methylation and hydroxymethylation landscapes in endodermal lineage intermediates during pancreatic differentiation of hESC. Nucleic Acids Research, 2018, 46, 2883-2900.	14.5	66
629	DNA methylation is not involved in dietary restriction induced lifespan extension in adult <i>Drosophila</i> . Genetical Research, 2018, 100, e1.	0.9	6
630	Neuroepigenetics., 2018,, 175-190.		0
631	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. Nature Neuroscience, 2018, 21, 432-439.	14.8	290
632	5-Hydroxymethylcytosine preferentially targets genes upregulated in isocitrate dehydrogenase 1 mutant high-grade glioma. Acta Neuropathologica, 2018, 135, 617-634.	7.7	15
633	Rescue of Fragile X Syndrome Neurons by DNA Methylation Editing of the FMR1 Gene. Cell, 2018, 172, 979-992.e6.	28.9	351
634	Distinct epigenetic programs regulate cardiac myocyte development and disease in the human heart in vivo. Nature Communications, 2018, 9, 391.	12.8	181
635	Large-scale comparative epigenomics reveals hierarchical regulation of non-CG methylation in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1069-E1074.	7.1	51
636	Contribution of transposable elements and distal enhancers to evolution of human-specific features of interphase chromatin architecture in embryonic stem cells. Chromosome Research, 2018, 26, 61-84.	2.2	28
637	The chromatin basis of neurodevelopmental disorders: Rethinking dysfunction along the molecular and temporal axes. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2018, 84, 306-327.	4.8	73
638	S-Adenosyl Methionine and Transmethylation Pathways in Neuropsychiatric Diseases Throughout Life. Neurotherapeutics, 2018, 15, 156-175.	4.4	68

#	Article	IF	CITATIONS
640	Puzzled Intelligence., 0,, 152-166.		0
641	Revisiting the genomic hypomethylation hypothesis of aging. Annals of the New York Academy of Sciences, 2018, 1418, 69-79.	3.8	72
642	Epigenetics and Genetics of Development. , 2018, , 153-210.		2
643	Effect of dC $\hat{a}$ † d(m5C) substitutions on the folding of intramolecular triplexes with mixed TAT and C+GC base triplets. Biochimie, 2018, 146, 156-165.	2.6	6
644	Methyl-CpG-Binding Domain Sequencing: MBD-seq. Methods in Molecular Biology, 2018, 1708, 171-189.	0.9	21
645	A role for activityâ€dependent epigenetics in the development and treatment of major depressive disorder. Genes, Brain and Behavior, 2018, 17, e12446.	2.2	41
646	Evolutionary expansion of DNA hypomethylation in the mammalian germline genome. Genome Research, 2018, 28, 145-158.	5.5	30
647	Analysis of DNA modifications in aging research. GeroScience, 2018, 40, 11-29.	4.6	39
648	Integrating 5hmC and gene expression data to infer regulatory mechanisms. Bioinformatics, 2018, 34, 1441-1447.	4.1	7
649	Epigenetics applied to psychiatry: Clinical opportunities and future challenges. Psychiatry and Clinical Neurosciences, 2018, 72, 195-211.	1.8	54
650	Epigenetic mechanisms in odontogenic tumors: A literature review. Archives of Oral Biology, 2018, 87, 211-217.	1.8	15
651	The effect of enriched environment across ages: A study of anhedonia and BDNF gene induction. Genes, Brain and Behavior, 2018, 17, e12485.	2.2	13
652	DNA Methylation and Psychiatric Disorders. Progress in Molecular Biology and Translational Science, 2018, 157, 175-232.	1.7	44
653	CpG Islands in Cancer: Heads, Tails, and Sides. Methods in Molecular Biology, 2018, 1766, 49-80.	0.9	19
654	DNA methylation loss in late-replicating domains is linked to mitotic cell division. Nature Genetics, 2018, 50, 591-602.	21.4	258
655	Epigenetic control of gene regulation during development and disease: A view from the retina. Progress in Retinal and Eye Research, 2018, 65, 1-27.	15.5	105
656	Aging Epigenetics., 2018,, 3-32.		7
657	Effects of developmental lead exposure on the hippocampal methylome: Influences of sex and timing and level of exposure. Toxicology Letters, 2018, 290, 63-72.	0.8	31

#	Article	IF	CITATIONS
658	DNA methylation signatures of educational attainment. Npj Science of Learning, 2018, 3, 7.	2.8	42
659	Generation of Whole Genome Bisulfite Sequencing Libraries for Comprehensive DNA Methylome Analysis. Methods in Molecular Biology, 2018, 1767, 291-298.	0.9	4
660	Zinc Fingers, TALEs, and CRISPR Systems: A Comparison of Tools for Epigenome Editing. Methods in Molecular Biology, 2018, 1767, 19-63.	0.9	73
661	Evaluating the Feasibility of DNA Methylation Analyses Using Long-Term Archived Brain Formalin-Fixed Paraffin-Embedded Samples. Molecular Neurobiology, 2018, 55, 668-681.	4.0	6
662	Epigenetics in epilepsy. Neuroscience Letters, 2018, 667, 40-46.	2.1	73
663	Variants of the EAAT2 Glutamate Transporter Gene Promoter Are Associated with Cerebral Palsy in Preterm Infants. Molecular Neurobiology, 2018, 55, 2013-2024.	4.0	15
664	Neuronal DNA Methyltransferases: Epigenetic Mediators between Synaptic Activity and Gene Expression?. Neuroscientist, 2018, 24, 171-185.	3.5	67
665	Epigenetics, nutrition and mental health. Is there a relationship?. Nutritional Neuroscience, 2018, 21, 602-613.	3.1	25
666	Past, present and future of epigenetics in brain sexual differentiation. Journal of Neuroendocrinology, 2018, 30, e12492.	2.6	25
667	Neuronal Expression of Opioid Gene is Controlled by Dual Epigenetic and Transcriptional Mechanism in Human Brain. Cerebral Cortex, 2018, 28, 3129-3142.	2.9	8
668	Epigenetic Regulation of the Kappa Opioid Receptor by Child Abuse. Biological Psychiatry, 2018, 84, 751-761.	1.3	68
669	Alcohol exposure promotes DNA methyltransferase DNMT3A upregulation through reactive oxygen species-dependent mechanisms. Cell Stress and Chaperones, 2018, 23, 115-126.	2.9	25
670	The impact of epigenomic nextâ€generation sequencing approaches on our understanding of neuropsychiatric disorders. Clinical Genetics, 2018, 93, 467-480.	2.0	11
671	Principles and Challenges of Applying Epigenetic Epidemiology to Psychology. Annual Review of Psychology, 2018, 69, 459-485.	17.7	65
672	Identification of Differentially Methylated Regions in the Genome of Arabidopsis thaliana. Methods in Molecular Biology, 2018, 1675, 61-69.	0.9	5
673	Disruption of AT-hook 1 domain in MeCP2 protein caused behavioral abnormality in mice. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 347-358.	3.8	11
674	The DNA methyltransferase family: a versatile toolkit for epigenetic regulation. Nature Reviews Genetics, 2018, 19, 81-92.	16.3	919
675	Plasticity of the epigenome during early-life stress. Seminars in Cell and Developmental Biology, 2018, 77, 115-132.	5.0	69

#	Article	IF	CITATIONS
676	Charting the dynamic epigenome during B-cell development. Seminars in Cancer Biology, 2018, 51, 139-148.	9.6	22
677	Nonâ€canonical Bases in the Genome: The Regulatory Information Layer in DNA. Angewandte Chemie - International Edition, 2018, 57, 4296-4312.	13.8	85
678	Nichtkanonische Basen im Genom: die regulative Informationsebene in der DNA. Angewandte Chemie, 2018, 130, 4377-4394.	2.0	14
679	Dynamism of an Astrocyte In Vivo: Perspectives on Identity and Function. Annual Review of Physiology, 2018, 80, 143-157.	13.1	44
680	Linking inter-individual variability to endocrine disruptors: insights for epigenetic inheritance. Mammalian Genome, 2018, 29, 141-152.	2.2	13
681	Target specificity of mammalian DNA methylation and demethylation machinery. Organic and Biomolecular Chemistry, 2018, 16, 1419-1435.	2.8	43
682	A comprehensive review of genetic and epigenetic mechanisms that regulate <i>BDNF</i> expression and function with relevance to major depressive disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 143-167.	1.7	100
683	DNA methylationâ€based biological aging and cancer risk and survival: Pooled analysis of seven prospective studies. International Journal of Cancer, 2018, 142, 1611-1619.	5.1	153
684	Microglia from offspring of dams with allergic asthma exhibit epigenomic alterations in genes dysregulated in autism. Glia, 2018, 66, 505-521.	4.9	54
685	Singleâ€base methylome analysis reveals dynamic epigenomic differences associated with water deficit in apple. Plant Biotechnology Journal, 2018, 16, 672-687.	8.3	130
686	Non-CpG Methylation Revised. Epigenomes, 2018, 2, 22.	1.8	6
687	DNA methylation and de-methylation using hybrid site-targeting proteins. Genome Biology, 2018, 19, 187.	8.8	45
688	DNA Methylation Assays Using Bisulphite Sequencing and Next-Generation Sequencing. Comprehensive Analytical Chemistry, 2018, , 107-136.	1.3	0
689	Characterization of human mosaic Rett syndrome brain tissue by single-nucleus RNA sequencing. Nature Neuroscience, 2018, 21, 1670-1679.	14.8	92
690	MECP2 Mutation Interrupts Nucleolin–mTOR–P70S6K Signaling in Rett Syndrome Patients. Frontiers in Genetics, 2018, 9, 635.	2.3	37
691	DNA methylation dynamics during embryonic development and postnatal maturation of the mouse auditory sensory epithelium. Scientific Reports, 2018, 8, 17348.	3.3	27
692	Age prediction of children and adolescents aged 6-17 years: an epigenome-wide analysis of DNA methylation. Aging, 2018, 10, 1015-1026.	3.1	22
693	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	12.6	516

#	Article	IF	CITATIONS
694	Mechanisms of DNA Methyltransferase Recruitment in Mammals. Genes, 2018, 9, 617.	2.4	37
695	Human Models Are Needed for Studying Human Neurodevelopmental Disorders. American Journal of Human Genetics, 2018, 103, 829-857.	6.2	103
696	Prenatal Alcohol Exposure: Profiling Developmental DNA Methylation Patterns in Central and Peripheral Tissues. Frontiers in Genetics, 2018, 9, 610.	2.3	27
697	Nondestructive, base-resolution sequencing of 5-hydroxymethylcytosine using a DNA deaminase. Nature Biotechnology, 2018, 36, 1083-1090.	17.5	154
698	Immunohistochemical Detection of 5-Methylcytosine and 5-Hydroxymethylcytosine in Developing and Postmitotic Mouse Retina. Journal of Visualized Experiments, 2018, , .	0.3	12
699	A unique role for DNA (hydroxy)methylation in epigenetic regulation of human inhibitory neurons. Science Advances, 2018, 4, eaau6190.	10.3	92
700	Dynamic DNA methylation: In the right place at the right time. Science, 2018, 361, 1336-1340.	12.6	469
701	Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells. ELife, 2018, 7, .	6.0	180
702	Immobilization of DNA with nitrogen mustard–biotin conjugate for global epigenetic analysis. Analytica Chimica Acta, 2018, 1043, 107-114.	5.4	10
703	Robust single-cell DNA methylome profiling with snmC-seq2. Nature Communications, 2018, 9, 3824.	12.8	138
704	Experienceâ€dependent transcriptional regulation in juvenile brain development. Development Growth and Differentiation, 2018, 60, 473-482.	1.5	8
705	Negative Evidence for a Functional Role of Neuronal DNMT3a in Persistent Pain. Frontiers in Molecular Neuroscience, 2018, 11, 332.	2.9	12
706	Activity-Regulated Transcription: Bridging the Gap between Neural Activity and Behavior. Neuron, 2018, 100, 330-348.	8.1	408
707	"lt was there all alongâ€. Situated uncertainty and the politics of publication in environmental epigenetics. BioSocieties, 2018, 13, 737-760.	1.3	5
708	Efficient Purification and LC-MS/MS-based Assay Development for Ten-Eleven Translocation-2 5-Methylcytosine Dioxygenase. Journal of Visualized Experiments, 2018, , .	0.3	3
709	X-Chromosome Inactivation and Escape from X Inactivation in Mouse. Methods in Molecular Biology, 2018, 1861, 205-219.	0.9	5
710	Genome-wide DNA methylation profiles of porcine ovaries in estrus and proestrus. Physiological Genomics, 2018, 50, 714-723.	2.3	6
711	Parallel Development of Chromatin Patterns, Neuron Morphology, and Connections: Potential for Disruption in Autism. Frontiers in Neuroanatomy, 2018, 12, 70.	1.7	21

#	Article	IF	Citations
712	Diverse facets of cortical interneuron migration regulation $\hat{a} \in$ Implications of neuronal activity and epigenetics. Brain Research, 2018, 1700, 160-169.	2.2	19
713	Maintenance DNA Methyltransferase Activity in the Presence of Oxidized Forms of 5-Methylcytosine: Structural Basis for Ten Eleven Translocation-Mediated DNA Demethylation. Biochemistry, 2018, 57, 6061-6069.	2.5	23
714	Cell Type and Species-specific Patterns in Neuronal and Non-neuronal Methylomes of Human and Chimpanzee Cortices. Cerebral Cortex, 2018, 28, 3724-3739.	2.9	7
715	TET mediated epigenetic regulation of iNKT cell lineage fate choice and function. Molecular Immunology, 2018, 101, 564-573.	2.2	6
716	The Vast Complexity of the Epigenetic Landscape during Neurodevelopment: An Open Frame to Understanding Brain Function. International Journal of Molecular Sciences, 2018, 19, 1333.	4.1	10
717	Genome-wide distribution of linker histone H1.0 is independent of MeCP2. Nature Neuroscience, 2018, 21, 794-798.	14.8	29
718	5-Hydroxymethylcytosine alterations in the human postmortem brains of autism spectrum disorder. Human Molecular Genetics, 2018, 27, 2955-2964.	2.9	28
719	DNA methylation landscape of the genes regulating D-serine and D-aspartate metabolism in post-mortem brain from controls and subjects with schizophrenia. Scientific Reports, 2018, 8, 10163.	3.3	29
720	CD4 <sup>+</sup> and CD8 <sup>+</sup> Tâ€Cellâ€Specific DNA Cytosine Methylation Differences Associated With Obesity. Obesity, 2018, 26, 1312-1321.	3.0	4
721	Aging and Disease., 2018,, 935-973.		1
722	Progress in Epigenetics of Depression. Progress in Molecular Biology and Translational Science, 2018, 157, 41-66.	1.7	65
723	Epigenetic Landscapes of the Adversity-Exposed Brain. Progress in Molecular Biology and Translational Science, 2018, 157, 1-19.	1.7	10
724	Emerging Role of Epigenetics in Human Neurodevelopmental Disorders. , 2018, , 269-304.		1
725	Exposure to environmental enrichment attenuates addiction-like behavior and alters molecular effects of heroin self-administration in rats. Neuropharmacology, 2018, 139, 26-40.	4.1	34
726	Epigenetic analysis of human postmortem brain tissue. Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn, 2018, 150, 237-261.	1.8	3
727	The Epigenetics of Early Life Adversity: Current Limitations and Possible Solutions. Progress in Molecular Biology and Translational Science, 2018, 157, 343-425.	1.7	31
728	Chronic social stress induces DNA methylation changes at an evolutionary conserved intergenic region in chromosome X. Epigenetics, 2018, 13, 627-641.	2.7	25
729	Physiology of Astroglia. Physiological Reviews, 2018, 98, 239-389.	28.8	1,044

#	ARTICLE	IF	CITATIONS
730	DNA methylation analysis on purified neurons and glia dissects age and Alzheimer's disease-specific changes in the human cortex. Epigenetics and Chromatin, 2018, 11, 41.	3.9	173
731	From 1D sequence to 3D chromatin dynamics and cellular functions: a phase separation perspective. Nucleic Acids Research, 2018, 46, 9367-9383.	14.5	51
732	Epigenetic Programming Effects of Early Life Stress: A Dual-Activation Hypothesis. Current Genomics, 2018, 19, 638-652.	1.6	19
733	Central Neuroepigenetic Regulation of the Hypothalamic–Pituitary–Adrenal Axis. Progress in Molecular Biology and Translational Science, 2018, 158, 105-127.	1.7	13
734	Sleep Deprivation and the Epigenome. Frontiers in Neural Circuits, 2018, 12, 14.	2.8	70
735	DNA-Methylation: Master or Slave of Neural Fate Decisions?. Frontiers in Neuroscience, 2018, 12, 5.	2.8	59
736	The Role of Activity-Dependent DNA Demethylation in the Adult Brain and in Neurological Disorders. Frontiers in Molecular Neuroscience, 2018, 11, 169.	2.9	45
737	The Methylome of Vertebrate Sex Chromosomes. Genes, 2018, 9, 230.	2.4	10
738	Dosage compensation and DNA methylation landscape of the X chromosome in mouse liver. Scientific Reports, 2018, 8, 10138.	3.3	38
739	DNA Methyltransferases, DNA Methylation, and Age-Associated Cognitive Function. International Journal of Molecular Sciences, 2018, 19, 1315.	4.1	105
740	DMRcaller: a versatile R/Bioconductor package for detection and visualization of differentially methylated regions in CpG and non-CpG contexts. Nucleic Acids Research, 2018, 46, e114.	14.5	66
741	A Lexicon of DNA Modifications: Their Roles in Embryo Development and the Germline. Frontiers in Cell and Developmental Biology, 2018, 6, 24.	3.7	16
742	Substantial Epigenetic Variation Causing Flower Color Chimerism in the Ornamental Tree Prunus mume Revealed by Single Base Resolution Methylome Detection and Transcriptome Sequencing. International Journal of Molecular Sciences, 2018, 19, 2315.	4.1	17
743	Chromatin-dependent allosteric regulation of DNMT3A activity by MeCP2. Nucleic Acids Research, 2018, 46, 9044-9056.	14.5	34
744	DNA methylation associated with healthy aging of elderly twins. GeroScience, 2018, 40, 469-484.	4.6	38
745	Diesel exhaust and house dust mite allergen lead to common changes in the airway methylome and hydroxymethylome. Environmental Epigenetics, 2018, 4, dvy020.	1.8	37
746	Hypersensitive quantification of global 5-hydroxymethylcytosine by chemoenzymatic tagging. Analytica Chimica Acta, 2018, 1038, 87-96.	5.4	22
747	Single-base resolution methylome analysis shows epigenetic changes in Arabidopsis seedlings exposed to microgravity spaceflight conditions on board the SJ-10 recoverable satellite. Npj Microgravity, 2018, 4, 12.	3.7	22

#	ARTICLE	IF	CITATIONS
748	DNA methylation reprogramming of functional elements during mammalian embryonic development. Cell Discovery, 2018, 4, 41.	6.7	51
749	DNA Methylation in Eukaryotes: Regulation and Function. , 2018, , 509-570.		0
750	A modular dCas9-SunTag DNMT3A epigenome editing system overcomes pervasive off-target activity of direct fusion dCas9-DNMT3A constructs. Genome Research, 2018, 28, 1193-1206.	5 <b>.</b> 5	123
751	Epigenetic mechanisms underlying nervous system diseases. Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn, 2018, 147, 43-58.	1.8	40
752	Neuroepigenetics of Schizophrenia. Progress in Molecular Biology and Translational Science, 2018, 158, 195-226.	1.7	20
<b>7</b> 53	Epigenetic Regulation in Neurodegenerative Diseases. Trends in Neurosciences, 2018, 41, 587-598.	8.6	248
754	Aging in the Brain: New Roles of Epigenetics in Cognitive Decline. Neuroscientist, 2018, 24, 516-525.	3.5	73
755	Epigenetics and Early Life Adversity: Current Evidence and Considerations for Epigenetic Studies in the Context of Child Maltreatment. Child Maltreatment Solutions Network, 2018, , 89-119.	0.4	3
756	An Epigenetic Spin to ALS and FTD. Advances in Neurobiology, 2018, 20, 1-29.	1.8	5
757	Linking genetics to epigenetics: The role of folate and folateâ€related pathways in neurodevelopmental disorders. Clinical Genetics, 2019, 95, 241-252.	2.0	32
758	Molecular windows into the human brain for psychiatric disorders. Molecular Psychiatry, 2019, 24, 653-673.	7.9	32
759	gemBS: high throughput processing for DNA methylation data from bisulfite sequencing. Bioinformatics, 2019, 35, 737-742.	4.1	39
760	Somatic mutations in the human brain: implications for psychiatric research. Molecular Psychiatry, 2019, 24, 839-856.	7.9	29
761	The diverse roles of DNA methylation in mammalian development and disease. Nature Reviews Molecular Cell Biology, 2019, 20, 590-607.	37.0	1,269
762	Differential olfactory bulb methylation and hydroxymethylation are linked to odor location memory bias in injured mice. Molecular Pain, 2019, 15, 174480691987347.	2.1	6
763	Epigenomic reprogramming of caloric restriction on aging. , 2019, , 251-267.		0
764	Analysis of genome-wide in cell free DNA methylation: progress and prospect. Analyst, The, 2019, 144, 5912-5922.	3.5	13
765	Global DNA Methylation Patterns in Human Gliomas and Their Interplay with Other Epigenetic Modifications. International Journal of Molecular Sciences, 2019, 20, 3478.	4.1	35

#	Article	IF	CITATIONS
766	Cell type-specific epigenetic links to schizophrenia risk in the brain. Genome Biology, 2019, 20, 135.	8.8	76
767	DNA hypermethylation in disease: mechanisms and clinical relevance. Epigenetics, 2019, 14, 1141-1163.	2.7	221
768	Plasticity at the DNA recognition site of the MeCP2 mCG-binding domain. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2019, 1862, 194409.	1.9	18
769	TET1 regulates fibroblast growth factor 8 transcription in gonadotropin releasing hormone neurons. PLoS ONE, 2019, 14, e0220530.	2.5	9
770	Somatic mutation: The hidden genetics of brain malformations and focal epilepsies. Epilepsy Research, 2019, 155, 106161.	1.6	45
771	Epigenetic signatures of Werner syndrome occur early in life and are distinct from normal epigenetic aging processes. Aging Cell, 2019, 18, e12995.	6.7	27
772	Different epigenetic clocks reflect distinct pathophysiological features of multiple sclerosis. Epigenomics, 2019, 11, 1429-1439.	2.1	22
773	Early-life DNA methylation profiles are indicative of age-related transcriptome changes. Epigenetics and Chromatin, 2019, 12, 58.	3.9	22
774	The Emergent-Context Emergent-Input Framework for Temporal Processing., 2019,,.		3
775	Nextâ€generation disease modeling with direct conversion: a new path to old neurons. FEBS Letters, 2019, 593, 3316-3337.	2.8	38
776	Genome Editing in Plants: Exploration of Technological Advancements and Challenges. Cells, 2019, 8, 1386.	4.1	115
777	Reprogramming of DNA methylation at NEUROD2-bound sequences during cortical neuron differentiation. Science Advances, 2019, 5, eaax0080.	10.3	32
778	Virtual methylome dissection facilitated by single-cell analyses. Epigenetics and Chromatin, 2019, 12, 66.	3.9	4
779	Selective demethylation of two CpG sites causes postnatal activation of the Dao gene and consequent removal of d-serine within the mouse cerebellum. Clinical Epigenetics, 2019, 11, 149.	4.1	22
780	Differences in DNA Methylation Between Disease-Resistant and Disease-Susceptible Chinese Tongue Sole (Cynoglossus semilaevis) Families. Frontiers in Genetics, 2019, 10, 847.	2.3	21
781	Epigenetic signatures of methylated DNA cytosine in Alzheimer's disease. Science Advances, 2019, 5, eaaw2880.	10.3	39
782	EGR1 recruits TET1 to shape the brain methylome during development and upon neuronal activity. Nature Communications, 2019, 10, 3892.	12.8	95
783	Epigenetics of the Synapse in Neurodegeneration. Current Neurology and Neuroscience Reports, 2019, 19, 72.	4.2	19

#	Article	IF	Citations
784	DNA methyltransferase isoforms expression in the temporal lobe of epilepsy patients with a history of febrile seizures. Clinical Epigenetics, 2019, 11, 118.	4.1	14
785	Tamoxifen induction of Cre recombinase does not cause long-lasting or sexually divergent responses in the CNS epigenome or transcriptome: implications for the design of aging studies. GeroScience, 2019, 41, 691-708.	4.6	20
786	Simultaneous profiling of 3D genome structure and DNA methylation in single human cells. Nature Methods, 2019, 16, 999-1006.	19.0	200
787	Epigenetic Delay in the Neurodevelopmental Trajectory of DNA Methylation States in Autism Spectrum Disorders. Frontiers in Genetics, 2019, 10, 907.	2.3	30
788	Cell type-specific transcriptional programs in mouse prefrontal cortex during adolescence and addiction. Nature Communications, 2019, 10, 4169.	12.8	100
789	A Novel Application of Mixed Effects Models for Reconciling Base-Pair Resolution 5-Methylcytosine and 5-Hydroxymethylcytosine Data in Neuroepigenetics. Frontiers in Genetics, 2019, 10, 801.	2.3	8
790	Base-Resolution Methylome of Retinal Pigment Epithelial Cells Used in the First Trial of Human Induced Pluripotent Stem Cell-Based Autologous Transplantation. Stem Cell Reports, 2019, 13, 761-774.	4.8	20
791	Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons. ELife, 2019, 8, .	6.0	64
792	Genome-Wide Alteration of 5-Hydroxymethylcytosine in Hypoxic-Ischemic Neonatal Rat Model of Cerebral Palsy. Frontiers in Molecular Neuroscience, 2019, 12, 214.	2.9	8
793	Divergent neuronal DNA methylation patterns across human cortical development reveal critical periods and a unique role of CpH methylation. Genome Biology, 2019, 20, 196.	8.8	67
794	Enhancer DNA methylation: implications for gene regulation. Essays in Biochemistry, 2019, 63, 707-715.	4.7	100
795	The isolation and molecular characterization of cerebral microvessels. Nature Protocols, 2019, 14, 3059-3081.	12.0	71
796	The distinct methylation landscape of maturing neurons and its role in Rett syndrome pathogenesis. Current Opinion in Neurobiology, 2019, 59, 180-188.	4.2	22
797	MeCP2: A Critical Regulator of Chromatin in Neurodevelopment and Adult Brain Function. International Journal of Molecular Sciences, 2019, 20, 4577.	4.1	39
798	ME-Class2 reveals context dependent regulatory roles for 5-hydroxymethylcytosine. Nucleic Acids Research, 2019, 47, e28-e28.	14.5	6
799	Adolescent Alcohol Exposure Epigenetically Suppresses Amygdala Arc Enhancer RNA Expression to Confer Adult Anxiety Susceptibility. Biological Psychiatry, 2019, 85, 904-914.	1.3	62
800	DNA Methylation and Susceptibility to Autism Spectrum Disorder. Annual Review of Medicine, 2019, 70, 151-166.	12.2	79
801	The contribution of active and passive mechanisms of 5mC and 5hmC removal in human T lymphocytes is differentiation―and activationâ€dependent. European Journal of Immunology, 2019, 49, 611-625.	2.9	16

#	Article	IF	CITATIONS
802	Dynamic Methylation of an L1 Transduction Family during Reprogramming and Neurodifferentiation. Molecular and Cellular Biology, 2019, 39, .	2.3	22
803	Cerebral Cortex Generated from Pluripotent Stem Cells to Model Corticogenesis and Rebuild Cortical Circuits: In Vitro Veritas?. Stem Cells and Development, 2019, 28, 361-369.	2.1	8
804	Maternal immune activation impairs cognitive flexibility and alters transcription in frontal cortex. Neurobiology of Disease, 2019, 125, 211-218.	4.4	41
805	Evolutionary transition between invertebrates and vertebrates via methylation reprogramming in embryogenesis. National Science Review, 2019, 6, 993-1003.	9.5	58
806	Comparative RNA-Sequencing and DNA Methylation Analyses of Apple ( <i>Malus domestica</i> Buds with Diverse Flowering Capabilities Reveal Novel Insights into the Regulatory Mechanisms of Flower Bud Formation. Plant and Cell Physiology, 2019, 60, 1702-1721.	3.1	27
807	Pharmacoepigenetics and Toxicoepigenetics in Neurodevelopmental Disorders., 2019,, 711-719.		0
808	Single-Cell Multi-omic Integration Compares and Contrasts Features of Brain Cell Identity. Cell, 2019, 177, 1873-1887.e17.	28.9	844
809	Neuronal methylome reveals CREB-associated neuro-axonal impairment in multiple sclerosis. Clinical Epigenetics, 2019, 11, 86.	4.1	24
810	Genetic and epigenetic influences on the phenotype of Rett syndrome. , 2019, , 183-217.		1
811	Chromatin and epigenetic signaling pathways. , 2019, , 1-23.		0
812	Insights Into the Epigenetics of Retinal Development and Diseases., 2019, , 355-383.		1
813	MeCP2: an epigenetic regulator of critical periods. Current Opinion in Neurobiology, 2019, 59, 95-101.	4.2	31
814	Sex Differences in the Epigenome: A Cause or Consequence of Sexual Differentiation of the Brain?. Genes, 2019, 10, 432.	2.4	38
815	Epigenetic dysregulation of enhancers in neurons is associated with Alzheimer's disease pathology and cognitive symptoms. Nature Communications, 2019, 10, 2246.	12.8	160
816	Recursive Motif Analyses Identify Brain Epigenetic Transcription Regulatory Modules. Computational and Structural Biotechnology Journal, 2019, 17, 507-515.	4.1	8
817	HOME: a histogram based machine learning approach for effective identification of differentially methylated regions. BMC Bioinformatics, 2019, 20, 253.	2.6	45
818	Structural basis for preferential binding of human TCF4 to DNA containing 5-carboxylcytosine. Nucleic Acids Research, 2019, 47, 8375-8387.	14.5	19
819	TET1 contributes to allergic airway inflammation and regulates interferon and aryl hydrocarbon receptor signaling pathways in bronchial epithelial cells. Scientific Reports, 2019, 9, 7361.	3.3	28

#	Article	IF	CITATIONS
820	Shaping the human brain: evolutionary cis-regulatory plasticity drives changes in synaptic activity-controlled adaptive gene expression. Current Opinion in Neurobiology, 2019, 59, 34-40.	4.2	4
821	The Yin and Yang of Arnt2 in Activity-Dependent Transcription. Neuron, 2019, 102, 270-272.	8.1	1
822	A DNMT3A PWWP mutation leads to methylation of bivalent chromatin and growth retardation in mice. Nature Communications, 2019, 10, 1884.	12.8	71
823	Age, but Not Amyloidosis, Induced Changes in Global Levels of Histone Modifications in Susceptible and Disease-Resistant Neurons in Alzheimer's Disease Model Mice. Frontiers in Aging Neuroscience, 2019, 11, 68.	3.4	12
824	Identification and sequencing of the gene encoding DNA methyltransferase 3 (DNMT3) from sea cucumber, Apostichopus japonicus. Molecular Biology Reports, 2019, 46, 3791-3800.	2.3	2
825	Epigenetic Changes in Cultures: Neurons and Astrocytes. Neuromethods, 2019, , 119-139.	0.3	0
826	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. Nature Communications, 2019, 10, 1749.	12.8	46
827	Epigenetic Regulations in Neuropsychiatric Disorders. Frontiers in Genetics, 2019, 10, 268.	2.3	116
828	CpG and Non-CpG Methylation in the Diet–Epigenetics–Neurodegeneration Connection. Current Nutrition Reports, 2019, 8, 74-82.	<b>4.</b> 3	26
829	ARNT2 Tunes Activity-Dependent Gene Expression through NCoR2-Mediated Repression and NPAS4-Mediated Activation. Neuron, 2019, 102, 390-406.e9.	8.1	35
830	Defining the Role of Nucleotide Flipping in Enzyme Specificity Using 19F NMR. Journal of the American Chemical Society, 2019, 141, 4952-4962.	13.7	23
831	Global Methylomic and Transcriptomic Analyses Reveal the Broad Participation of DNA Methylation in Daily Gene Expression Regulation of Populus trichocarpa. Frontiers in Plant Science, 2019, 10, 243.	3.6	21
832	The bZIP mutant CEBPB (V285A) has sequence specific DNA binding propensities similar to CREB1. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2019, 1862, 486-492.	1.9	3
833	Extensive Recovery of Embryonic Enhancer and Gene Memory Stored in Hypomethylated Enhancer DNA. Molecular Cell, 2019, 74, 542-554.e5.	9.7	65
834	Developmental Dieldrin Exposure Alters DNA Methylation at Genes Related to Dopaminergic Neuron Development and Parkinson's Disease in Mouse Midbrain. Toxicological Sciences, 2019, 169, 593-607.	3.1	33
835	Increased intron retention is a postâ€transcriptional signature associated with progressive aging and Alzheimer's disease. Aging Cell, 2019, 18, e12928.	6.7	80
836	Epigenetic modification: a regulatory mechanism in essential hypertension. Hypertension Research, 2019, 42, 1099-1113.	2.7	57
837	Does Gender Leave an Epigenetic Imprint on the Brain?. Frontiers in Neuroscience, 2019, 13, 173.	2.8	33

#	Article	IF	Citations
838	Histone Deacetylase Inhibitors as Multitarget Ligands: New Players in Alzheimer's Disease Drug Discovery?. ChemMedChem, 2019, 14, 1067-1073.	3.2	48
839	Evolution of Brain Connections: Integrating Diffusion MR Tractography With Gene Expression Highlights Increased Corticocortical Projections in Primates. Cerebral Cortex, 2019, 29, 5150-5165.	2.9	12
840	Hypomethylation at non-CpG/CpG sites in the promoter of HIF- $1\hat{l}\pm$ gene combined with enhanced H3K9Ac modification contribute to maintain higher HIF- $1\hat{l}\pm$ expression in breast cancer. Oncogenesis, 2019, 8, 26.	4.9	22
841	Stress Marks on the Genome: Use or Lose?. International Journal of Molecular Sciences, 2019, 20, 364.	4.1	23
842	Retinal-input-induced epigenetic dynamics in the developing mouse dorsal lateral geniculate nucleus. Epigenetics and Chromatin, 2019, 12, 13.	3.9	6
843	Bisulfite-free direct detection of 5-methylcytosine and 5-hydroxymethylcytosine at base resolution. Nature Biotechnology, 2019, 37, 424-429.	17.5	267
844	The DNA modification N6-methyl-2'-deoxyadenosine (m6dA) drives activity-induced gene expression and is required for fear extinction. Nature Neuroscience, 2019, 22, 534-544.	14.8	51
845	DNA (Hydroxy)Methylation in T Helper Lymphocytes. Trends in Biochemical Sciences, 2019, 44, 589-598.	7.5	6
846	The DNA methylation landscape in cancer. Essays in Biochemistry, 2019, 63, 797-811.	4.7	169
847	BEST: a web server for brain expression Spatio-temporal pattern analysis. BMC Bioinformatics, 2019, 20, 632.	2.6	13
848	Active Demethylation of Non-CpG Moieties in Animals: A Neglected Research Area. International Journal of Molecular Sciences, 2019, 20, 6272.	4.1	6
849	Integrated Epigenome, Exome, and Transcriptome Analyses Reveal Molecular Subtypes and Homeotic Transformation in Uterine Fibroids. Cell Reports, 2019, 29, 4069-4085.e6.	6.4	49
850	DNA methylation in AgRP neurons regulates voluntary exercise behavior in mice. Nature Communications, 2019, 10, 5364.	12.8	26
851	Neuronal and glial DNA methylation and gene expression changes in early epileptogenesis. PLoS ONE, 2019, 14, e0226575.	2.5	22
852	Epigenome-wide meta-analysis of blood DNA methylation and its association with subcortical volumes: findings from the ENIGMA Epigenetics Working Group. Molecular Psychiatry, 2021, 26, 3884-3895.	7.9	34
853	Selection-Corrected Statistical Inference for Region Detection With High-Throughput Assays. Journal of the American Statistical Association, 2019, 114, 1351-1365.	3.1	2
854	Children's biobehavioral reactivity to challenge predicts DNA methylation in adolescence and emerging adulthood. Developmental Science, 2019, 22, e12739.	2.4	6
855	Neuroepigenetics and addictive behaviors: Where do we stand?. Neuroscience and Biobehavioral Reviews, 2019, 106, 58-72.	6.1	27

#	Article	IF	CITATIONS
856	Like father like daughter: sex-specific parent-of-origin effects in the transmission of liability for psychotic symptoms to offspring. Journal of Developmental Origins of Health and Disease, 2019, 10, 100-107.	1.4	9
857	Structural basis for effects of CpA modifications on C/EBP $\hat{l}^2$ binding of DNA. Nucleic Acids Research, 2019, 47, 1774-1785.	14.5	23
858	Epigenetic Tools in Chronic Pain Studies. , 2019, , 1-48.		0
859	Perinatal exposure to the SSRI paroxetine alters the methylome landscape of the developing dentate gyrus. European Journal of Neuroscience, 2019, 50, 1843-1870.	2.6	12
860	DNA methyltransferase <i>BmDnmt1</i> and <i>BmDnmt2</i> in silkworm ( <i>Bombyx mori</i> ) and the regulation of silkworm embryonic development. Archives of Insect Biochemistry and Physiology, 2019, 100, e21529.	1.5	13
861	Adverse neuropsychiatric development following perinatal brain injury: from a preclinical perspective. Pediatric Research, 2019, 85, 198-215.	2.3	11
862	Clinical epigenetics: seizing opportunities for translation. Nature Reviews Genetics, 2019, 20, 109-127.	16.3	353
863	Early life stress and voluntary alcohol consumption in relation to Maoa methylation in male rats. Alcohol, 2019, 79, 7-16.	1.7	16
864	Exogenous adrenocorticotropic hormone affects genomeâ€wide DNA methylation and transcriptome of corpus luteum in sows. FASEB Journal, 2019, 33, 3264-3278.	0.5	6
865	Neuronal brain-region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric trait heritability. Nature Neuroscience, 2019, 22, 307-316.	14.8	120
866	Early-life epigenetic changes along the corticotropin-releasing hormone (CRH) gene influence resilience or vulnerability to heat stress later in life. Molecular Psychiatry, 2019, 24, 1013-1026.	7.9	37
867	Epigenetics in eating disorders: a systematic review. Molecular Psychiatry, 2019, 24, 901-915.	7.9	63
868	Perspectives on defining cell types in the brain. Current Opinion in Neurobiology, 2019, 56, 61-68.	4.2	44
869	A Novel Mecp2Y120D Knock-in Model Displays Similar Behavioral Traits But Distinct Molecular Features Compared to the Mecp2-Null Mouse Implying Precision Medicine for the Treatment of Rett Syndrome. Molecular Neurobiology, 2019, 56, 4838-4854.	4.0	19
870	DNA methylation correlates of PTSD: Recent findings and technical challenges. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2019, 90, 223-234.	4.8	28
871	It is a complex issue: emerging connections between epigenetic regulators in drug addiction. European Journal of Neuroscience, 2019, 50, 2477-2491.	2.6	16
872	Epigenetic cues modulating the generation of cellâ€type diversity in the cerebral cortex. Journal of Neurochemistry, 2019, 149, 12-26.	3.9	19
873	Detecting differential DNA methylation from sequencing of bisulfite converted DNA of diverse species. Briefings in Bioinformatics, 2019, 20, 33-46.	6.5	17

#	Article	IF	CITATIONS
874	Schizophrenia risk variants influence multiple classes of transcripts of sorting nexin 19 (SNX19). Molecular Psychiatry, 2020, 25, 831-843.	7.9	36
875	Epigenetic mechanisms related to cognitive decline during aging. Journal of Neuroscience Research, 2020, 98, 234-246.	2.9	50
876	Prenatal exposure to environmental insults and enhanced risk of developing Schizophrenia and Autism Spectrum Disorder: focus on biological pathways and epigenetic mechanisms. Neuroscience and Biobehavioral Reviews, 2020, 117, 253-278.	6.1	88
877	Sevoflurane Exposure Results in Sex-Specific Transgenerational Upregulation of Target IEGs in the Subiculum. Molecular Neurobiology, 2020, 57, 11-22.	4.0	26
878	Mechanisms of early placental development in mouse and humans. Nature Reviews Genetics, 2020, 21, 27-43.	16.3	274
879	Biological embedding of experience: A primer on epigenetics. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23261-23269.	7.1	148
880	Developmental changes and sex differences in DNA methylation and demethylation in hypothalamic regions of the mouse brain. Epigenetics, 2020, 15, 72-84.	2.7	40
881	Chronic Ethanol Exposure Alters DNA Methylation in Neural Stem Cells: Role of Mouse Strain and Sex. Molecular Neurobiology, 2020, 57, 650-667.	4.0	28
882	Singleâ€base methylome profiling of the giant kelp <i>Saccharina japonica</i> reveals significant differences in DNA methylation to microalgae and plants. New Phytologist, 2020, 225, 234-249.	7.3	38
883	DNA Methylation in Epidermal Differentiation, Aging, and Cancer. Journal of Investigative Dermatology, 2020, 140, 38-47.	0.7	54
884	Age-related DNA hydroxymethylation is enriched for gene expression and immune system processes in human peripheral blood. Epigenetics, 2020, 15, 294-306.	2.7	8
885	Possible involvement of DNA methylation in hippocampal synaptophysin gene expression during postnatal development of mice. Neurochemistry International, 2020, 132, 104587.	3.8	5
886	Stress and its effects across generations. , 2020, , 269-290.		4
887	Evolution of DNA Methylome Diversity in Eukaryotes. Journal of Molecular Biology, 2020, 432, 1687-1705.	4.2	82
888	The Molecular Basis of MeCP2 Function in the Brain. Journal of Molecular Biology, 2020, 432, 1602-1623.	4.2	89
889	Epigenetic mechanism in search for the pathomechanism of diabetic neuropathy development in diabetes mellitus type 1 (T1DM). Endocrine, 2020, 68, 235-240.	2.3	14
890	DNA Methylation Readers in Plants. Journal of Molecular Biology, 2020, 432, 1706-1717.	4.2	18
891	DNA Modification Readers and Writers and Their Interplay. Journal of Molecular Biology, 2020, 432, 1731-1746.	4.2	48

#	Article	IF	CITATIONS
892	Identification and functional characterization of methyl-CpG binding domain protein from Tribolium castaneum. Genomics, 2020, 112, 2223-2232.	2.9	12
893	Precision Medicine in Neurodegenerative Diseases: Some Promising Tips Coming from the microRNAs' World. Cells, 2020, 9, 75.	4.1	10
894	Neurobiological functions of transcriptional enhancers. Nature Neuroscience, 2020, 23, 5-14.	14.8	83
895	MBD-seq - realities of a misunderstood method for high-quality methylome-wide association studies. Epigenetics, 2020, 15, 431-438.	2.7	17
896	Memory and neuromodulation: A perspective of DNA methylation. Neuroscience and Biobehavioral Reviews, 2020, 111, 57-68.	6.1	15
897	Discovery of a new predominant cytosine DNA modification that is linked to gene expression in malaria parasites. Nucleic Acids Research, 2020, 48, 184-199.	14.5	24
898	Neonatal Inhibition of DNA Methylation Disrupts Testosterone-Dependent Masculinization of Neurochemical Phenotype. Endocrinology, 2020, $161$ , .	2.8	21
899	Alteration of the brain methylation landscape following postnatal inflammatory injury in rat pups. FASEB Journal, 2020, 34, 432-445.	0.5	17
900	MeCP2 Represses the Rate of Transcriptional Initiation of Highly Methylated Long Genes. Molecular Cell, 2020, 77, 294-309.e9.	9.7	72
901	MeCP2 Represses Enhancers through Chromosome Topology-Associated DNA Methylation. Molecular Cell, 2020, 77, 279-293.e8.	9.7	49
902	Dioxin Disrupts Dynamic DNA Methylation Patterns in Genes That Govern Cardiomyocyte Maturation. Toxicological Sciences, 2020, 178, 325-337.	3.1	7
903	Transgenerational accumulation of methylome changes discovered in commercially reared honey bee (Apis mellifera) queens. Insect Biochemistry and Molecular Biology, 2020, 127, 103476.	2.7	4
904	Selective loss of 5hmC promotes neurodegeneration in the mouse model of Alzheimer's disease. FASEB Journal, 2020, 34, 16364-16382.	0.5	29
905	Suppression of DNA Double-Strand Break Formation by DNA Polymerase $\hat{l}^2$ in Active DNA Demethylation Is Required for Development of Hippocampal Pyramidal Neurons. Journal of Neuroscience, 2020, 40, 9012-9027.	3.6	5
906	Characterization of universal features of partially methylated domains across tissues and species. Epigenetics and Chromatin, 2020, 13, 39.	3.9	16
907	Quantitative analysis questions the role of MeCP2 as a global regulator of alternative splicing. PLoS Genetics, 2020, 16, e1009087.	3.5	10
908	Reliable tumor detection by whole-genome methylation sequencing of cell-free DNA in cerebrospinal fluid of pediatric medulloblastoma. Science Advances, 2020, 6, .	10.3	42
909	Emerging Insights into the Distinctive Neuronal Methylome. Trends in Genetics, 2020, 36, 816-832.	6.7	22

#	Article	IF	CITATIONS
910	Gender-Affirming Hormone Therapy Modifies the CpG Methylation Pattern of the ESR1 Gene Promoter After Six Months of Treatment in Transmen. Journal of Sexual Medicine, 2020, 17, 1795-1806.	0.6	13
911	Epigenomic programming in early fetal brain development. Epigenomics, 2020, 12, 1053-1070.	2.1	9
912	Analysis of DNA methylation using pyrosequencing. , 2020, , 37-62.		3
913	<scp>TCF</scp> 20 dysfunction leads to cortical neurogenesis defects and autisticâ€like behaviors in mice. EMBO Reports, 2020, 21, e49239.	4.5	16
914	Inducible cell-specific mouse models for paired epigenetic and transcriptomic studies of microglia and astroglia. Communications Biology, 2020, 3, 693.	4.4	27
915	A map of cis-regulatory elements and 3D genome structures in zebrafish. Nature, 2020, 588, 337-343.	27.8	80
916	DNMT3A Haploinsufficiency Results in Behavioral Deficits and Global Epigenomic Dysregulation Shared across Neurodevelopmental Disorders. Cell Reports, 2020, 33, 108416.	6.4	37
917	A human tissue map of 5-hydroxymethylcytosines exhibits tissue specificity through gene and enhancer modulation. Nature Communications, 2020, 11, 6161.	12.8	76
918	Developmental remodelling of non-CG methylation at satellite DNA repeats. Nucleic Acids Research, 2020, 48, 12675-12688.	14.5	17
919	Epigenetics and Heart Failure. International Journal of Molecular Sciences, 2020, 21, 9010.	4.1	10
920	Epigenetics of Muscle- and Brain-Specific Expression of KLHL Family Genes. International Journal of Molecular Sciences, 2020, 21, 8394.	4.1	14
921	Genome-Wide Differential DNA Methylation and miRNA Expression Profiling Reveals Epigenetic Regulatory Mechanisms Underlying Nitrogen-Limitation-Triggered Adaptation and Use Efficiency Enhancement in Allotetraploid Rapeseed. International Journal of Molecular Sciences, 2020, 21, 8453.	4.1	10
922	DNA Methyltransferase 1 (DNMT1) Acts on Neurodegeneration by Modulating Proteostasis-Relevant Intracellular Processes. International Journal of Molecular Sciences, 2020, 21, 5420.	4.1	14
923	Epigenomic Dysregulation in Schizophrenia: In Search of Disease Etiology and Biomarkers. Cells, 2020, 9, 1837.	4.1	55
924	Leveraging epigenetics to examine differences in developmental trajectories of social attention: A proof-of-principle study of DNA methylation in infants with older siblings with autism., 2020, 60, 101409.		10
925	The Role of Epigenetic Dysregulation in Suicidal Behaviors. Current Topics in Behavioral Neurosciences, 2020, 46, 41-61.	1.7	5
926	Role of environmental factors and epigenetics in autism spectrum disorders. Progress in Molecular Biology and Translational Science, 2020, 173, 35-60.	1.7	22
927	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. Nature, 2020, 583, 752-759.	27.8	84

#	Article	IF	CITATIONS
928	RGS6 Mediates Effects of Voluntary Running on Adult Hippocampal Neurogenesis. Cell Reports, 2020, 32, 107997.	6.4	19
929	Recent advancements in understanding the role of epigenetics in the auditory system. Gene, 2020, 761, 144996.	2.2	12
930	Thyroid Hormone Induces DNA Demethylation in <i>Xenopus</i> Tadpole Brain. Endocrinology, 2020, 161, .	2.8	14
931	Cell Reprogramming Preserving Epigenetic Age: Advantages and Limitations. Biochemistry (Moscow), 2020, 85, 1035-1047.	1.5	7
932	Existence and possible roles of independent non-CpG methylation in the mammalian brain. DNA Research, 2020, 27, .	3.4	10
933	Tumor Necrosis Factor α Influences Phenotypic Plasticity and Promotes Epigenetic Changes in Human Basal Forebrain Cholinergic Neuroblasts. International Journal of Molecular Sciences, 2020, 21, 6128.	4.1	17
934	Contiguous and stochastic CHH methylation patterns of plant DRM2 and CMT2 revealed by single-read methylome analysis. Genome Biology, 2020, 21, 194.	8.8	15
935	A conceptual framework for plasticity in the developing brain. Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn, 2020, 173, 57-66.	1.8	1
936	Epigenomic analysis of Parkinson's disease neurons identifies Tet2 loss as neuroprotective. Nature Neuroscience, 2020, 23, 1203-1214.	14.8	57
937	Epigenetics modifiers: potential hub for understanding and treating neurodevelopmental disorders from hypoxic injury. Journal of Neurodevelopmental Disorders, 2020, 12, 37.	3.1	9
938	Exposure to different early-life stress experiences results in differentially altered DNA methylation in the brain and immune system. Neurobiology of Stress, 2020, 13, 100249.	4.0	30
939	Transposable Elements: A Common Feature of Neurodevelopmental and Neurodegenerative Disorders. Trends in Genetics, 2020, 36, 610-623.	6.7	64
940	DNA methylation dynamics underlie metamorphic gene regulation programs in Xenopus tadpole brain. Developmental Biology, 2020, 462, 180-196.	2.0	9
941	Genetic and epigenetic <i>MTHFR</i> gene variants in the mothers of attention-deficit/hyperactivity disorder affected children as possible risk factors for neurodevelopmental disorders. Epigenomics, 2020, 12, 813-823.	2.1	2
942	Deciphering the Enigma of the Histone H2A.Z-1/H2A.Z-2 Isoforms: Novel Insights and Remaining Questions. Cells, 2020, 9, 1167.	4.1	7
943	TET2-mediated Cdkn2A DNA hydroxymethylation in midbrain dopaminergic neuron injury of Parkinson's disease. Human Molecular Genetics, 2020, 29, 1239-1252.	2.9	21
944	Brain Wiring and Supragranular-Enriched Genes Linked to Protracted Human Frontal Cortex Development. Cerebral Cortex, 2020, 30, 5654-5666.	2.9	11
945	DEMETER-mediated DNA Demethylation in Gamete Companion Cells and the Endosperm, and its Possible Role in Embryo Development in Arabidopsis. Journal of Plant Biology, 2020, 63, 321-329.	2.1	6

#	Article	IF	Citations
946	Subacute cannabidiol alters genomeâ€wide <scp>DNA</scp> methylation in adult mouse hippocampus. Environmental and Molecular Mutagenesis, 2020, 61, 890-900.	2.2	19
947	Pharmacological DNA Demethylation Weakens Inhibitory Synapses in the Auditory Cortex and Re-opens the Critical Period for Frequency Map Plasticity. Neuroscience, 2020, 440, 239-248.	2.3	0
948	Genome-wide DNA Methylation Signatures Are Determined by DNMT3A/B Sequence Preferences. Biochemistry, 2020, 59, 2541-2550.	2.5	16
949	Closing the gap from transcription to the structural connectome enhances the study of connections in the human brain. Developmental Dynamics, 2020, 249, 1047-1061.	1.8	11
950	DNA Methylation-Mediated Modulation of Endocytosis as Potential Mechanism for Synaptic Function Regulation in Murine Inhibitory Cortical Interneurons. Cerebral Cortex, 2020, 30, 3921-3937.	2.9	42
951	Hemispheric asymmetry in the human brain and in Parkinson's disease is linked to divergent epigenetic patterns in neurons. Genome Biology, 2020, 21, 61.	8.8	40
952	Skewed X-Chromosome Inactivation and Compensatory Upregulation of Escape Genes Precludes Major Clinical Symptoms in a Female With a Large Xq Deletion. Frontiers in Genetics, 2020, 11, 101.	2.3	19
953	Target of Rapamycin Regulates Genome Methylation Reprogramming to Control Plant Growth in Arabidopsis. Frontiers in Genetics, 2020, 11, 186.	2.3	22
954	Epigenetics of suicidal behaviors. , 2020, , 301-323.		0
955	Environmental Pressures on Transgenerational Epigenetic Inheritance. , 2020, , 97-122.		0
956	BDNF deficiency and enriched environment treatment affect neurotransmitter gene expression differently across ages. Journal of Neurochemistry, 2020, 154, 41-55.	3.9	23
957	Epigenomic Regulatory Mechanism in Vegetative Phase Transition of <i>Malus hupehensis</i> . Journal of Agricultural and Food Chemistry, 2020, 68, 4812-4829.	5.2	10
958	An Activity-Mediated Transition in Transcription in Early Postnatal Neurons. Neuron, 2020, 107, 874-890.e8.	8.1	41
959	Exploring DNA Methylation Diversity in the Honey Bee Brain by Ultra-Deep Amplicon Sequencing. Epigenomes, 2020, 4, 10.	1.8	12
960	Identification of cell type-specific methylation signals in bulk whole genome bisulfite sequencing data. Genome Biology, 2020, 21, 156.	8.8	22
961	Gene regulatory networks controlling neuronal development. , 2020, , 699-730.		0
962	Comparative whole genome DNA methylation profiling across cattle tissues reveals global and tissue-specific methylation patterns. BMC Biology, 2020, 18, 85.	3.8	34
963	Interplay between Metabolism, Nutrition and Epigenetics in Shaping Brain DNA Methylation, Neural Function and Behavior. Genes, 2020, 11, 742.	2.4	18

#	Article	IF	CITATIONS
964	Klotho and the Treatment of Human Malignancies. Cancers, 2020, 12, 1665.	3.7	23
965	Antisense oligonucleotide modulation of non-productive alternative splicing upregulates gene expression. Nature Communications, 2020, 11, 3501.	12.8	103
966	Epigenetic regulation of neuronal cell specification inferred with single cell "Omics―data. Computational and Structural Biotechnology Journal, 2020, 18, 942-952.	4.1	6
967	Comprehensive structure-function characterization of DNMT3B and DNMT3A reveals distinctive de novo DNA methylation mechanisms. Nature Communications, 2020, 11, 3355.	12.8	94
968	DeepH&M: Estimating single-CpG hydroxymethylation and methylation levels from enrichment and restriction enzyme sequencing methods. Science Advances, 2020, 6, .	10.3	8
969	Wandering along the epigenetic timeline. Clinical Epigenetics, 2020, 12, 97.	4.1	16
970	Interactions between the combined genotypes of 5-HTTLPR and BDNF Val66Met polymorphisms and parenting on adolescent depressive symptoms: A three-year longitudinal study. Journal of Affective Disorders, 2020, 265, 104-111.	4.1	7
971	Global DNA methylation and cognitive and behavioral outcomes at 4 years of age: A crossâ€sectional study. Brain and Behavior, 2020, 10, e01579.	2.2	6
972	When function follows form: Nuclear compartment structure and the epigenetic landscape of the aging neuron. Experimental Gerontology, 2020, 133, 110876.	2.8	11
973	Absence of MeCP2 binding to non-methylated GT-rich sequences in vivo. Nucleic Acids Research, 2020, 48, 3542-3552.	14.5	10
974	Epigenetic insights into multiple sclerosis disease progression. Journal of Internal Medicine, 2020, 288, 82-102.	6.0	21
975	Epigenetics, Development, and Psychopathology. Annual Review of Clinical Psychology, 2020, 16, 327-350.	12.3	38
976	Regenerating zebrafish fin epigenome is characterized by stable lineage-specific DNA methylation and dynamic chromatin accessibility. Genome Biology, 2020, 21, 52.	8.8	44
977	Invited Review: Epigenetics in neurodevelopment. Neuropathology and Applied Neurobiology, 2020, 46, 6-27.	3.2	34
978	DNA Methylation Is Correlated with Gene Expression during Diapause Termination of Early Embryonic Development in the Silkworm (Bombyx mori). International Journal of Molecular Sciences, 2020, 21, 671.	4.1	14
979	H3K36 Methylation in Neural Development and Associated Diseases. Frontiers in Genetics, 2019, 10, 1291.	2.3	32
980	DNA methylation in Schwann cells and in oligodendrocytes. Glia, 2020, 68, 1568-1583.	4.9	10
981	Understanding the Relevance of DNA Methylation Changes in Immune Differentiation and Disease. Genes, 2020, 11, 110.	2.4	54

#	Article	IF	CITATIONS
982	Signals, epigenetics, regulation of gene expression. , 2020, , 109-138.		0
983	The Impact of Environmental Factors on 5-Hydroxymethylcytosine in the Brain. Current Environmental Health Reports, 2020, 7, 109-120.	6.7	13
984	Intellectual and Developmental Disabilities Research Centers: A Multidisciplinary Approach to Understand the Pathogenesis of Methyl-CpG Binding Protein 2-related Disorders. Neuroscience, 2020, 445, 190-206.	2.3	11
985	Genome-wide Profiling Identifies DNA Methylation Signatures of Aging in Rod Photoreceptors Associated with Alterations in Energy Metabolism. Cell Reports, 2020, 31, 107525.	6.4	20
986	A viral toolkit for recording transcription factor–DNA interactions in live mouse tissues.  Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10003-10014.	7.1	17
987	Identification of a novel Shank2 transcriptional variant in Shank2 knockout mouse model of autism spectrum disorder. Molecular Brain, 2020, 13, 54.	2.6	8
988	Cortical cellular diversity and development in schizophrenia. Molecular Psychiatry, 2021, 26, 203-217.	7.9	11
989	Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex. Epigenetics, 2021, 16, 1-13.	2.7	19
990	Effects of commercial queen rearing methods on queen fecundity and genome methylation. Apidologie, 2021, 52, 282-291.	2.0	3
991	Epigenetic mechanisms underlying enhancer modulation of neuronal identity, neuronal activity and neurodegeneration. Neurobiology of Disease, 2021, 147, 105155.	4.4	15
992	Parsing the Functional Impact of Noncoding Genetic Variants in the Brain Epigenome. Biological Psychiatry, 2021, 89, 65-75.	1.3	8
993	Epigenetic Neuropharmacology: Drugs Affecting the Epigenome in the Brain. Annual Review of Pharmacology and Toxicology, 2021, 61, 181-201.	9.4	12
994	Epigenetic regulation of cancer stem cell formation and maintenance. International Journal of Cancer, 2021, 148, 2884-2897.	5.1	37
995	Metabolomics study of cerebrospinal fluid from diabetic rats with cognitive impairment simultaneously treated with Panax quinquefolius and Acorus gramineus. Biomedical Chromatography, 2021, 35, e5041.	1.7	6
996	Epigenetic regulation of neural lineage elaboration: Implications for therapeutic reprogramming. Neurobiology of Disease, 2021, 148, 105174.	4.4	8
997	Predictive modeling of single-cell DNA methylome data enhances integration with transcriptome data. Genome Research, 2021, 31, 101-109.	5.5	12
998	Flanking sequence preference modulates <i>de novo</i> DNA methylation in the mouse genome. Nucleic Acids Research, 2021, 49, 145-157.	14.5	14
999	The Molecular Têteâ€Ãâ€₹ête between Gâ€Quadruplexes and the iâ€motif in the Human Genome. ChemBioChe 2021, 22, 1517-1537.	m 2.6	13

#	Article	IF	CITATIONS
1000	Changes in genome architecture and transcriptional dynamics progress independently of sensory experience during post-natal brain development. Cell, 2021, 184, 741-758.e17.	28.9	115
1001	DNA methylation mediates differentiation in thermal responses of Pacific oyster (Crassostrea gigas) derived from different tidal levels. Heredity, 2021, 126, 10-22.	2.6	38
1003	Brain plasticity. , 2021, , 77-98.		0
1004	The epigenetics of suicide: The critical impact of environment on epigenetic regulation in suicide. , 2021, , 393-427.		1
1005	Histone modifications, DNA methylation, and the epigenetic code of alcohol use disorder. International Review of Neurobiology, 2021, 156, 1-62.	2.0	21
1006	MeCP2: The Genetic Driver of Rett Syndrome Epigenetics. Frontiers in Genetics, 2021, 12, 620859.	2.3	67
1007	DNA methylation at birth potentially mediates the association between prenatal lead (Pb) exposure and infant neurodevelopmental outcomes. Environmental Epigenetics, 2021, 7, dvab005.	1.8	15
1009	Experience and the genome: the role of epigenetics. , 2021, , 45-75.		0
1010	TAB-seq and ACE-seq Data Processing for Genome-Wide DNA hydroxymethylation Profiling. Methods in Molecular Biology, 2021, 2272, 163-178.	0.9	2
1011	Single-Cell Sequencing of Brain Cell Transcriptomes and Epigenomes. Neuron, 2021, 109, 11-26.	8.1	135
1012	Cerebrospinal fluid liquid biopsy for detecting somatic mosaicism in brain. Brain Communications, 2021, 3, fcaa235.	3.3	42
1013	A comprehensive epigenome atlas reveals DNA methylation regulating skeletal muscle development. Nucleic Acids Research, 2021, 49, 1313-1329.	14.5	68
1014	Epigenetics in intellectual disability., 2021,, 489-517.		0
1015	Role of epigenetics in the brain. , 2021, , 85-109.		1
1016	Neuroblastoma and the epigenome. Cancer and Metastasis Reviews, 2021, 40, 173-189.	5.9	49
1017	The emergence of the brain non-CpG methylation system in vertebrates. Nature Ecology and Evolution, 2021, 5, 369-378.	7.8	63
1018	Nondestructive enzymatic deamination enables single-molecule long-read amplicon sequencing for the determination of 5-methylcytosine and 5-hydroxymethylcytosine at single-base resolution. Genome Research, 2021, 31, 291-300.	5.5	63
1019	Epigenetic landscape of stress surfeit disorders: Key role for DNA methylation dynamics. International Review of Neurobiology, 2021, 156, 127-183.	2.0	8

#	Article	IF	Citations
1020	TET-Mediated Epigenetic Regulation in Immune Cell Development and Disease. Frontiers in Cell and Developmental Biology, 2020, 8, 623948.	3.7	27
1021	5-Methylcytosine and 5-hydroxymethylcytosine in psychiatric epigenetics. , 2021, , 275-308.		0
1022	Epigenetics in child psychiatry., 2021, , 553-573.		0
1023	Splicing alterations in healthy aging and disease. Wiley Interdisciplinary Reviews RNA, 2021, 12, e1643.	6.4	29
1024	Mechanistic insights into recognition of symmetric methylated cytosines in CpG and non-CpG DNA by UHRF1 SRA. International Journal of Biological Macromolecules, 2021, 170, 514-522.	7.5	6
1025	Conserved dual-mode gene regulation programs in higher eukaryotes. Nucleic Acids Research, 2021, 49, 2583-2597.	14.5	2
1027	Targeting Epigenetic Mechanisms to Treat Alcohol Use Disorders (AUD). Current Pharmaceutical Design, 2021, 27, 3252-3272.	1.9	2
1028	Cross-species examination of X-chromosome inactivation highlights domains of escape from silencing. Epigenetics and Chromatin, 2021, 14, 12.	3.9	23
1029	Gene expression and epigenetics reveal species-specific mechanisms acting upon common molecular pathways in the evolution of task division in bees. Scientific Reports, 2021, 11, 3654.	3.3	12
1030	Non-CG methylation and multiple histone profiles associate child abuse with immune and small GTPase dysregulation. Nature Communications, 2021, 12, 1132.	12.8	24
1031	Cutting across structural and transcriptomic scales translates time across the lifespan in humans and chimpanzees. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20202987.	2.6	9
1032	TET Enzymes and 5-Hydroxymethylcytosine in Neural Progenitor Cell Biology and Neurodevelopment. Frontiers in Cell and Developmental Biology, 2021, 9, 645335.	3.7	29
1033	Comprehensive analysis of single cell ATAC-seq data with SnapATAC. Nature Communications, 2021, 12, 1337.	12.8	253
1034	DNA Methyltransferase 1 (DNMT1) Shapes Neuronal Activity of Human iPSC-Derived Glutamatergic Cortical Neurons. International Journal of Molecular Sciences, 2021, 22, 2034.	4.1	12
1035	Resilience to Stress: Lessons from Rodents about Nature versus Nurture. Neuroscientist, 2022, 28, 283-298.	3.5	3
1037	Wholeâ€genome characterization of chronological ageâ€associated changes in methylome and circular RNAs in moso bamboo ( <i>Phyllostachys edulis</i> ) from vegetative to floral growth. Plant Journal, 2021, 106, 435-453.	5.7	27
1038	Maternal intermittent fasting before mating alters hepatic DNA methylation in offspring. Epigenomics, 2021, 13, 341-356.	2.1	1
1039	Developmental Accumulation of Gene Body and Transposon Non-CpG Methylation in the Zebrafish Brain. Frontiers in Cell and Developmental Biology, 2021, 9, 643603.	3.7	10

#	Article	IF	CITATIONS
1040	DNA Methylation Regulates Transcription Factor-Specific Neurodevelopmental but Not Sexually Dimorphic Gene Expression Dynamics in Zebra Finch Telencephalon. Frontiers in Cell and Developmental Biology, 2021, 9, 583555.	3.7	8
1041	Functional enhancer elements drive subclass-selective expression from mouse to primate neocortex. Cell Reports, 2021, 34, 108754.	6.4	88
1043	How do established developmental risk-factors for schizophrenia change the way the brain develops?. Translational Psychiatry, 2021, 11, 158.	4.8	24
1044	Cellular response to endogenous DNA damage: DNA base modifications in gene expression regulation. DNA Repair, 2021, 99, 103051.	2.8	22
1045	Neuronal non-CG methylation is an essential target for MeCP2 function. Molecular Cell, 2021, 81, 1260-1275.e12.	9.7	24
1046	Loss of ten-eleven translocation 2 induces cardiac hypertrophy and fibrosis through modulating ERK signaling pathway. Human Molecular Genetics, 2021, 30, 865-879.	2.9	12
1047	Conservation of Aging and Cancer Epigenetic Signatures across Human and Mouse. Molecular Biology and Evolution, 2021, 38, 3415-3435.	8.9	5
1048	Epigenome-wide study of brain DNA methylation following acute opioid intoxication. Drug and Alcohol Dependence, 2021, 221, 108658.	3.2	15
1049	Genomeâ€wide hypermethylation is closely associated with abnormal expression of genes involved in neural development in induced pluripotent stem cells derived from a Down syndrome mouse model. Cell Biology International, 2021, 45, 1383-1392.	3.0	0
1050	scMET: Bayesian modeling of DNA methylation heterogeneity at single-cell resolution. Genome Biology, 2021, 22, 114.	8.8	14
1051	MicroRNA-29 is an essential regulator of brain maturation through regulation of CH methylation. Cell Reports, 2021, 35, 108946.	6.4	25
1052	Human brain region-specific variably methylated regions are enriched for heritability of distinct neuropsychiatric traits. Genome Biology, 2021, 22, 116.	8.8	22
1053	A ride through the epigenetic landscape: aging reversal by reprogramming. GeroScience, 2021, 43, 463-485.	4.6	12
1054	Rett Syndrome: A Timely Review From Recognition to Current Clinical Approaches and Clinical Study Updates. Seminars in Pediatric Neurology, 2021, 37, 100881.	2.0	11
1055	Tissue-specific regulatory mechanism of LncRNAs and methylation in sheep adipose and muscle induced by Allium mongolicum Regel extracts. Scientific Reports, 2021, 11, 9186.	3.3	8
1056	Sedentary Life and Reduced Mastication Impair Spatial Learning and Memory and Differentially Affect Dentate Gyrus Astrocyte Subtypes in the Aged Mice. Frontiers in Neuroscience, 2021, 15, 632216.	2.8	5
1057	Evolution of DNA methylation in the human brain. Nature Communications, 2021, 12, 2021.	12.8	53
1058	Decreased DNA methylation at promoters and gene-specific neuronal hypermethylation in the prefrontal cortex of patients with bipolar disorder. Molecular Psychiatry, 2021, 26, 3407-3418.	7.9	23

#	Article	IF	Citations
1059	Low biological fluctuation of mitochondrial CpG and non-CpG methylation at the single-molecule level. Scientific Reports, 2021, 11, 8032.	3.3	27
1060	Drug Response-Related DNA Methylation Changes in Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. Frontiers in Neuroscience, 2021, 15, 674273.	2.8	29
1061	Genome-wide DNA methylation analysis and biochemical responses provide insights into the initial domestication of halophyte Puccinellia tenuiflora. Plant Cell Reports, 2021, 40, 1181-1197.	5.6	2
1062	Genetics and Epigenetics of One-Carbon Metabolism Pathway in Autism Spectrum Disorder: A Sex-Specific Brain Epigenome?. Genes, 2021, 12, 782.	2.4	22
1063	Sulfur amino acid metabolism and related metabotypes of autism spectrum disorder: A review of biochemical evidence for a hypothesis. Biochimie, 2021, 184, 143-157.	2.6	13
1064	Pesticides as endocrine distruptors of the reproductive system (literature review and own research). Journal of the National Academy of Medical Sciences of Ukraine, 2021, , 49-62.	0.3	0
1065	DNA methylation in stress and depression: from biomarker to therapeutics. Acta Neuropsychiatrica, 2021, 33, 217-241.	2.1	11
1066	Genomeâ€wide DNA methylation and transcription analysis in tongue and biceps femoris muscles of cloned pigs with macroglossia. Animal Genetics, 2021, 52, 608-620.	1.7	1
1067	Transcriptomic and Epigenomic Landscape in Rett Syndrome. Biomolecules, 2021, 11, 967.	4.0	10
1068	Pregnancy Induces an Immunological Memory Characterized by Maternal Immune Alterations Through Specific Genes Methylation. Frontiers in Immunology, 2021, 12, 686676.	4.8	6
1069	Direct and heritable effects of natural tidal environments on DNA methylation in Pacific oysters (Crassostrea gigas). Environmental Research, 2021, 197, 111058.	7.5	15
1070	Analysis of Methylation Dynamics Reveals a Tissue-Specific, Age-Dependent Decline in 5-Methylcytosine Within the Genome of the Vertebrate Aging Model Nothobranchius furzeri. Frontiers in Molecular Biosciences, 2021, 8, 627143.	3.5	7
1071	TET1-mediated DNA hydroxymethylation regulates adult remyelination in mice. Nature Communications, 2021, 12, 3359.	12.8	47
1072	Single-molecule micromanipulation studies of methylated DNA. Biophysical Journal, 2021, 120, 2148-2155.	0.5	13
1073	MeCP2 is a microsatellite binding protein that protects CA repeats from nucleosome invasion. Science, 2021, 372, .	12.6	36
1074	Comparative Analysis of Skeletal Muscle DNA Methylation and Transcriptome of the Chicken Embryo at Different Developmental Stages. Frontiers in Physiology, 2021, 12, 697121.	2.8	5
1075	Bisulfite Amplicon Sequencing Can Detect Glia and Neuron Cell-Free DNA in Blood Plasma. Frontiers in Molecular Neuroscience, 2021, 14, 672614.	2.9	12
1076	Tissue-specific 5-hydroxymethylcytosine landscape of the human genome. Nature Communications, 2021, 12, 4249.	12.8	50

#	Article	IF	CITATIONS
1077	UHRF2 commissions the completion of DNA demethylation through allosteric activation by 5hmC and K33-linked ubiquitination of XRCC1. Molecular Cell, 2021, 81, 2960-2974.e7.	9.7	16
1078	The Molecular Basis of Depression: Implications of Sex-Related Differences in Epigenetic Regulation. Frontiers in Molecular Neuroscience, 2021, 14, 708004.	2.9	11
1079	Gly, GlyGly, and GlyAsp Modulate Expression of Genes of the SNF2 Family and DNA Methyltransferases in Regenerants from Calluses of Tobacco Nicotiana tabacum. Biology Bulletin, 2021, 48, 450-458.	0.5	1
1080	Introduction to Single-Cell DNA Methylation Profiling Methods. Biomolecules, 2021, 11, 1013.	4.0	35
1081	Human non-CpG methylation patterns display both tissue-specific and inter-individual differences suggestive of underlying function. Epigenetics, 2022, 17, 653-664.	2.7	8
1082	Aging biomarkers and the brain. Seminars in Cell and Developmental Biology, 2021, 116, 180-193.	5.0	33
1083	Epigenetic inactivation of the autophagy–lysosomal system in appendix in Parkinson's disease. Nature Communications, 2021, 12, 5134.	12.8	18
1084	The Zebrafish Model to Understand Epigenetics in Renal Diseases. International Journal of Molecular Sciences, 2021, 22, 9152.	4.1	2
1085	Proteomeâ€Wide Profiling of Readers for DNA Modification. Advanced Science, 2021, 8, e2101426.	11.2	7
1086	The epigenetic mechanisms involved in mitochondrial dysfunction: Implication for Parkinson's disease. Brain Pathology, 2022, 32, e13012.	4.1	11
1087	DNA methylation signatures in autism spectrum disorders. Nucleus (India), 2021, 64, 359-372.	2.2	2
1088	Multi-omics in mesial temporal lobe epilepsy with hippocampal sclerosis: Clues into the underlying mechanisms leading to disease. Seizure: the Journal of the British Epilepsy Association, 2021, 90, 34-50.	2.0	19
1089	Neurodegenerative movement disorders: An epigenetics perspective and promise for the future. Neuropathology and Applied Neurobiology, 2021, 47, 897-909.	3.2	16
1090	Examination of CA1 Hippocampal DNA Methylation as a Mechanism for Closing of Estrogen's Critical Window. Frontiers in Aging Neuroscience, 2021, 13, 717032.	3.4	4
1091	Current and Future Perspectives of Noncoding RNAs in Brain Function and Neuropsychiatric Disease. Biological Psychiatry, 2022, 91, 183-193.	1.3	15
1092	Proteomic and transcriptional changes associated with MeCP2 dysfunction reveal nodes for therapeutic intervention in Rett syndrome. Neurochemistry International, 2021, 148, 105076.	3.8	7
1093	Methylation of the tyrosine hydroxylase gene is dysregulated by cocaine dependence in the human striatum. IScience, 2021, 24, 103169.	4.1	8
1095	Progressive Domain Segregation in Early Embryonic Development and Underlying Correlation to Genetic and Epigenetic Changes. Cells, 2021, 10, 2521.	4.1	4

#	Article	IF	CITATIONS
1096	Multiomics Analysis of Neuroblastoma Cells Reveals a Diversity of Malignant Transformations. Frontiers in Cell and Developmental Biology, 2021, 9, 727353.	3.7	5
1097	Combined Profiling of Transcriptome and DNA Methylome Reveal Genes Involved in Accumulation of Soluble Sugars and Organic Acid in Apple Fruits. Foods, 2021, 10, 2198.	4.3	11
1099	DNA Methylation and Demethylation Underlie the Sex Difference in Estrogen Receptor Alpha in the Arcuate Nucleus. Neuroendocrinology, 2022, 112, 636-648.	2.5	7
1100	Adolescent Substance Abuse, Transgenerational Consequences and Epigenetics. Current Neuropharmacology, 2021, 19, 1560-1569.	2.9	13
1101	Deep Enzymology Studies on DNA Methyltransferases Reveal Novel Connections between Flanking Sequences and Enzyme Activity. Journal of Molecular Biology, 2021, 433, 167186.	4.2	18
1102	Differences in DNA methylation between slow and fast muscle in Takifugu rubripes. Gene, 2021, 801, 145853.	2.2	4
1103	Molecular impacts of childhood abuse on the human brain. Neurobiology of Stress, 2021, 15, 100343.	4.0	12
1104	The role of TET proteins in stress-induced neuroepigenetic and behavioural adaptations. Neurobiology of Stress, 2021, 15, 100352.	4.0	10
1105	Stress-Mediated Regulation of the DNA Methylome. , 2021, , 37-47.		0
1106	Principles of Management of Drug-Induced Neurological Disorders. , 2021, , 79-87.		0
1107	Genomeâ€wide variation in DNA methylation linked to developmental stage and chromosomal suppression of recombination in whiteâ€throated sparrows. Molecular Ecology, 2021, 30, 3453-3467.	3.9	12
1108	Perinatal stress and epigenetics. Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn, 2021, 180, 125-148.	1.8	14
1109	Epigenetic and non-coding regulation of alcohol abuse and addiction. International Review of Neurobiology, 2021, 156, 63-86.	2.0	8
1110	Genome-wide prediction of topoisomerase $ll\hat{l}^2$ binding by architectural factors and chromatin accessibility. PLoS Computational Biology, 2021, 17, e1007814.	3.2	8
1111	The Role of H3K4 Trimethylation in CpG Islands Hypermethylation in Cancer. Biomolecules, 2021, 11, 143.	4.0	11
1112	Regulation of DNA methyltransferase gene expression by short peptides in nicotiana tabacum regenerants. AIMS Biophysics, 2021, 8, 66-79.	0.6	1
1113	Other omics approaches to the study of rare diseases. , 2021, , 229-262.		0
1114	Genomic Targeting of TET Activity for Targeted Demethylation Using. Methods in Molecular Biology, 2021, 2272, 181-194.	0.9	6

#	Article	IF	CITATIONS
1115	Laboratory techniques in psychiatric epigenetics. , 2021, , 197-231.		0
1116	DNA methyltransferase inhibitors and psychiatric disorders. , 2021, , 639-656.		0
1117	Differential DNA Methylation Profiles in Patients with Temporal Lobe Epilepsy and Hippocampal Sclerosis ILAE Type I. Journal of Molecular Neuroscience, 2021, 71, 1951-1966.	2.3	11
1118	Functional roles of antisense enhancer RNA for promoting prostate cancer progression. Theranostics, 2021, 11, 1780-1794.	10.0	24
1120	Genes that escape from Xâ€chromosome inactivation: Potential contributors to Klinefelter syndrome. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2020, 184, 226-238.	1.6	44
1121	Integrated Analysis of DNA Methylation, Hydroxymethylation, and Gene Expression Data Using ME-Class2. Methods in Molecular Biology, 2021, 2198, 467-489.	0.9	1
1122	Whole-Genome DNA Methylation Profiling with Nucleotide Resolution. Methods in Molecular Biology, 2015, 1284, 27-40.	0.9	4
1123	Functional Implications of Dynamic DNA Methylation for the Developing, Aging and Diseased Brain. RNA Technologies, 2019, , 141-163.	0.3	20
1124	17Î <sup>2</sup> -Estradiol Increases Non-CpG Methylation in Exon 1 of the Rainbow Trout (Oncorhynchus mykiss) MyoD Gene. Marine Biotechnology, 2017, 19, 321-327.	2.4	14
1125	Naloxone Facilitates Contextual Learning and Memory in a Receptor-Independent and Tet1-Dependent Manner. Cellular and Molecular Neurobiology, 2021, 41, 1031-1038.	3.3	3
1126	Introduction to Epigenetic Mechanisms. , 2016, , 49-62.		2
1127	Epigenetic processes and DNA repair in embryonic stem cells. , 2020, , 1-23.		1
1128	Genome-wide profiling of gene expression and DNA methylation provides insight into low-altitude acclimation in Tibetan pigs. Gene, 2018, 642, 522-532.	2.2	18
1129	Establishment, maintenance, and biological roles of non-CG methylation in plants. Essays in Biochemistry, 2019, 63, 743-755.	4.7	49
1130	The influence of DNA methylation on monoallelic expression. Essays in Biochemistry, 2019, 63, 663-676.	4.7	39
1131	CpG and non-CpG Presenilin1 methylation pattern in course of neurodevelopment and neurodegeneration is associated with gene expression in human and murine brain. Epigenetics, 2020, 15, 781-799.	2.7	39
1132	DNA Methyltransferase 3A Is Involved in the Sustained Effects of Chronic Stress on Synaptic Functions and Behaviors. Cerebral Cortex, 2021, 31, 1998-2012.	2.9	11
1176	Epigenetic reprogramming of immune cells in injury, repair, and resolution. Journal of Clinical Investigation, 2019, 129, 2994-3005.	8.2	55

#	Article	IF	CITATIONS
1177	MECP2 disorders: from the clinic to mice and back. Journal of Clinical Investigation, 2015, 125, 2914-2923.	8.2	172
1178	The emerging landscape of in vitro and in vivo epigenetic allelic effects. F1000Research, 2017, 6, 2108.	1.6	11
1179	DNA Methylation Signatures of the Plant Chromomethyltransferases. PLoS Genetics, 2016, 12, e1006526.	3.5	149
1180	MeCP2 recognizes cytosine methylated tri-nucleotide and di-nucleotide sequences to tune transcription in the mammalian brain. PLoS Genetics, 2017, 13, e1006793.	3.5	117
1181	Methy-Pipe: An Integrated Bioinformatics Pipeline for Whole Genome Bisulfite Sequencing Data Analysis. PLoS ONE, 2014, 9, e100360.	2.5	54
1182	Coordinated Gene Expression of Neuroinflammatory and Cell Signaling Markers in Dorsolateral Prefrontal Cortex during Human Brain Development and Aging. PLoS ONE, 2014, 9, e110972.	2.5	44
1183	Disclosing Bias in Bisulfite Assay: MethPrimers Underestimate High DNA Methylation. PLoS ONE, 2015, 10, e0118318.	2.5	42
1184	Impacts of Chromatin States and Long-Range Genomic Segments on Aging and DNA Methylation. PLoS ONE, 2015, 10, e0128517.	2.5	27
1185	Cardiac Myocyte De Novo DNA Methyltransferases 3a/3b Are Dispensable for Cardiac Function and Remodeling after Chronic Pressure Overload in Mice. PLoS ONE, 2015, 10, e0131019.	2.5	35
1186	Evaluation of Methyl-Binding Domain Based Enrichment Approaches Revisited. PLoS ONE, 2015, 10, e0132205.	2.5	26
1187	Coordinated Expression of Phosphoinositide Metabolic Genes during Development and Aging of Human Dorsolateral Prefrontal Cortex. PLoS ONE, 2015, 10, e0132675.	2.5	16
1188	Genome-Wide Mapping of 5mC and 5hmC Identified Differentially Modified Genomic Regions in Late-Onset Severe Preeclampsia: A Pilot Study. PLoS ONE, 2015, 10, e0134119.	2.5	22
1189	Subsets of Visceral Adipose Tissue Nuclei with Distinct Levels of 5-Hydroxymethylcytosine. PLoS ONE, 2016, 11, e0154949.	2.5	9
1190	The sequence preference of DNA methylation variation in mammalians. PLoS ONE, 2017, 12, e0186559.	2.5	8
1191	Single-cell analysis of transcriptome and DNA methylome in human oocyte maturation. PLoS ONE, 2020, 15, e0241698.	2.5	27
1192	MicroRNA-137 Drives Epigenetic Reprogramming in the Adult Amygdala and Behavioral Changes after Adolescent Alcohol Exposure. ENeuro, 2019, 6, ENEURO.0401-19.2019.	1.9	23
1193	The role of epigenetics in hypothalamic energy balance control: implications for obesity. Cell Stress, 2019, 3, 208-220.	3.2	20
1194	Hippocampal and cortical tissue-specific epigenetic clocks indicate an increased epigenetic age in a mouse model for Alzheimer's disease. Aging, 2020, 12, 20817-20834.	3.1	22

#	Article	IF	CITATIONS
1195	Genetics and epigenetic factors of Wilson disease. Annals of Translational Medicine, 2019, 7, S58-S58.	1.7	33
1196	DNA methylation, environmental exposures and early embryo development. Animal Reproduction, 2019, 16, 465-474.	1.0	41
1197	Childhood Maltreatment and Stress-Related Psychopathology: The Epigenetic Memory Hypothesis. Current Pharmaceutical Design, 2015, 21, 1413-1417.	1.9	39
1198	Epigenetic Regulation of Cytochrome P450 Enzymes and Clinical Implication. Current Drug Metabolism, 2015, 16, 86-96.	1.2	65
1199	Energizing Genetics and Epi-genetics: Role in the Regulation of Mitochondrial Function. Current Genomics, 2015, 15, 436-456.	1.6	10
1200	Epigenetic Changes Associated with Early Life Experiences: Saliva, A Biospecimen for DNA Methylation Signatures. Current Genomics, 2018, 19, 676-698.	1.6	14
1201	Epigenetic Basis of Neuronal and Synaptic Plasticity. Current Topics in Medicinal Chemistry, 2017, 17, 771-793.	2.1	30
1202	Intra-individual methylomics detects the impact of early-life adversity. Life Science Alliance, 2019, 2, e201800204.	2.8	8
1203	Assessment and site-specific manipulation of DNA (hydroxy-)methylation during mouse corticogenesis. Life Science Alliance, 2019, 2, e201900331.	2.8	20
1204	New approaches to manipulating the epigenome. Dialogues in Clinical Neuroscience, 2014, 16, 345-357.	3.7	24
1205	Role of DNA methylation and the DNA methyltransferases in learning and memory. Dialogues in Clinical Neuroscience, 2014, 16, 359-371.	3.7	66
1206	Epigenetic mechanisms in schizophrenia. Dialogues in Clinical Neuroscience, 2014, 16, 405-417.	3.7	74
1207	Unraveling the epigenetic landscape of depression: focus on early life stress. Dialogues in Clinical Neuroscience, 2019, 21, 341-357.	3.7	75
1208	A review of epigenetic contributions †to post-traumatic stress disorder. Dialogues in Clinical Neuroscience, 2019, 21, 417-428.	3.7	46
1209	Whole-Genome DNA Methylation Associated With Differentially Expressed Genes Regulated Anthocyanin Biosynthesis Within Flower Color Chimera of Ornamental Tree Prunus mume. Forests, 2020, 11, 90.	2.1	12
1210	Astonishing advances in mouse genetic tools for biomedical research. Swiss Medical Weekly, 2015, 145, w14186.	1.6	15
1211	Enzymatic DNA oxidation: mechanisms and biological significance. BMB Reports, 2014, 47, 609-618.	2.4	20
1212	A concise review of human brain methylome during aging and neurodegenerative diseases. BMB Reports, 2019, 52, 577-588.	2.4	26

#	Article	IF	CITATIONS
1213	Epigenomic landscapes of retinal rods and cones. ELife, 2016, 5, e11613.	6.0	106
1214	5-hydroxymethylcytosine marks regions with reduced mutation frequency in human DNA. ELife, 2016, 5,	6.0	28
1215	OGT binds a conserved C-terminal domain of TET1 to regulate TET1 activity and function in development. ELife, $2018, 7, \ldots$	6.0	46
1216	Species and cell-type properties of classically defined human and rodent neurons and glia. ELife, 2018, 7, .	6.0	66
1217	A whole lifespan mouse multi-tissue DNA methylation clock. ELife, 2018, 7, .	6.0	140
1218	MeCP2 nuclear dynamics in live neurons results from low and high affinity chromatin interactions. ELife, 2019, $8$ , .	6.0	29
1219	Losing Dnmt3a dependent methylation in inhibitory neurons impairs neural function by a mechanism impacting Rett syndrome. ELife, 2020, 9, .	6.0	44
1220	Identification and characterization of the cytosine-5 DNA methyltransferase gene family in <i>Salvia miltiorrhiza</i> . PeerJ, 2018, 6, e4461.	2.0	8
1221	Proteins in DNA methylation and their role in neural stem cell proliferation and differentiation. Cell Regeneration, 2021, 10, 7.	2.6	8
1222	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 2021, 598, 103-110.	27.8	166
1223	MicroRNAs in the Onset of Schizophrenia. Cells, 2021, 10, 2679.	4.1	23
1224	Transposable Element Dynamics and Regulation during Zygotic Genome Activation in Mammalian Embryos and Embryonic Stem Cell Model Systems. Stem Cells International, 2021, 2021, 1-17.	2.5	3
1226	SIRT6 Through the Brain Evolution, Development, and Aging. Frontiers in Aging Neuroscience, 2021, 13, 747989.	3.4	13
1227	Epigenetic Regulatory Dynamics in Models of Methamphetamine-Use Disorder. Genes, 2021, 12, 1614.	2.4	12
1228	Developmental Temporal Patterns and Molecular Network Features in the Transcriptome of Rat Spinal Cord. Engineering, 2021, 7, 1592-1602.	6.7	4
1229	DNA methylation atlas of the mouse brain at single-cell resolution. Nature, 2021, 598, 120-128.	27.8	135
1230	Epigenomic diversity of cortical projection neurons in the mouse brain. Nature, 2021, 598, 167-173.	27.8	47
1231	The Potential Brain Drain from Environmental Exposures on the Methylome and Genome Across Generations., 2014,, 375-406.		O

#	Article	IF	CITATIONS
1232	An Overview of Methods Used in Neurogenomics and Their Applications. Neuromethods, 2015, , 1-59.	0.3	0
1233	Epigenetic of Somatic Cells Reprogramming. Cancer Genetics and Epigenetics, 0, , .	0.0	0
1234	The Insight of Regulation Mechanism from DNA Methylation Based on Single Base Resolution Sequencing Data. Cancer Genetics and Epigenetics, $0, \dots$	0.0	0
1235	Epigenetics Advances in the Nervous System. QianRen Biology, 2015, 02, 1-9.	0.0	0
1237	Epigenomic Measurements in Brain Tissues. , 2015, , 1-41.		0
1238	Personalized Management of Neurological Disorders. , 2015, , 409-460.		0
1240	Epigenomic Measurements in Brain Tissues. , 2016, , 2857-2897.		0
1244	DNA Methylation in Eukaryotes: Regulation and Function. , 2017, , 1-62.		1
1245	Unraveling the Role of Long Noncoding RNAs in Pluripotent Stem Cell-Based Neuronal Commitment and Neurogenesis., 2017,, 43-59.		0
1246	Parental Responsibility and the Principle of Procreative Beneficence in Light of Assisted Reproductive Technologies. International Library of Ethics, Law, and the New Medicine, 2017, , 167-187.	0.5	0
1252	Analog Genetics. , 2018, , 223-255.		0
1253	The Developmental Neuroepigenetics of Substance Abuse. Journal of Drug and Alcohol Research, 2018, 7, 1-27.	0.9	3
1261	Mecp2 Nuclear Dynamics in Live Neurons Results from Low and High Affinity Chromatin Interactions. SSRN Electronic Journal, 0, , .	0.4	2
1262	Neuroepigenetics., 2019,, 101-111.		0
1266	Epigénesis: secuelas de una infancia adversa. Revista Digital Universitaria, 2019, 20, .	0.0	0
1279	Ageing, Drosophila melanogaster and Epigenetics. The Malaysian Journal of Medical Sciences, 2020, 27, 7-19.	0.5	5
1282	DNA Methylation and Schizophrenia: Current Literature and Future Perspective. Cells, 2021, 10, 2890.	4.1	26
1283	Epigenetic interaction of microbes with their mammalian hosts. Journal of Biosciences, $2021$ , $46$ , $1$ .	1.1	5

#	Article	IF	CITATIONS
1284	Early-Life Iron Deficiency Anemia Programs the Hippocampal Epigenomic Landscape. Nutrients, 2021, 13, 3857.	4.1	14
1285	Tecnologia REAC: abordagem bioelétrica do processo saúde doença Brazilian Journal of Implantology and Health Sciences, 2020, 2, 01-06.	0.1	0
1287	Whole-genome bisulfite sequencing of abdominal adipose reveals DNA methylation pattern variations in broiler lines divergently selected for fatness. Journal of Animal Science, 2021, 99, .	0.5	1
1289	Possible existence of a system similar to bacterial restriction–modification in plants. AIMS Molecular Science, 2020, 7, 396-413.	0.5	1
1290	An overview of Rett syndrome. , 2020, , 299-310.		0
1294	The Epigenome in Neurodevelopmental Disorders. Frontiers in Neuroscience, 2021, 15, 776809.	2.8	38
1295	Human iPSC-Derived Neurons as A Platform for Deciphering the Mechanisms behind Brain Aging. Biomedicines, 2021, 9, 1635.	3.2	5
1297	Alternative splicing at neuroligin site A regulates glycan interaction and synaptogenic activity. ELife, 2020, 9, .	6.0	10
1299	DNA methylation-based age estimation in pediatric healthy tissues and brain tumors. Aging, 2020, 12, 21037-21056.	3.1	22
1300	Differential Glial Activation in Early Epileptogenesis—Insights From Cell-Specific Analysis of DNA Methylation and Gene Expression in the Contralateral Hippocampus. Frontiers in Neurology, 2020, 11, 573575.	2.4	5
1301	Towards a Role for Clinical Pathology Diagnostics for Childhood Maltreatment. Austin Journal of Clinical Pathology, 2015, 2, .	0.0	3
1302	Editing the Neuronal Genome: a CRISPR View of Chromatin Regulation in Neuronal Development, Function, and Plasticity. Yale Journal of Biology and Medicine, 2016, 89, 457-470.	0.2	4
1304	Autosomal dominant retinitis pigmentosa rhodopsin mutant Q344X drives specific alterations in chromatin complex gene transcription. Molecular Vision, 2018, 24, 153-164.	1.1	5
1305	Cell-type-specific brain methylomes profiled via ultralow-input microfluidics. Nature Biomedical Engineering, 2018, 2, 183-194.	22.5	15
1306	Epigenetic regulation of nervous system development and function. Neurochemistry International, 2022, 152, 105249.	3.8	2
1307	Dynamic Changes of DNA Methylation During Wild Strawberry (Fragaria nilgerrensis) Tissue Culture. Frontiers in Plant Science, 2021, 12, 765383.	3.6	5
1308	Prenatal Adversity Alters the Epigenetic Profile of the Prefrontal Cortex: Sexually Dimorphic Effects of Prenatal Alcohol Exposure and Food-Related Stress. Genes, 2021, 12, 1773.	2.4	10
1309	An epigenetic rheostat of experience: DNA methylation of OXTR as a mechanism of early life allostasis. Comprehensive Psychoneuroendocrinology, 2021, 8, 100098.	1.7	12

#	Article	IF	CITATIONS
1310	Integrated Transcriptome Analysis and Single-Base Resolution Methylomes of Watermelon (Citrullus) Tj ETQq0 0 2021, 12, 769712.	0 rgBT /O	verlock 10 T
1311	Human brain organogenesis: Toward a cellular understanding of development and disease. Cell, 2022, 185, 42-61.	28.9	97
1313	Repeated Ethanol Exposure Alters DNA Methylation Status and Dynorphin/Kappa-Opioid Receptor Expression in Nucleus Accumbens of Alcohol-Preferring AA Rats. Frontiers in Genetics, 2021, 12, 750142.	2.3	10
1314	Impact of medical imaging on the epigenome – low-dose exposure in the course of computed tomography does not induce detectable changes of DNA-methylation profiles in peripheral blood cells. International Journal of Radiation Biology, 2022, 98, 980-985.	1.8	3
1315	Effect of DNA modifications on the transition between canonical and non-canonical DNA structures in CpG islands during senescence. RSC Advances, 2021, 11, 37205-37217.	3.6	7
1316	Experimental and Bioinformatic Approaches to Studying DNA Methylation in Cancer. Cancers, 2022, 14, 349.	3.7	9
1317	The roles of epigenetic modifications in neurodegenerative diseases. Zhejiang Da Xue Xue Bao Yi Xue Ban = Journal of Zhejiang University Medical Sciences, 2021, 50, 642-650.	0.3	0
1319	Flanking sequences influence the activity of TET1 and TET2 methylcytosine dioxygenases and affect genomic 5hmC patterns. Communications Biology, 2022, 5, 92.	4.4	15
1320	The Epigenetic Role of Vitamin C in Neurodevelopment. International Journal of Molecular Sciences, 2022, 23, 1208.	4.1	22
1321	DNA Epigenetics in Addiction Susceptibility. Frontiers in Genetics, 2022, 13, 806685.	2.3	7
1322	Methionine- and Choline-Deficient Diet Identifies an Essential Role for DNA Methylation in Plasmacytoid Dendritic Cell Biology. Journal of Immunology, 2022, 208, 881-897.	0.8	2
1323	Developmental Iron Deficiency Dysregulates TET Activity and DNA Hydroxymethylation in the Rat Hippocampus and Cerebellum. Developmental Neuroscience, 2022, 44, 80-90.	2.0	8
1324	Developmental and Injury-induced Changes in DNA Methylation in Regenerative versus Non-regenerative Regions of the Vertebrate Central Nervous System. BMC Genomics, 2022, 23, 2.	2.8	8
1326	Candidate Epigenetic Biomarker of Cognitive Trajectory: The Chicken or the Egg?. Biological Psychiatry, 2022, 91, 332-334.	1.3	O
1327	DNA Methylation in Depression and Depressive-Like Phenotype: Biomarker or Target of Pharmacological Intervention?. Current Neuropharmacology, 2022, 20, 2267-2291.	2.9	3
1328	Developmental nicotine exposure and masculinization of the rat preoptic area. NeuroToxicology, 2022, 89, 41-54.	3.0	2
1329	Whole Genome DNA Methylation Profiling of D2 Medium Spiny Neurons in Mouse Nucleus Accumbens Using Two Independent Library Preparation Methods. Genes, 2022, 13, 306.	2.4	1
1330	Epigenetic reorganization during early embryonic lineage specification. Genes and Genomics, 2022, 44, 379-387.	1.4	4

#	Article	IF	Citations
1331	Tcf12 and NeuroD1 cooperatively drive neuronal migration during cortical development. Development (Cambridge), 2022, 149, .	2.5	11
1333	Epigenetic interaction of microbes with their mammalian hosts. Journal of Biosciences, 2021, 46, .	1.1	0
1334	A Multi-Omics Approach to Visualize Early Neuronal Differentiation in 4D. SSRN Electronic Journal, 0,	0.4	0
1335	Brain-derived cell-free DNA. Neural Regeneration Research, 2022, 17, 2213.	3.0	2
1337	Multi-tissue DNA methylation microarray signature is predictive of gene function. Epigenetics, 2022, , 1-15.	2.7	0
1338	scMelody: An Enhanced Consensus-Based Clustering Model for Single-Cell Methylation Data by Reconstructing Cell-to-Cell Similarity. Frontiers in Bioengineering and Biotechnology, 2022, 10, 842019.	4.1	4
1339	The Role of MeCP2 in Regulating Synaptic Plasticity in the Context of Stress and Depression. Cells, 2022, 11, 748.	4.1	12
1340	Cerebellar and Striatal Implications in Autism Spectrum Disorders: From Clinical Observations to Animal Models. International Journal of Molecular Sciences, 2022, 23, 2294.	4.1	27
1341	Cholinergic and Neuroimmune Signaling Interact to Impact Adult Hippocampal Neurogenesis and Alcohol Pathology Across Development. Frontiers in Pharmacology, 2022, 13, 849997.	3.5	9
1342	The Biological Basis of Gender Incongruence. , 0, , .		0
1343	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. Cell Genomics, 2022, 2, 100107.	6.5	58
1344	More of less: Novel multi-ome profiling of single human neurons. Cell Genomics, 2022, 2, 100110.	6.5	0
1345	DNA Methylation Malleability and Dysregulation in Cancer Progression: Understanding the Role of PARP1. Biomolecules, 2022, 12, 417.	4.0	6
1346	Exploring crucial molecular events in pearl oyster after pre-grafting conditioning by genome-wide bisulfite sequencing for DNA methylation analysis. Fish and Shellfish Immunology, 2022, 123, 10-19.	3.6	2
1347	Evaluating the challenges and reproducibility of studies investigating DNA methylation signatures of psychological stress. Epigenomics, 2022, 14, 405-421.	2.1	5
1348	Epigenetic function in neurodevelopment and cognitive impairment. Neuroforum, 2022, 28, 41-53.	0.3	O
1349	Exploration of the Effect on Genome-Wide DNA Methylation by miR-143 Knock-Out in Mice Liver. International Journal of Molecular Sciences, 2021, 22, 13075.	4.1	5
1350	Crosstalk of DNA Methylation Triggered by Pathogen in Poplars With Different Resistances. Frontiers in Microbiology, 2021, 12, 750089.	3.5	8

#	Article	IF	CITATIONS
1351	5-Hydroxymethylcytosine-mediated active demethylation is required for mammalian neuronal differentiation and function. ELife, $2021$ , $10$ , .	6.0	21
1354	Epigenetic Epidemiology of Autism and Other Neurodevelopmental Disorders. , 2022, , 405-426.		1
1402	BCurve: Bayesian Curve Credible Bands Approach for the Detection of Differentially Methylated Regions. Methods in Molecular Biology, 2022, 2432, 167-185.	0.9	0
1403	Identification of differential hypothalamic DNA methylation and gene expression associated with sexual partner preferences in rams. PLoS ONE, 2022, 17, e0263319.	2.5	3
1404	Making sense of the ageing methylome. Nature Reviews Genetics, 2022, 23, 585-605.	16.3	86
1406	Alpha-synuclein overexpression induces epigenomic dysregulation of glutamate signaling and locomotor pathways. Human Molecular Genetics, 2022, 31, 3694-3714.	2.9	5
1407	Differential Regulation of Mouse Hippocampal Gene Expression Sex Differences by Chromosomal Content and Gonadal Sex. Molecular Neurobiology, 2022, 59, 4669-4702.	4.0	11
1409	Dnmt3a knockout in excitatory neurons impairs postnatal synapse maturation and increases the repressive histone modification H3K27me3. ELife, 0, $11$ , .	6.0	10
1410	Genome-wide DNA methylation reveals potential epigenetic mechanism of age-dependent viral susceptibility in grass carp. Immunity and Ageing, 2022, 19, .	4.2	6
1411	Evolution of genetic mechanisms regulating cortical neurogenesis. Developmental Neurobiology, 2022, 82, 428-453.	3.0	17
1412	The Role of Genetics, Epigenetics, and the Environment in ASD: A Mini Review. Epigenomes, 2022, 6, 15.	1.8	9
1413	Key questions on the epigenetics of herpes simplex virus latency. PLoS Pathogens, 2022, 18, e1010587.	4.7	3
1414	Mitochondrial DNA methylation profiling of the human prefrontal cortex and nucleus accumbens: correlations with aging and drug use. Clinical Epigenetics, 2022, 14, .	4.1	4
1416	Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. Nature Genetics, 2022, 54, 1037-1050.	21.4	26
1417	A timely, user-friendly analysis of the mouse DNA methylome. Cell Genomics, 2022, 2, 100153.	6.5	1
1418	Genetic and Epigenetic Regulation of Brain Organoids. Frontiers in Cell and Developmental Biology, 0, 10, .	3.7	3
1419	Effect of acute heat shock on stress gene expression and DNA methylation in zebu (Bos indicus) and crossbred (Bos indicus × Bos taurus) dairy cattle. International Journal of Biometeorology, 2022, 66, 1797-1809.	3.0	5
1420	Applications of singleâ€cell multiâ€omics sequencing in deep understanding of brain diseases. Clinical and Translational Discovery, 2022, 2, .	0.5	O

#	Article	IF	CITATIONS
1421	Identification of Prefrontal Cortex and Amygdala Expressed Genes Associated With Sevoflurane Anesthesia on Non-human Primate. Frontiers in Integrative Neuroscience, 0, 16, .	2.1	2
1423	Circulating Cell-Free DNA Methylation Mirrors AlterationsÂln Cerebral Patterns in Epilepsy. SSRN Electronic Journal, 0, , .	0.4	0
1424	The potential role of DNA methylation as preventive treatment target of epileptogenesis. Frontiers in Cellular Neuroscience, $0,16,.$	3.7	3
1425	5-methylcytosine turnover: Mechanisms and therapeutic implications in cancer. Frontiers in Molecular Biosciences, 0, 9, .	3.5	8
1427	Cell-type specific DNA methylome signatures reveal epigenetic mechanisms for neuronal diversity and neurodevelopmental disorder. Human Molecular Genetics, 0, , .	2.9	1
1428	Inference of putative cell-type-specific imprinted regulatory elements and genes during human neuronal differentiation. Human Molecular Genetics, 2023, 32, 402-416.	2.9	2
1429	Temporal analysis of enhancers during mouse cerebellar development reveals dynamic and novel regulatory functions. ELife, 0, $11$ , .	6.0	7
1430	Community engagement in epigenomic and neurocognitive research on post-traumatic stress disorder in Rwandans exposed to the 1994 genocide against the Tutsi: lessons learned. Epigenomics, 2022, 14, 887-895.	2.1	1
1431	DNA methylation as a mediator of genetic and environmental influences on Parkinson's disease susceptibility: Impacts of alpha-Synuclein, physical activity, and pesticide exposure on the epigenome. Frontiers in Genetics, 0, 13, .	2.3	15
1433	An Association Study of DNA Methylation and Gene Expression in Angelman Syndrome: A Bioinformatics Approach. International Journal of Molecular Sciences, 2022, 23, 9139.	4.1	0
1434	Epigenetic regulation of fetal brain development in pig. Gene, 2022, 844, 146823.	2.2	5
1435	Abnormal transcriptome-wide DNA demethylation induced by folate deficiency causes neural tube defects. Frontiers in Genetics, 0, 13, .	2.3	3
1436	Role of DNA De-methylation intermediate  5-hydroxymethylcytosine' in ovarian cancer management: A comprehensive review. Biomedicine and Pharmacotherapy, 2022, 155, 113674.	5.6	3
1437	Genes and pathways associated with fear discrimination identified by genome-wide DNA methylation and RNA-seq analyses in nucleus accumbens in mice. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2023, 120, 110643.	4.8	2
1438	Epigenetics of Brain Disorders. , 2023, , 737-759.		0
1439	DNA Methylation as an Epigenetic Mechanism of Anticipation. Cognitive Systems Monographs, 2022, , 7-26.	0.1	0
1440	A critique of the hypothesis that CA repeats are primary targets of neuronal MeCP2. Life Science Alliance, 2022, 5, e202201522.	2.8	1
1441	Sex-specific epigenetic development in the mouse hypothalamic arcuate nucleus pinpoints human genomic regions associated with body mass index. Science Advances, 2022, 8, .	10.3	6

#	Article	IF	CITATIONS
1442	Melatonin and cancer suppression: insights into its effects on DNA methylation. Cellular and Molecular Biology Letters, 2022, 27, .	7.0	15
1444	Truncated Tau caused by intron retention is enriched in Alzheimer's disease cortex and exhibits altered biochemical properties. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	12
1445	Sex-biased effects on hippocampal circuit development by perinatal SERT expression in CA3 pyramidal neurons. Development (Cambridge), 2022, 149, .	2.5	5
1446	A multi-omics approach to visualize early neuronal differentiation from hESCs in 4D. IScience, 2022, 25, 105279.	4.1	4
1447	Epigenomic Measurements in Brain Tissues. , 2022, , 3221-3261.		0
1448	Modulation of DNA/RNA Methylation Signaling Mediating Metabolic Homeostasis in Cancer. Sub-Cellular Biochemistry, 2022, , 201-237.	2.4	1
1451	Epigenetics of neural differentiation: Spotlight on enhancers. Frontiers in Cell and Developmental Biology, $0,10,1$	3.7	5
1452	The 5-Hydroxymethylcytosine Landscape of Prostate Cancer. Cancer Research, 2022, 82, 3888-3902.	0.9	22
1453	MethBank 4.0: an updated database of DNA methylation across a variety of species. Nucleic Acids Research, 2023, 51, D208-D216.	14.5	7
1454	Enzymology of Mammalian DNA Methyltransferases. Advances in Experimental Medicine and Biology, 2022, , 69-110.	1.6	3
1455	Structure and Function of TET Enzymes. Advances in Experimental Medicine and Biology, 2022, , 239-267.	1.6	7
1456	Domain Structure of the Dnmt1, Dnmt3a, and Dnmt3b DNA Methyltransferases. Advances in Experimental Medicine and Biology, 2022, , 45-68.	1.6	5
1457	Role of DNMTs in the Brain. Advances in Experimental Medicine and Biology, 2022, , 363-394.	1.6	5
1458	DNA Methylation in Honey Bees and the Unresolved Questions in Insect Methylomics. Advances in Experimental Medicine and Biology, 2022, , 159-176.	1.6	1
1459	Role of primary aging hallmarks in AlzheimerÂ's disease. Theranostics, 2023, 13, 197-230.	10.0	8
1460	Prelimbic Cortical Stimulation with L-methionine Enhances Cognition through Hippocampal DNA Methylation and Neuroplasticity Mechanisms. , 2023, 14, 112.		4
1461	Genetic dissection of the soybean dwarf mutant dm with integrated genomic, transcriptomic and methylomic analyses. Frontiers in Plant Science, 0, 13, .	3.6	0
1463	Rett Syndrome and MECP2 Duplication Syndrome: Disorders of MeCP2 Dosage. Neuropsychiatric Disease and Treatment, 0, Volume 18, 2813-2835.	2.2	16

#	Article	IF	CITATIONS
1464	Sex-Specific Differences in the Transcriptome of the Human Dorsolateral Prefrontal Cortex in Schizophrenia. Molecular Neurobiology, 2023, 60, 1083-1098.	4.0	7
1465	Homeorhesis: envisaging the logic of life trajectories in molecular research on trauma and its effects. History and Philosophy of the Life Sciences, 2022, 44, .	1.1	1
1466	NSC Physiological Features in Spinal Muscular Atrophy: SMN Deficiency Effects on Neurogenesis. International Journal of Molecular Sciences, 2022, 23, 15209.	4.1	2
1467	The Chromatin Structure at the MECP2 Gene and In Silico Prediction of Potential Coding and Non-Coding MECP2 Splice Variants. International Journal of Molecular Sciences, 2022, 23, 15643.	4.1	5
1468	Induced pluripotent stem cell-derived and directly reprogrammed neurons to study neurodegenerative diseases: The impact of aging signatures. Frontiers in Aging Neuroscience, 0, 14, .	3.4	9
1470	Evolutionary Implications of Environmental Toxicant Exposure. Biomedicines, 2022, 10, 3090.	3.2	0
1471	Evidence that direct inhibition of transcription factor binding is the prevailing mode of gene and repeat repression by DNA methylation. Nature Genetics, 2022, 54, 1895-1906.	21.4	39
1472	Integrative Approaches of DNA Methylation Patterns according to Age, Sex, and Longitudinal Changes. Current Genomics, 2022, 24, .	1.6	0
1473	DNA methylation and hydroxymethylation characterize the identity of D1 and D2 striatal projection neurons. Communications Biology, 2022, 5, .	4.4	4
1474	Mammalian DNA methylome dynamics: mechanisms, functions and new frontiers. Development (Cambridge), 2022, 149, .	2.5	6
1475	Tet Enzyme-Mediated Response in Environmental Stress and Stress-Related Psychiatric Diseases. Molecular Neurobiology, 0, , .	4.0	0
1476	DNA Methylation Variation Is a Possible Mechanism in the Response of Haemaphysalis longicornis to Low-Temperature Stress. International Journal of Molecular Sciences, 2022, 23, 15207.	4.1	3
1477	The global dynamic of DNA methylation in response to heat stress revealed epigenetic mechanism of heat acclimation in <i>Saccharina japonica</i> . Journal of Phycology, 2023, 59, 249-263.	2.3	1
1478	Curcumin Combats against Gastrointestinal Cancer: A Review of Current Knowledge Regarding Epigenetics Mechanisms with a Focus on DNA Methylation. Current Medicinal Chemistry, 2023, 30, 4374-4388.	2.4	1
1479	Single-cell DNA methylation sequencing by combinatorial indexing and enzymatic DNA methylation conversion. Cell and Bioscience, 2023, $13$ , .	4.8	10
1480	Early-life exercise primes the murine neural epigenome to facilitate gene expression and hippocampal memory consolidation. Communications Biology, 2023, 6, .	4.4	2
1481	DNA Methylation in Algae and Its Impact on Abiotic Stress Responses. Plants, 2023, 12, 241.	3 <b>.</b> 5	3
1482	Genome-wide characterization of mitochondrial DNA methylation in human brain. Frontiers in Endocrinology, 0, 13, .	3.5	4

#	Article	IF	Citations
1483	Differential expression of m5C RNA methyltransferase genes NSUN6 and NSUN7 in Alzheimer's disease and traumatic brain injury. Molecular Neurobiology, 2023, 60, 2223-2235.	4.0	4
1484	Circulating cell-free DNA methylation mirrors alterations in cerebral patterns in epilepsy. Clinical Epigenetics, 2022, 14, .	4.1	2
1485	Role of epigenetics in shaping sex differences in brain development and behavior. , 2023, , 209-239.		3
1486	DNA Methylation: Genomewide Distribution, Regulatory Mechanism and Therapy Target., 2022, 14, 4-19.		2
1488	Dynamic Regulation of DNA Methylation and Brain Functions. Biology, 2023, 12, 152.	2.8	9
1489	The impact of spatial correlation on methylation entropy with application to mouse brain methylome. Epigenetics and Chromatin, 2023, 16, .	3.9	1
1490	Transgenerational effects of intertidal environment on physiological phenotypes and DNA methylation in Pacific oysters. Science of the Total Environment, 2023, 871, 162112.	8.0	11
1491	Databases and prospects of dynamic gene regulation in eukaryotes: A mini review. Computational and Structural Biotechnology Journal, 2023, 21, 2147-2159.	4.1	1
1492	DNA methylation and demethylation shape sexual differentiation of neurochemical phenotype. Hormones and Behavior, 2023, 151, 105349.	2.1	2
1493	Transcriptome and methylome dynamics in the gills of large yellow croaker (Larimichthys crocea) during low-salinity adaption. Frontiers in Marine Science, $0,10,.$	2.5	1
1494	Neuron–Glia-Ratio-Like Approach Evidenced for Limited Variability and In-Aggregate Circadian Shifts in Cortical Cell-Specific Transcriptomes. Journal of Molecular Neuroscience, 2023, 73, 159-170.	2.3	0
1495	Large Language Models and the Reverse Turing Test. Neural Computation, 2023, 35, 309-342.	2.2	31
1496	Immunity of turbot Induced by inactivated vaccine of Aeromonas salmonicida from the perspective of DNA methylation. Frontiers in Immunology, 0, $14$ , .	4.8	0
1497	Changes in Mitochondrial Epigenome in Type 2 Diabetes Mellitus. , 0, 80, .		2
1498	DNA methylation variation is crucial to restore adventitious rooting ability during <i>in vitro</i> shoot cultureâ€induced rejuvenation in apple rootstock. Plant Journal, 2023, 114, 554-569.	5.7	3
1500	Epigenetic regulation of plastin 3 expression by the macrosatellite DXZ4 and the transcriptional regulator CHD4. American Journal of Human Genetics, 2023, 110, 442-459.	6.2	2
1503	Histone lysine methyltransferase-related neurodevelopmental disorders: current knowledge and saRNA future therapies. Frontiers in Cell and Developmental Biology, $0,11,.$	3.7	0
1504	Crosstalk between microRNAs and epigenetics during brain development and neurological diseases. , 2023, , 173-207.		0

#	Article	IF	CITATIONS
1505	Maternal Epigenetic Dysregulation as a Possible Risk Factor for Neurodevelopmental Disorders. Genes, 2023, 14, 585.	2.4	2
1507	Reassessment of weak parent-of-origin expression bias shows it rarely exists outside of known imprinted regions. ELife, $0,12,12$	6.0	9
1508	Single substitution in H3.3G34 alters DNMT3A recruitment to cause progressive neurodegeneration. Cell, 2023, 186, 1162-1178.e20.	28.9	17
1509	The Chromatin Remodeling Factor BrCHR39 Targets DNA Methylation to Positively Regulate Apical Dominance in Brassica rapa. Plants, 2023, 12, 1384.	3.5	1
1510	Epigenetic and epitranscriptomic regulation of axon regeneration. Molecular Psychiatry, 2023, 28, 1440-1450.	7.9	3
1511	Buffering of transcription rate by mRNA half-life is a conserved feature of Rett syndrome models. Nature Communications, 2023, 14, .	12.8	3
1512	The methylation landscape of giga-genome and the epigenetic timer of age in Chinese pine. Nature Communications, 2023, 14, .	12.8	10
1513	Capture Methylation-Sensitive Restriction Enzyme Sequencing (Capture MRE-Seq) for Methylation Analysis of Highly Degraded DNA Samples. Methods in Molecular Biology, 2023, , 73-89.	0.9	0
1514	A pilot investigation of differential hydroxymethylation levels in patient-derived neural stem cells implicates altered cortical development in bipolar disorder. Frontiers in Psychiatry, 0, 14, .	2.6	0
1515	Epigenetics and Disease., 2023,, 197-210.		0
1517	How can we modulate aging through nutrition and physical exercise? An epigenetic approach. Aging, 0,	3.1	1
1518	Genes, environments, and epigenetics., 2023,, 181-200.		0
1519	Embryonic Stem Cell-Derived Neurons as a Model System for Epigenome Maturation during Development. Genes, 2023, 14, 957.	2.4	0
1520	NSD1 deposits histone H3 lysine 36 dimethylation to pattern non-CG DNA methylation in neurons. Molecular Cell, 2023, 83, 1412-1428.e7.	9.7	10
1521	Increasing Specificity of Targeted DNA Methylation Editing by Non-Enzymatic CRISPR/dCas9-Based Steric Hindrance. Biomedicines, 2023, 11, 1238.	3.2	3
1523	Drugs For Relapse Prevention in Addiction: Review of Psychological and Neurological Factors, Genetics and Neurobiological Mechanisms. Frontiers in Clinical Drug Research CNS and Neurological Disorders, 2023, , 158-237.	0.1	0
1524	Association between methylation in the promoter region of the GAD2 gene and opioid use disorder. Brain Research, 2023, 1812, 148407.	2.2	0
1525	Reduced non-CpG methylation is a potential epigenetic target after spinal cord injury. Neural Regeneration Research, 2023, 18, 2489-2496.	3.0	1

#	Article	IF	Citations
1526	Epigenetic regulation of human-specific gene expression in the prefrontal cortex. BMC Biology, 2023, 21, .	3.8	1
1527	Epigenetics of cognition and behavior: insights from Mendelian disorders of epigenetic machinery. Journal of Neurodevelopmental Disorders, 2023, 15, .	3.1	4
1529	Epigenetics and Brain Plasticity: Back to Function. Contemporary Clinical Neuroscience, 2023, , 237-252.	0.3	0
1531	Dynamic DNA methylation modification in peanut seed development. IScience, 2023, 26, 107062.	4.1	0
1533	Identification of epigenetically active L1 promoters in the human brain and their relationship with psychiatric disorders. Neuroscience Research, 2023, 195, 37-51.	1.9	0
1536	Prenatal exposure to legacy PFAS and neurodevelopment in preschool-aged Canadian children: The MIREC cohort. Neurotoxicology and Teratology, 2023, 98, 107181.	2.4	9
1537	Sex-specific variations in global DNA methylation levels with age: a population-based exploratory study from North India. Frontiers in Genetics, 0, 14, .	2.3	3
1541	Integrative mapping of the dog epigenome: Reference annotation for comparative intertissue and cross-species studies. Science Advances, 2023, 9, .	10.3	3
1542	Cangfu Daotan Wan alleviates polycystic ovary syndrome with phlegm-dampness syndrome via disruption of the PKP3/ERCC1/MAPK axis. Journal of Ovarian Research, 2023, 16, .	3.0	1
1544	Epigenetic Reprogramming in Mice and Humans: From Fertilization to Primordial Germ Cell Development. Cells, 2023, 12, 1874.	4.1	2
1546	Modeling epigenetic lesions that cause gliomas. Cell, 2023, 186, 3674-3685.e14.	28.9	10
1547	Parallel shift of DNA methylation and gene expression toward the mean in mouse spleen with aging. Aging, 0, , .	3.1	0
1548	Droplet-based bisulfite sequencing for high-throughput profiling of single-cell DNA methylomes. Nature Communications, 2023, 14, .	12.8	3
1549	The computational power of the human brain. Frontiers in Cellular Neuroscience, 0, 17, .	3.7	0
1550	Evolutionary conservation of embryonic DNA methylome remodelling in distantly related teleost species. Nucleic Acids Research, 2023, 51, 9658-9671.	14.5	3
1551	Functional genomics in Spiralia. Briefings in Functional Genomics, 2023, 22, 487-497.	2.7	2
1552	Joint single-cell profiling resolves 5mC and 5hmC and reveals their distinct gene regulatory effects. Nature Biotechnology, 0, , .	17.5	4
1553	The neuronal epigenome is special. Nature Reviews Molecular Cell Biology, 0, , .	37.0	0

#	Article	IF	CITATIONS
1554	Direct Conversion of Fibroblast into Neurons for Alzheimer's Disease Research: A Systematic Review. Journal of Alzheimer's Disease, 2023, , 1-24.	2.6	0
1555	Epigenetic regulation in major depression and other stress-related disorders: molecular mechanisms, clinical relevance and therapeutic potential. Signal Transduction and Targeted Therapy, 2023, 8, .	17.1	5
1556	Emergence and influence of sequence bias in evolutionarily malleable, mammalian tandem arrays. BMC Biology, 2023, 21, .	3.8	0
1559	DNA methylation and reader or writer proteins: Differentiation and disease. , 2024, , 343-368.		0
1560	Whole-genome bisulfite sequencing reveals the function of DNA methylation in the allotransplantation immunity of pearl oysters. Frontiers in Immunology, 0, 14, .	4.8	1
1561	Single-cell DNA methylation and 3D genome architecture in the human brain. Science, 2023, 382, .	12.6	10
1562	Unidirectional alteration of methylation and hydroxymethylation at the promoters and differential gene expression in oral squamous cell carcinoma. Frontiers in Genetics, $0,14,.$	2.3	0
1563	Epigenomic mechanisms and episignature biomarkers in rare diseases. , 2024, , 1031-1076.		0
1564	Aging and disease. , 2024, , 1177-1218.		0
1565	Integration of FUNDC1-associated mitochondrial protein import and mitochondrial quality control contributes to TDP-43 degradation. Cell Death and Disease, 2023, 14, .	6.3	2
1566	Distinct disease mutations in DNMT3A result in a spectrum of behavioral, epigenetic, and transcriptional deficits. Cell Reports, 2023, 42, 113411.	6.4	1
1567	Human neuronal maturation comes of age: cellular mechanisms and species differences. Nature Reviews Neuroscience, 2024, 25, 7-29.	10.2	3
1568	Sex difference of pre- and post-natal exposure to six developmental neurotoxicants on intellectual abilities: a systematic review and meta-analysis of human studies. Environmental Health, 2023, 22, .	4.0	2
1569	Differential usage of DNA modifications in neurons, astrocytes, and microglia. Epigenetics and Chromatin, 2023, 16, .	3.9	1
1570	Epigenetic mechanisms underlying sex differences in the brain and behavior. Trends in Neurosciences, 2024, 47, 18-35.	8.6	3
1571	Histone methylation mediated by NSD1 is required for the establishment and maintenance of neuronal identities. Cell Reports, 2023, 42, 113496.	6.4	2
1572	Epigenetic and transcriptional landscapes during cerebral cortex development in a microcephaly mouse model. Journal of Genetics and Genomics, 2023, , .	3.9	0
1575	Out of the Silence: Insights into How Genes Escape X-Chromosome Inactivation. Epigenomes, 2023, 7, 29.	1.8	1

#	Article	IF	CITATIONS
1576	ICF1-Syndrome-Associated DNMT3B Mutations Prevent De Novo Methylation at a Subset of Imprinted Loci during iPSC Reprogramming. Biomolecules, 2023, 13, 1717.	4.0	0
1577	Drug addiction and treatment: An epigenetic perspective. Biomedicine and Pharmacotherapy, 2024, 170, 115951.	5.6	1
1578	Single-cell methylation analysis of brain tissue prioritizes mutations that alter transcription. Cell Genomics, 2023, , 100454.	6.5	0
1579	Quantification of cytosine modifications in the aged mouse brain. Neuropsychopharmacology Reports, 0, , .	2.3	0
1580	Early social isolation differentially affects the glucocorticoid receptor system and alcohol-seeking behavior in male and female Marchigian Sardinian alcohol-preferring rats. Neurobiology of Stress, 2024, 28, 100598.	4.0	O
1581	MeCP2 represses the activity of topoisomerase IIβ in long neuronal genes. Cell Reports, 2023, 42, 113538.	6.4	0
1582	Outcomes of early social experiences on glucocorticoid and endocannabinoid systems in the prefrontal cortex of male and female adolescent rats. Frontiers in Cellular Neuroscience, 0, 17, .	3.7	1
1583	Brain-wide correspondence of neuronal epigenomics and distant projections. Nature, 2023, 624, 355-365.	27.8	2
1584	Single-cell DNA methylome and 3D multi-omic atlas of the adult mouse brain. Nature, 2023, 624, 366-377.	27.8	5
1586	Transcription factor-mediated direct cellular reprogramming yields cell-type specific DNA methylation signature. Scientific Reports, 2023, $13$ , .	3.3	0
1588	5-Hydroxymethylcytosine: the many faces of the sixth base of mammalian DNA. Chemical Society Reviews, 2024, 53, 2264-2283.	38.1	0
1589	MSCAN: multi-scale self- and cross-attention network for RNA methylation site prediction. BMC Bioinformatics, 2024, 25, .	2.6	1
1590	Neuropsin promotes hippocampal synaptogenesis by regulating the expression and cleavage of L1CAM. Journal of Cell Science, 2024, 137, .	2.0	0
1591	Association of prenatal exposure to perfluorinated and polyfluoroalkyl substances with childhood neurodevelopment: A systematic review and meta-analysis. Ecotoxicology and Environmental Safety, 2024, 271, 115939.	6.0	O
1592	Environmental factors and epigenetics of neuropsychiatric disorders., 2024, , 11-35.		0
1593	DNA methylation-mediated energy metabolism provides new insight into the quality losses during oyster reproductive process. Aquaculture, 2024, 583, 740595.	3.5	O
1594	Epigenetics and Down syndrome. , 2024, , 139-181.		0
1595	Uncovering the roles of DNA hemi-methylation in transcriptional regulation using MspJl-assisted hemi-methylation sequencing. Nucleic Acids Research, 2024, 52, e24-e24.	14.5	O

#	Article	IF	Citations
1597	Identification of DNA methylation biomarkers for evaluating cardiovascular disease risk from epigenome profiles altered by low-dose ionizing radiation. Clinical Epigenetics, 2024, 16, .	4.1	0
1598	Potential Role of DNA Methylation as a Driver of Plastic Responses to the Environment Across Cells, Organisms, and Populations. Genome Biology and Evolution, 2024, 16, .	2.5	0
1599	Epigenetic regulators controlling osteogenic lineage commitment and bone formation. Bone, 2024, 181, 117043.	2.9	0
1600	Emerging Functional Connections Between Metabolism and Epigenetic Remodeling in Neural Differentiation. Molecular Neurobiology, 0, , .	4.0	0
1601	Loss of NSD2 causes dysregulation of synaptic genes and altered H3K36 dimethylation in mice. Frontiers in Genetics, 0, $15$ , .	2.3	0
1602	Genome-wide comparative methylation analysis reveals the fate of germ stem cells after surrogate production in teleost. BMC Biology, 2024, 22, .	3.8	1
1603	Epigenetic mechanisms in depression: Implications for pathogenesis and treatment. Current Opinion in Neurobiology, 2024, 85, 102854.	4.2	0
1604	BISCUIT: an efficient, standards-compliant tool suite for simultaneous genetic and epigenetic inference in bulk and single-cell studies. Nucleic Acids Research, 2024, 52, e32-e32.	14.5	0
1605	Overcoming genetic and cellular complexity to study the pathophysiology of X-linked intellectual disabilities. Journal of Neurodevelopmental Disorders, 2024, 16, .	3.1	0
1606	Epigenetic Regulation in Schizophrenia: Focus on Methylation and Histone Modifications in Human Studies. Genes, 2024, 15, 272.	2.4	0
1607	Epigenomic tomography for probing spatially defined chromatin state in the brain. Cell Reports Methods, 2024, 4, 100738.	2.9	0
1609	Multi-omics provide insights into the regulation of DNA methylation in pear fruit metabolism. Genome Biology, 2024, 25, .	8.8	O