

DNA methylation landscapes: provocative insights from

Nature Reviews Genetics

9, 465-476

DOI: 10.1038/nrg2341

Citation Report

#	ARTICLE	IF	CITATIONS
1	THE EXCAVATION OF THE GRAND CANON OF THE COLORADO RIVER. <i>Science</i> , 1881, os-2, 453-454.	6.0	0
2	Epigenetics and dermatological disease. <i>Pharmacogenomics</i> , 2008, 9, 1835-1850.	0.6	52
3	Epigenome dynamics: a quantitative genetics perspective. <i>Nature Reviews Genetics</i> , 2008, 9, 883-890.	7.7	183
4	The evolving functions of DNA methylation. <i>Current Opinion in Plant Biology</i> , 2008, 11, 554-559.	3.5	83
5	Different methylation of the TNF-alpha promoter in cortex and substantia nigra: Implications for selective neuronal vulnerability. <i>Neurobiology of Disease</i> , 2008, 32, 521-527.	2.1	92
6	DNA methylation-based biomarkers for early detection of non-small cell lung cancer: an update. <i>Molecular Cancer</i> , 2008, 7, 81.	7.9	135
7	Epigenetic remodeling and stem cells. <i>Drug Discovery Today: Technologies</i> , 2008, 5, e139-e142.	4.0	0
8	Reduced-representation methylation mapping. <i>Genome Biology</i> , 2008, 9, 231.	13.9	26
9	Epigenetic modifications in rheumatoid arthritis. <i>Arthritis Research and Therapy</i> , 2008, 10, 219.	1.6	53
10	DNA Cytosine Demethylation: Are We Getting Close?. <i>Cell</i> , 2008, 135, 1167-1169.	13.5	30
11	A Charged Performance by gp17 in Viral Packaging. <i>Cell</i> , 2008, 135, 1169-1171.	13.5	4
12	Epigenetics, an emerging discipline with broad implications. <i>Comptes Rendus - Biologies</i> , 2008, 331, 837-843.	0.1	17
13	Relics of repeat-induced point mutation direct heterochromatin formation in <i>Neurospora crassa</i> . <i>Genome Research</i> , 2009, 19, 427-437.	2.4	137
14	RNA cytosine methylation analysis by bisulfite sequencing. <i>Nucleic Acids Research</i> , 2008, 37, e12-e12.	6.5	304
15	Epigenetic mechanisms in health and disease. <i>Annals of the Rheumatic Diseases</i> , 2008, 67, iii97-iii100.	0.5	39
16	Prospects for Epigenetic Epidemiology. <i>American Journal of Epidemiology</i> , 2008, 169, 389-400.	1.6	209
17	Identifying genetic components of drug response in mice. <i>Pharmacogenomics</i> , 2008, 9, 1323-1330.	0.6	2
18	New clustering module in BDPC bisulfite sequencing data presentation and compilation web application for DNA methylation analyses. <i>BioTechniques</i> , 2009, 47, 781-783.	0.8	9

#	ARTICLE	IF	CITATIONS
19	Many paths to one goal? The proteins that recognize methylated DNA in eukaryotes. <i>International Journal of Developmental Biology</i> , 2009, 53, 323-334.	0.3	76
20	Parp1 Localizes within the Dnmt1 Promoter and Protects Its Unmethylated State by Its Enzymatic Activity. <i>PLoS ONE</i> , 2009, 4, e4717.	1.1	97
21	Discovery of Novel Hypermethylated Genes in Prostate Cancer Using Genomic CpG Island Microarrays. <i>PLoS ONE</i> , 2009, 4, e4830.	1.1	81
22	Epigenetic Differences in Cortical Neurons from a Pair of Monozygotic Twins Discordant for Alzheimer's Disease. <i>PLoS ONE</i> , 2009, 4, e6617.	1.1	258
23	The Genome of the Stick Insect <i>Medauroidea extradentata</i> Is Strongly Methylated within Genes and Repetitive DNA. <i>PLoS ONE</i> , 2009, 4, e7223.	1.1	29
24	Computational approaches for understanding the evolution of DNA methylation in animals. <i>Epigenetics</i> , 2009, 4, 551-556.	1.3	55
25	Can epigenetics help in the discovery of therapeutics for psychiatric disorders, especially schizophrenia?. <i>Expert Opinion on Drug Discovery</i> , 2009, 4, 621-627.	2.5	5
26	Epigenetic biomarker development. <i>Epigenomics</i> , 2009, 1, 99-110.	1.0	112
27	DNA methylation is widespread and associated with differential gene expression in castes of the honeybee, <i>Apis mellifera</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11206-11211.	3.3	303
28	An in vitro ES cell imprinting model shows that imprinted expression of the <i>Igf2r</i> gene arises from an allele-specific expression bias. <i>Development (Cambridge)</i> , 2009, 136, 437-448.	1.2	58
29	Epigenetics: poly(ADP-ribose)ation of PARP1 regulates genomic methylation patterns. <i>FASEB Journal</i> , 2009, 23, 672-678.	0.2	154
30	A human B cell methylome at 100~base pair resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 671-678.	3.3	319
31	Deciphering Rett Syndrome with Mouse Genetics, Epigenomics, and Human Neurons. <i>International Review of Neurobiology</i> , 2009, 89, 147-160.	0.9	9
32	Distinct DNA methylation patterns characterize differentiated human embryonic stem cells and developing human fetal liver. <i>Genome Research</i> , 2009, 19, 1044-1056.	2.4	266
33	CpG-island promoters drive transcription of human telomeres. <i>Rna</i> , 2009, 15, 2186-2194.	1.6	203
34	Genome-wide screen of promoter methylation identifies novel markers in melanoma. <i>Genome Research</i> , 2009, 19, 1462-1470.	2.4	179
35	Paramutation: A Heritable Change in Gene Expression by Allelic Interactions In Trans. <i>Molecular Plant</i> , 2009, 2, 578-588.	3.9	36
36	Tissue- and Expression Level-Specific Chromatin Looping at Maize <i>b1</i> Epialleles. <i>Plant Cell</i> , 2009, 21, 832-842.	3.1	126

#	ARTICLE	IF	CITATIONS
37	High definition profiling of mammalian DNA methylation by array capture and single molecule bisulfite sequencing. <i>Genome Research</i> , 2009, 19, 1593-1605.	2.4	198
38	Molluscan Memory of Injury: Evolutionary Insights into Chronic Pain and Neurological Disorders. <i>Brain, Behavior and Evolution</i> , 2009, 74, 206-218.	0.9	69
39	High-resolution genome-wide cytosine methylation profiling with simultaneous copy number analysis and optimization for limited cell numbers. <i>Nucleic Acids Research</i> , 2009, 37, 3829-3839.	6.5	141
40	Promoting gene expression in plants by permissive histone lysine methylation. <i>Plant Signaling and Behavior</i> , 2009, 4, 484-488.	1.2	26
41	Reversing DNA Methylation: New Insights from Neuronal Activity-Induced Gadd45b in Adult Neurogenesis. <i>Science Signaling</i> , 2009, 2, pe17.	1.6	34
42	DNA Methylation Analysis of Chromosome 21 Gene Promoters at Single Base Pair and Single Allele Resolution. <i>PLoS Genetics</i> , 2009, 5, e1000438.	1.5	143
43	Dynamic regulation of DNA methylation during mammalian development. <i>Epigenomics</i> , 2009, 1, 81-98.	1.0	40
44	Epstein-Barr Virus Latency in B Cells Leads to Epigenetic Repression and CpG Methylation of the Tumour Suppressor Gene Bim. <i>PLoS Pathogens</i> , 2009, 5, e1000492.	2.1	158
45	Open chromatin encoded in DNA sequence is the signature of "master" replication origins in human cells. <i>Nucleic Acids Research</i> , 2009, 37, 6064-6075.	6.5	52
46	Survival motor neuron gene 2 silencing by DNA methylation correlates with spinal muscular atrophy disease severity and can be bypassed by histone deacetylase inhibition. <i>Human Molecular Genetics</i> , 2009, 18, 304-317.	1.4	116
47	DNA hypomethylation restricted to the murine forebrain induces cortical degeneration and impairs postnatal neuronal maturation. <i>Human Molecular Genetics</i> , 2009, 18, 2875-2888.	1.4	169
48	Epigenomic profiling indicates a role for DNA methylation in early postnatal liver development. <i>Human Molecular Genetics</i> , 2009, 18, 3026-3038.	1.4	60
49	Prediction of novel families of enzymes involved in oxidative and other complex modifications of bases in nucleic acids. <i>Cell Cycle</i> , 2009, 8, 1698-1710.	1.3	345
50	Evolving role of MeCP2 in Rett syndrome and autism. <i>Epigenomics</i> , 2009, 1, 119-130.	1.0	89
51	RNA polymerase II interacts with the Hspa1b promoter in mouse epididymal spermatozoa. <i>Reproduction</i> , 2009, 137, 923-929.	1.1	15
52	Inactive X chromosome-specific reduction in placental DNA methylation. <i>Human Molecular Genetics</i> , 2009, 18, 3544-3552.	1.4	66
53	ROS1 5-methylcytosine DNA glycosylase is a slow-turnover catalyst that initiates DNA demethylation in a distributive fashion. <i>Nucleic Acids Research</i> , 2009, 37, 4264-4274.	6.5	42
55	Genetics and epigenetics: stability and plasticity during cellular differentiation. <i>Trends in Genetics</i> , 2009, 25, 129-136.	2.9	271

#	ARTICLE	IF	CITATIONS
56	ContDist: a tool for the analysis of quantitative gene and promoter properties. <i>BMC Bioinformatics</i> , 2009, 10, 7.	1.2	8
57	Analysis of fine-scale mammalian evolutionary breakpoints provides new insight into their relation to genome organisation. <i>BMC Genomics</i> , 2009, 10, 335.	1.2	58
58	Fish sex: why so diverse?. <i>Current Opinion in Neurobiology</i> , 2009, 19, 648-653.	2.0	39
59	Kaiso is a bimodal modulator for Wnt/ β -catenin signaling. <i>FEBS Letters</i> , 2009, 583, 627-632.	1.3	30
60	Epigenetics and the embodiment of race: Developmental origins of US racial disparities in cardiovascular health. <i>American Journal of Human Biology</i> , 2009, 21, 2-15.	0.8	561
61	Use of Adsorptive Transfer Stripping Voltammetry for Analyzing Variations of Cytosine Methylation in DNA. <i>Electroanalysis</i> , 2009, 21, 2685-2692.	1.5	6
62	DNA methylation-mediated epigenetic control. <i>Journal of Cellular Biochemistry</i> , 2009, 108, 43-51.	1.2	111
63	Epigenetic control. <i>Journal of Cellular Physiology</i> , 2009, 219, 243-250.	2.0	319
64	Methylation analysis by DNA immunoprecipitation. <i>Journal of Cellular Physiology</i> , 2010, 222, 522-531.	2.0	23
65	DNA hypomethylation in the origin and pathogenesis of human diseases. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 2249-2261.	2.4	187
66	Interindividual variation in epigenomic phenomena in humans. <i>Mammalian Genome</i> , 2009, 20, 604-611.	1.0	3
67	Gene body DNA methylation in plants: a means to an end or an end to a means?. <i>EMBO Journal</i> , 2009, 28, 997-998.	3.5	58
68	Chromatin maps, histone modifications and leukemia. <i>Leukemia</i> , 2009, 23, 1243-1251.	3.3	54
69	Targeted bisulfite sequencing reveals changes in DNA methylation associated with nuclear reprogramming. <i>Nature Biotechnology</i> , 2009, 27, 353-360.	9.4	458
70	Targeted and genome-scale strategies reveal gene-body methylation signatures in human cells. <i>Nature Biotechnology</i> , 2009, 27, 361-368.	9.4	985
71	Dynamic DNA methylation programs persistent adverse effects of early-life stress. <i>Nature Neuroscience</i> , 2009, 12, 1559-1566.	7.1	1,066
72	Linking DNA methylation and histone modification: patterns and paradigms. <i>Nature Reviews Genetics</i> , 2009, 10, 295-304.	7.7	1,944
74	The role of predictive modelling in rationally re-engineering biological systems. <i>Nature Reviews Microbiology</i> , 2009, 7, 297-305.	13.6	55

#	ARTICLE	IF	CITATIONS
75	Studies on functional role of DNA methylation within the FXYD5-COX7A1 region of human chromosome 19. <i>Biochemistry (Moscow)</i> , 2009, 74, 874-881.	0.7	0
76	Chordate roots of the vertebrate nervous system: expanding the molecular toolkit. <i>Nature Reviews Neuroscience</i> , 2009, 10, 736-746.	4.9	102
77	Methylation profiles of 22 candidate genes in breast cancer using high-throughput MALDI-TOF mass array. <i>Oncogene</i> , 2009, 28, 2969-2978.	2.6	96
78	Epigenetic Regulation of Mammalian Genomes by Transposable Elements. <i>Annals of the New York Academy of Sciences</i> , 2009, 1178, 276-284.	1.8	36
79	Vitaminâ€regulated cytokines and growth factors in the CNS and elsewhere. <i>Journal of Neurochemistry</i> , 2009, 111, 1309-1326.	2.1	24
80	Preparation of genome-wide DNA fragment libraries using bisulfite in polyacrylamide gel electrophoresis slices with formamide denaturation and quality control for massively parallel sequencing by oligonucleotide ligation and detection. <i>Analytical Biochemistry</i> , 2009, 390, 126-135.	1.1	17
81	Methods in DNA methylation profiling. <i>Epigenomics</i> , 2009, 1, 331-345.	1.0	80
82	Epigenetic mechanisms for nutrition determinants of later health outcomes. <i>American Journal of Clinical Nutrition</i> , 2009, 89, 1488S-1493S.	2.2	171
83	Inflammatory signalling as mediator of epigenetic modulation in tissue-specific chronic inflammation. <i>International Journal of Biochemistry and Cell Biology</i> , 2009, 41, 176-184.	1.2	117
84	Coregulated expression of loline alkaloid-biosynthesis genes in <i>Neotyphodium uncinatum</i> cultures. <i>Fungal Genetics and Biology</i> , 2009, 46, 517-530.	0.9	16
85	A Unifying Model for the Selective Regulation of Inducible Transcription by CpG Islands and Nucleosome Remodeling. <i>Cell</i> , 2009, 138, 114-128.	13.5	528
86	Teeing Up Transcription on CpG Islands. <i>Cell</i> , 2009, 138, 14-16.	13.5	7
87	CpG islands: Algorithms and applications in methylation studies. <i>Biochemical and Biophysical Research Communications</i> , 2009, 382, 643-645.	1.0	49
88	A Shore Sign of Reprogramming. <i>Cell Stem Cell</i> , 2009, 5, 571-572.	5.2	7
89	Discovering sequences with potential regulatory characteristics. <i>Genomics</i> , 2009, 93, 314-322.	1.3	13
90	Acceleration of 5-Methylcytosine Deamination in Cyclobutane Dimers by G and Its Implications for UV-Induced C-to-T Mutation Hotspots. <i>Journal of Molecular Biology</i> , 2009, 392, 1145-1157.	2.0	76
91	Large-Scale Structural Biology of the Human Proteome. <i>Annual Review of Biochemistry</i> , 2009, 78, 541-568.	5.0	49
92	Epigenetic Regulation in Human Brainâ€Focus on Histone Lysine Methylation. <i>Biological Psychiatry</i> , 2009, 65, 198-203.	0.7	206

#	ARTICLE	IF	CITATIONS
93	Lasting Epigenetic Influence of Early-Life Adversity on the BDNF Gene. <i>Biological Psychiatry</i> , 2009, 65, 760-769.	0.7	1,115
94	Characterization of QKI Gene Expression, Genetics, and Epigenetics in Suicide Victims with Major Depressive Disorder. <i>Biological Psychiatry</i> , 2009, 66, 824-831.	0.7	67
95	Epigenetics: A Molecular Link Between Environmental Factors and Type 2 Diabetes. <i>Diabetes</i> , 2009, 58, 2718-2725.	0.3	521
96	Regulation of Stem Cell Pluripotency and Differentiation Involves a Mutual Regulatory Circuit of the Nanog, OCT4, and SOX2 Pluripotency Transcription Factors With Polycomb Repressive Complexes and Stem Cell microRNAs. <i>Stem Cells and Development</i> , 2009, 18, 1093-1108.	1.1	375
97	New Trends in Molecular Biomarker Discovery for Breast Cancer. <i>Genetic Testing and Molecular Biomarkers</i> , 2009, 13, 565-571.	0.3	34
98	Molecular Endocrinology. <i>Methods in Molecular Biology</i> , 2009, , .	0.4	4
99	Short-Read Sequencing Technologies for Transcriptional Analyses. <i>Annual Review of Plant Biology</i> , 2009, 60, 305-333.	8.6	118
100	Gene-body hypermethylation of ATM in peripheral blood DNA of bilateral breast cancer patients. <i>Human Molecular Genetics</i> , 2009, 18, 1332-1342.	1.4	124
101	Epigenetic mechanisms in cancer. <i>Biomarkers in Medicine</i> , 2009, 3, 397-410.	0.6	32
102	Development of a Novel Output Value for Quantitative Assessment in Methylated DNA Immunoprecipitation-CpG Island Microarray Analysis. <i>DNA Research</i> , 2009, 16, 275-286.	1.5	35
103	Infra- and Transspecific Clues to Understanding the Dynamics of Transposable Elements. <i>Genome Dynamics and Stability</i> , 2009, , 21-43.	1.1	5
104	Genomic and Epigenomic Instability, Fragile Sites, Schizophrenia and Autism. <i>Current Genomics</i> , 2010, 11, 447-469.	0.7	64
105	Early demethylation of non-CpG, CpC-rich, elements in the myogenin 5' flanking region. <i>Cell Cycle</i> , 2010, 9, 3965-3976.	1.3	76
107	DNA methylation for subtype classification and prediction of treatment outcome in patients with childhood acute lymphoblastic leukemia. <i>Blood</i> , 2010, 115, 1214-1225.	0.6	129
108	High-definition mapping of retroviral integration sites identifies active regulatory elements in human multipotent hematopoietic progenitors. <i>Blood</i> , 2010, 116, 5507-5517.	0.6	150
109	Structure, evolution and dynamics of transcriptional regulatory networks. <i>Biochemical Society Transactions</i> , 2010, 38, 1155-1178.	1.6	21
110	Demethylating Agents in the Treatment of Cancer. <i>Pharmaceuticals</i> , 2010, 3, 2022-2044.	1.7	50
111	Genome-Wide Evolutionary Analysis of Eukaryotic DNA Methylation. <i>Science</i> , 2010, 328, 916-919.	6.0	1,598

#	ARTICLE	IF	CITATIONS
112	Comparison of the DNA methylation profiles of human peripheral blood cells and transformed B-lymphocytes. <i>Human Genetics</i> , 2010, 127, 651-658.	1.8	53
113	Control of genic DNA methylation in <i>Arabidopsis</i> . <i>Journal of Plant Research</i> , 2010, 123, 299-302.	1.2	16
114	DNA methylation pattern in a barley reconstructed karyotype with deleted ribosomal gene cluster of chromosome 6H. <i>Protoplasma</i> , 2010, 242, 13-18.	1.0	4
115	Les folates dans la prÃ©vention et dans le dÃ©terminisme du cancer. <i>Journal Africain Du Cancer</i> , 2010, 2, 171-177.	0.1	0
116	The epigenetics of social adversity in early life: Implications for mental health outcomes. <i>Neurobiology of Disease</i> , 2010, 39, 66-72.	2.1	246
117	Cannabinoids and the gut: New developments and emerging concepts. , 2010, 126, 21-38.		365
118	Evolution of Eukaryotic DNA Methylation and the Pursuit of Safer Sex. <i>Current Biology</i> , 2010, 20, R780-R785.	1.8	160
119	Cancer chemoprevention by dietary polyphenols: Promising role for epigenetics. <i>Biochemical Pharmacology</i> , 2010, 80, 1771-1792.	2.0	411
120	To Infinium, and Beyond!. <i>Cancer Cell</i> , 2010, 17, 419-420.	7.7	10
121	More is less: Inactivation and deletion events and the search for tumor suppressor genes. <i>Journal of Cellular Biochemistry</i> , 2010, 110, 281-287.	1.2	2
122	How the epigenome contributes to the development of psychiatric disorders. <i>Developmental Psychobiology</i> , 2010, 52, 331-342.	0.9	43
123	Identification of methylated regions with peak search based on Poisson model from massively parallel methylated DNA immunoprecipitationâ€™sequencing data. <i>Electrophoresis</i> , 2010, 31, 3537-3544.	1.3	4
124	Vasa genes: Emerging roles in the germ line and in multipotent cells. <i>BioEssays</i> , 2010, 32, 626-637.	1.2	142
125	Mammalian methylâ€™binding proteins: What might they do?. <i>BioEssays</i> , 2010, 32, 1025-1032.	1.2	19
126	Unveiling the methylation status of CpG dinucleotides in the substituted segment of the human p53 knockâ€™in (<i>Hupki</i>) mouse genome. <i>Molecular Carcinogenesis</i> , 2010, 49, 999-1006.	1.3	5
127	Genome-wide DNA methylation analysis for diabetic nephropathy in type 1 diabetes mellitus. <i>BMC Medical Genomics</i> , 2010, 3, 33.	0.7	261
128	Transcription-dependent silencing of inducible convergent transgenes in transgenic mice. <i>Epigenetics and Chromatin</i> , 2010, 3, 3.	1.8	27
129	Epigenetic histone modifications of human transposable elements: genome defense versus exaptation. <i>Mobile DNA</i> , 2010, 1, 2.	1.3	60

#	ARTICLE	IF	CITATIONS
130	Genome-wide DNA methylation profiling. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 210-223.	6.6	85
131	DNA methylation and gene expression. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 362-371.	6.6	138
132	By 2020. <i>Prenatal Diagnosis</i> , 2010, 30, 710-711.	1.1	3
133	Epigenetic control of expression of the human <i>hMLH1</i> and <i>hMSH2</i> pigment genes. <i>Ophthalmic and Physiological Optics</i> , 2010, 30, 446-453.	1.0	9
134	Genome-wide DNA methylation profiles in precancerous conditions and cancers. <i>Cancer Science</i> , 2010, 101, 36-45.	1.7	107
135	Molecular genetic and epigenetic analysis of <i>NCX2</i> and <i>SLC8A2</i> at 19q13.3 in human gliomas. <i>Neuropathology and Applied Neurobiology</i> , 2010, 36, 198-210.	1.8	13
136	Ploidy and DNA methylation: new tools available. <i>Molecular Ecology</i> , 2010, 19, 213-215.	2.0	21
137	Environmentally induced phenotypes and DNA methylation: how to deal with unpredictable conditions until the next generation and after. <i>Molecular Ecology</i> , 2010, 19, 1283-1295.	2.0	293
138	Regulation of major histocompatibility complex class II gene expression, genetic variation and disease. <i>Genes and Immunity</i> , 2010, 11, 99-112.	2.2	122
139	Epigenetic regulation of neurogenesis in the adult hippocampus. <i>Heredity</i> , 2010, 105, 122-134.	1.2	70
140	Repeat elements and the Arabidopsis DNA methylation landscape. <i>Heredity</i> , 2010, 105, 14-23.	1.2	80
141	Chromatin remodelling during development. <i>Nature</i> , 2010, 463, 474-484.	13.7	936
142	CpG islands influence chromatin structure via the CpG-binding protein Cfp1. <i>Nature</i> , 2010, 464, 1082-1086.	13.7	577
143	Single base-resolution methylome of the silkworm reveals a sparse epigenomic map. <i>Nature Biotechnology</i> , 2010, 28, 516-520.	9.4	349
144	Epigenetic modification of fetal baboon hepatic phosphoenolpyruvate carboxykinase following exposure to moderately reduced nutrient availability. <i>Journal of Physiology</i> , 2010, 588, 1349-1359.	1.3	111
145	Core promoters as an example of the effect of whole-genome information on the evolution of views on molecular mechanisms of vital activity. <i>Molecular Biology</i> , 2010, 44, 682-692.	0.4	2
146	Tackling the epigenome: challenges and opportunities for collaboration. <i>Nature Biotechnology</i> , 2010, 28, 1039-1044.	9.4	82
147	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010, 28, 1045-1048.	9.4	1,705

#	ARTICLE	IF	CITATIONS
148	DNA methylation and memory formation. <i>Nature Neuroscience</i> , 2010, 13, 1319-1323.	7.1	432
149	Establishing, maintaining and modifying DNA methylation patterns in plants and animals. <i>Nature Reviews Genetics</i> , 2010, 11, 204-220.	7.7	3,201
150	Looking beyond promoters. <i>Nature Reviews Genetics</i> , 2010, 11, 596-596.	7.7	4
151	Epigenetics in heart failure. <i>Annals of the New York Academy of Sciences</i> , 2010, 1188, 159-164.	1.8	19
152	Epigenetic reprogramming: Enforcer or enabler of developmental fate?. <i>Development Growth and Differentiation</i> , 2010, 52, 483-491.	0.6	13
153	Epigenetic performers in plants. <i>Development Growth and Differentiation</i> , 2010, 52, 555-566.	0.6	65
154	Grain Yield Heterosis in <i>Zea mays</i> L. Shows Positive Correlation with Parental Difference in CHG Methylation. <i>Crop Science</i> , 2010, 50, 2338-2346.	0.8	10
155	DNA Methylation and Genome Evolution in Honeybee: Gene Length, Expression, Functional Enrichment Covary with the Evolutionary Signature of DNA Methylation. <i>Genome Biology and Evolution</i> , 2010, 2, 770-780.	1.1	45
156	An epigenetic hypothesis of aging-related cognitive dysfunction. <i>Frontiers in Aging Neuroscience</i> , 2010, 2, 9.	1.7	120
157	SETDB1 Is Involved in Postembryonic DNA Methylation and Gene Silencing in <i>Drosophila</i> . <i>PLoS ONE</i> , 2010, 5, e10581.	1.1	22
158	Integrated Genetic and Epigenetic Analysis Identifies Haplotype-Specific Methylation in the FTO Type 2 Diabetes and Obesity Susceptibility Locus. <i>PLoS ONE</i> , 2010, 5, e14040.	1.1	215
159	F5HD: copy number variations on the theme of muscular dystrophy. <i>Journal of Cell Biology</i> , 2010, 191, 1049-1060.	2.3	112
160	EPIGENETIC PROGRAMMING AND FETAL GROWTH RESTRICTIONS. <i>Fetal and Maternal Medicine Review</i> , 2010, 21, 204-224.	0.3	1
161	Chemical discrimination between dC and 5Me dC via their hydroxylamine adducts. <i>Nucleic Acids Research</i> , 2010, 38, e192-e192.	6.5	34
162	DNA methylation and epigenetic control of cellular differentiation. <i>Cell Cycle</i> , 2010, 9, 3880-3883.	1.3	127
163	Confining euchromatin/heterochromatin territory: <i>jumonji</i> crosses the line. <i>Genes and Development</i> , 2010, 24, 1465-1478.	2.7	82
164	Domain structure of the DEMETER 5-methylcytosine DNA glycosylase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19225-19230.	3.3	66
165	A single amino acid substitution confers enhanced methylation activity of mammalian Dnmt3b on chromatin DNA. <i>Nucleic Acids Research</i> , 2010, 38, 6054-6064.	6.5	9

#	ARTICLE	IF	CITATIONS
166	Application of OMICS technologies in occupational and environmental health research; current status and projections. <i>Occupational and Environmental Medicine</i> , 2010, 67, 136-143.	1.3	107
167	Methylation Regulates Alpha-Synuclein Expression and Is Decreased in Parkinson's Disease Patients' Brains. <i>Journal of Neuroscience</i> , 2010, 30, 6355-6359.	1.7	364
168	Identification and characterization of putative methylation targets in the MAOA locus using bioinformatic approaches. <i>Epigenetics</i> , 2010, 5, 325-342.	1.3	28
169	A homogeneous method for investigation of methylation-dependent protein-protein interactions in epigenetics. <i>Nucleic Acids Research</i> , 2010, 38, e11-e11.	6.5	51
170	Chromatin Remodeling in Mammary Gland Differentiation and Breast Tumorigenesis. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010, 2, a004515-a004515.	2.3	33
171	Multivalent epigenetic marks confer microenvironment-responsive epigenetic plasticity to ovarian cancer cells. <i>Epigenetics</i> , 2010, 5, 716-729.	1.3	51
172	Do different neurons age differently? Direct genome-wide analysis of aging in single identified cholinergic neurons. <i>Frontiers in Aging Neuroscience</i> , 2010, 2, .	1.7	65
173	DNA Adenine Methylation Is Required to Replicate Both <i>Vibrio cholerae</i> Chromosomes Once per Cell Cycle. <i>PLoS Genetics</i> , 2010, 6, e1000939.	1.5	61
174	Interplay between DNA Methylation and Transcription Factor Availability: Implications for Developmental Activation of the Mouse Myogenin Gene. <i>Molecular and Cellular Biology</i> , 2010, 30, 3805-3815.	1.1	71
175	MetMap Enables Genome-Scale Methylation Typing for Determining Methylation States in Populations. <i>PLoS Computational Biology</i> , 2010, 6, e1000888.	1.5	11
176	Aging and Chronic Sun Exposure Cause Distinct Epigenetic Changes in Human Skin. <i>PLoS Genetics</i> , 2010, 6, e1000971.	1.5	217
177	Heterodimeric DNA methyltransferases as a platform for creating designer zinc finger methyltransferases for targeted DNA methylation in cells. <i>Nucleic Acids Research</i> , 2010, 38, 1749-1759.	6.5	29
178	Epigenetics and Obesity. <i>Progress in Molecular Biology and Translational Science</i> , 2010, 94, 291-347.	0.9	81
179	The DNA Methylome of Human Peripheral Blood Mononuclear Cells. <i>PLoS Biology</i> , 2010, 8, e1000533.	2.6	290
180	VEZF1 Elements Mediate Protection from DNA Methylation. <i>PLoS Genetics</i> , 2010, 6, e1000804.	1.5	91
181	A yeast one-hybrid system to screen for methylated DNA-binding proteins. <i>Nucleic Acids Research</i> , 2010, 38, e189-e189.	6.5	12
182	Two thymidine hydroxylases differentially regulate the formation of glucosylated DNA at regions flanking polymerase II polycistronic transcription units throughout the genome of <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2010, 38, 3923-3935.	6.5	84
183	Genome-wide analysis of epigenetic signatures for kidney-specific transporters. <i>Kidney International</i> , 2010, 78, 569-577.	2.6	27

#	ARTICLE	IF	CITATIONS
184	Reconciling the positive and negative roles of histone H2A.Z in gene transcription. <i>Epigenetics</i> , 2010, 5, 267-272.	1.3	94
185	Challenges ahead for mass spectrometry and proteomics applications in epigenetics. <i>Epigenomics</i> , 2010, 2, 163-167.	1.0	2
186	Epigenetic control of inducible gene expression in the immune system. <i>Epigenomics</i> , 2010, 2, 775-795.	1.0	16
187	Functional Conservation of DNA Methylation in the Pea Aphid and the Honeybee. <i>Genome Biology and Evolution</i> , 2010, 2, 719-728.	1.1	109
188	Epigenetic approaches for the detection of fetal DNA in maternal plasma. <i>Chimerism</i> , 2010, 1, 30-35.	0.7	26
189	Comparing genome-wide chromatin profiles using ChIP-chip or ChIP-seq. <i>Bioinformatics</i> , 2010, 26, 1000-1006.	1.8	28
190	Metabolic memory and diabetic nephropathy: potential role for epigenetic mechanisms. <i>Nature Reviews Nephrology</i> , 2010, 6, 332-341.	4.1	107
191	Methylation of DNA in Cancer. <i>Advances in Clinical Chemistry</i> , 2010, 52, 145-167.	1.8	120
192	Epigenetics of Schizophrenia. <i>Current Topics in Behavioral Neurosciences</i> , 2010, 4, 611-628.	0.8	54
193	Detection of Food-Derived Damaged Nucleosides with Possible Adverse Effects on Human Health Using a Global Adductomics Approach. <i>Journal of Agricultural and Food Chemistry</i> , 2010, 58, 6370-6375.	2.4	16
194	Function and detection of 5-methylcytosine in eukaryotic RNA. <i>Epigenomics</i> , 2010, 2, 709-715.	1.0	43
195	Perinatal folate-related exposures and risk of psychotic symptoms in the ALSPAC birth cohort. <i>Schizophrenia Research</i> , 2010, 120, 177-183.	1.1	16
196	Variation, patterns, and temporal stability of DNA methylation: considerations for epigenetic epidemiology. <i>FASEB Journal</i> , 2010, 24, 3135-3144.	0.2	287
197	Epigenetics in asthma and other inflammatory lung diseases. <i>Epigenomics</i> , 2010, 2, 523-537.	1.0	25
198	Investigation of DNA damage response and apoptotic gene methylation pattern in sporadic breast tumors using high throughput quantitative DNA methylation analysis technology. <i>Molecular Cancer</i> , 2010, 9, 303.	7.9	31
199	Nutrition, Epigenomics and the Development of Obesity. , 2010, , 191-201.		3
200	Small-Molecule-Based Inhibition of Histone Demethylation in Cells Assessed by Quantitative Mass Spectrometry. <i>Journal of Proteome Research</i> , 2010, 9, 4082-4092.	1.8	56
201	The epigenomic interface between genome and environment in common complex diseases. <i>Briefings in Functional Genomics</i> , 2010, 9, 477-485.	1.3	55

#	ARTICLE	IF	CITATIONS
202	Combined Proteomic and Transcriptomic Analysis Identifies Differentially Expressed Pathways Associated to <i>Pinus radiata</i> Needle Maturation. <i>Journal of Proteome Research</i> , 2010, 9, 3954-3979.	1.8	56
203	Dnmt3a-Dependent Nonpromoter DNA Methylation Facilitates Transcription of Neurogenic Genes. <i>Science</i> , 2010, 329, 444-448.	6.0	544
204	Epigenome Mapping in Normal and Disease States. <i>Circulation Research</i> , 2010, 107, 327-339.	2.0	164
205	Extending the maternal-zygotic effect with genomic imprinting. <i>Molecular Human Reproduction</i> , 2010, 16, 695-703.	1.3	9
206	Genomic imprinting in diabetes. <i>Genome Medicine</i> , 2010, 2, 55.	3.6	11
207	Molecular aspects of steroidogenic factor 1 (SF-1). <i>Molecular and Cellular Endocrinology</i> , 2010, 315, 27-39.	1.6	126
208	The molecular pathology of schizophrenia—Focus on histone and DNA modifications. <i>Brain Research Bulletin</i> , 2010, 83, 103-107.	1.4	37
209	Odd-skipped related 2 is epigenetically regulated in cellular quiescence. <i>Biochemical and Biophysical Research Communications</i> , 2010, 396, 831-836.	1.0	4
210	The obesity-associated Fto gene is a transcriptional coactivator. <i>Biochemical and Biophysical Research Communications</i> , 2010, 401, 390-395.	1.0	87
211	Histone Methyl Transferases and Demethylases; Can They Link Metabolism and Transcription?. <i>Cell Metabolism</i> , 2010, 12, 321-327.	7.2	231
212	Epigenetic changes in Alzheimer's disease: Decrements in DNA methylation. <i>Neurobiology of Aging</i> , 2010, 31, 2025-2037.	1.5	336
213	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. <i>Cell Stem Cell</i> , 2010, 6, 479-491.	5.2	747
214	Epigenetic reprogramming of host genes in viral and microbial pathogenesis. <i>Trends in Microbiology</i> , 2010, 18, 439-447.	3.5	239
215	Targeting DNA methylation for epigenetic therapy. <i>Trends in Pharmacological Sciences</i> , 2010, 31, 536-546.	4.0	275
216	A-Z of methylome analysis. <i>Methods</i> , 2010, 52, 201-202.	1.9	2
217	Methylation of TFAM gene promoter in peripheral white blood cells is associated with insulin resistance in adolescents. <i>Molecular Genetics and Metabolism</i> , 2010, 100, 83-87.	0.5	60
218	Autism Spectrum Disorders and Epigenetics. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2010, 49, 794-809.	0.3	197
219	DNA methylation in cell differentiation and reprogramming: an emerging systematic view. <i>Regenerative Medicine</i> , 2010, 5, 531-544.	0.8	64

#	ARTICLE	IF	CITATIONS
220	5-methylcytosine in RNA: detection, enzymatic formation and biological functions. <i>Nucleic Acids Research</i> , 2010, 38, 1415-1430.	6.5	300
221	Bisulfite methylation profiling of large genomes. <i>Epigenomics</i> , 2010, 2, 209-220.	1.0	16
222	DNA cytosine methylation in plant development. <i>Journal of Genetics and Genomics</i> , 2010, 37, 1-12.	1.7	172
223	Dietary Methionine Affect Meat Quality and Myostatin Gene Exon 1 Region Methylation in Skeletal Muscle Tissues of Broilers. <i>Agricultural Sciences in China</i> , 2010, 9, 1338-1346.	0.6	22
224	CpG island clusters and pro-epigenetic selection for CpGs in protein-coding exons of HOX and other transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 15485-15490.	3.3	51
225	Conservation and divergence of methylation patterning in plants and animals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8689-8694.	3.3	1,160
226	Epigenome manipulation as a pathway to new natural product scaffolds and their congeners. <i>Natural Product Reports</i> , 2010, 27, 11-22.	5.2	266
227	The Application of Next Generation Sequencing in DNA Methylation Analysis. <i>Genes</i> , 2010, 1, 85-101.	1.0	51
228	Phylogeny of Methylomes. <i>Science</i> , 2010, 328, 837-838.	6.0	64
229	Emergence of the osteo-epigenome in bone biology. <i>IBMS BoneKEy</i> , 2010, 7, 314-324.	0.1	5
230	Emerging promise of epigenetics and DNA methylation for the diagnosis and management of women's cancers. <i>Epigenomics</i> , 2010, 2, 9-38.	1.0	25
231	Bioinformatics approaches for genomics and post genomics applications of next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2010, 11, 181-197.	3.2	141
232	Epigenetics of Aging. , 2010, , .		10
233	Epigenetics in cancer. <i>Carcinogenesis</i> , 2010, 31, 27-36.	1.3	2,119
235	Chromatin-Based Treatments for Affective Disorders – Insight or Utopia. <i>Modern Problems of Pharmacopsychiatry</i> , 2010, , 182-198.	2.5	1
236	Functional genomics and rheumatoid arthritis: where have we been and where should we go?. <i>Genome Medicine</i> , 2010, 2, 44.	3.6	11
237	DNA manipulation, sorting, and mapping in nanofluidic systems. <i>Chemical Society Reviews</i> , 2010, 39, 1133.	18.7	158
238	Aging Hair. , 2010, , .		22

#	ARTICLE	IF	CITATIONS
239	Behavioral Neurobiology of Schizophrenia and Its Treatment. Current Topics in Behavioral Neurosciences, 2010, , .	0.8	8
240	Mammalian <i>Su(Hw)</i> Genes in Chromatin Control. Annual Review of Cell and Developmental Biology, 2010, 26, 471-501.	4.0	91
241	Discrimination of N6-methyl adenine in a specific DNA sequence. Chemical Communications, 2010, 46, 5530.	2.2	17
242	Introduction into the analysis of high-throughput-sequencing based epigenome data. Briefings in Bioinformatics, 2010, 11, 512-523.	3.2	27
243	Identification of CpG islands in DNA sequences using supervised classification. , 2011, , .		1
244	Epigenetic regulation of satellite cell activation during muscle regeneration. Stem Cell Research and Therapy, 2011, 2, 18.	2.4	55
245	Genomic DNA Hypomethylation by Histone Deacetylase Inhibition Implicates DNMT1 Nuclear Dynamics. Molecular and Cellular Biology, 2011, 31, 4119-4128.	1.1	57
246	DNA Methylation: Superior or Subordinate in the Epigenetic Hierarchy?. Genes and Cancer, 2011, 2, 607-617.	0.6	564
247	Divergent DNA Methylation Patterns Associated with Abiotic Stress in Hevea brasiliensis. Molecular Plant, 2011, 4, 996-1013.	3.9	63
248	Mechanisms and functions of Tet protein-mediated 5-methylcytosine oxidation. Genes and Development, 2011, 25, 2436-2452.	2.7	565
250	Broad Epigenetic Signature of Maternal Care in the Brain of Adult Rats. PLoS ONE, 2011, 6, e14739.	1.1	406
251	Mechanisms of Epigenetic Gene Activation in Disease: Dynamics of DNA Methylation and Demethylation. , 2011, , 55-73.		0
252	The Epigenome and Plant Development. Annual Review of Plant Biology, 2011, 62, 411-435.	8.6	172
253	DNA methylation directly silences genes with non-CpG island promoters and establishes a nucleosome occupied promoter. Human Molecular Genetics, 2011, 20, 4299-4310.	1.4	172
254	Generation and replication-dependent dilution of 5fC and 5caC during mouse preimplantation development. Cell Research, 2011, 21, 1670-1676.	5.7	244
255	Genome-Wide Epigenetic Modifications in Cancer. , 2011, 67, 25-49.		43
256	Recruitment of Dnmt1. Progress in Molecular Biology and Translational Science, 2011, 101, 289-310.	0.9	29
257	Mechanistic and Functional Links Between Histone Methylation and DNA Methylation. Progress in Molecular Biology and Translational Science, 2011, 101, 335-348.	0.9	12

#	ARTICLE	IF	CITATIONS
258	Biological Functions of Methyl-CpG-Binding Proteins. Progress in Molecular Biology and Translational Science, 2011, 101, 377-398.	0.9	80
259	Evaluation of the Infinium Methylation 450K technology. Epigenomics, 2011, 3, 771-784.	1.0	514
260	DNA Methylation and Cancer. , 2011, 67, 1-23.		89
261	Epigenetics and Disease. , 2011, , .		5
262	Turn-On DNA Damage Sensors for the Direct Detection of 8-Oxoguanine and Photoproducts in Native DNA. Journal of the American Chemical Society, 2011, 133, 12518-12527.	6.6	27
264	Reprogramming of the paternal genome upon fertilization involves genome-wide oxidation of 5-methylcytosine. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3642-3647.	3.3	618
265	DNA Methylation Detection: Bisulfite Genomic Sequencing Analysis. Methods in Molecular Biology, 2011, 791, 11-21.	0.4	212
266	New concepts of old epigenetic phenomena and their implications for selecting specific cell populations for epigenomic research. Epigenomics, 2011, 3, 383-386.	1.0	10
267	Synthesis and Biochemical Evaluation of β -Isoxazoline Derivatives as DNA Methyltransferase 1 Inhibitors. Journal of Medicinal Chemistry, 2011, 54, 7663-7677.	2.9	154
268	Hydroxylation of 5-Methylcytosine by TET1 Promotes Active DNA Demethylation in the Adult Brain. Cell, 2011, 145, 423-434.	13.5	1,196
269	Epigenetic regulation of transposable element derived human gene promoters. Gene, 2011, 475, 39-48.	1.0	42
270	Heterogeneity and degree of TIMP4, GATA4, SOX18, and EGFL7 gene promoter methylation in non-small cell lung cancer and surrounding tissues. Cancer Genetics, 2011, 204, 492-500.	0.2	33
271	Amyloid protein-mediated differential DNA methylation status regulates gene expression in Alzheimer's disease model cell line. Biochemical and Biophysical Research Communications, 2011, 414, 700-705.	1.0	37
272	Neuronal activity modifies the DNA methylation landscape in the adult brain. Nature Neuroscience, 2011, 14, 1345-1351.	7.1	601
273	Direct lineage conversions: unnatural but useful?. Nature Biotechnology, 2011, 29, 892-907.	9.4	240
274	Genome-wide Regulation of 5hmC, 5mC, and Gene Expression by Tet1 Hydroxylase in Mouse Embryonic Stem Cells. Molecular Cell, 2011, 42, 451-464.	4.5	551
275	Regulation of Primary Response Genes. Molecular Cell, 2011, 44, 348-360.	4.5	196
276	Epigenetic modifications induced by early enrichment are associated with changes in timing of induction of BDNF expression. Neuroscience Letters, 2011, 495, 168-172.	1.0	76

#	ARTICLE	IF	CITATIONS
277	Differential Methylation of Imprinted Genes in Growth-Restricted Placentas. <i>Reproductive Sciences</i> , 2011, 18, 1111-1117.	1.1	38
278	Uhrf1 and Dnmt1 are required for development and maintenance of the zebrafish lens. <i>Developmental Biology</i> , 2011, 350, 50-63.	0.9	76
279	Comprehensive analysis of DNA-methylation in mammalian tissues using MeDIP-chip. <i>Methods</i> , 2011, 53, 175-184.	1.9	28
280	Epigenetic mechanisms in Alzheimer's disease: progress but much to do. <i>Neurobiology of Aging</i> , 2011, 32, 1181-1187.	1.5	19
281	Epigenetic gene regulation in the adult mammalian brain: Multiple roles in memory formation. <i>Neurobiology of Learning and Memory</i> , 2011, 96, 68-78.	1.0	59
282	The supply of choline is important for fetal progenitor cells. <i>Seminars in Cell and Developmental Biology</i> , 2011, 22, 624-628.	2.3	53
284	Down-regulation of UHRF1, associated with re-expression of tumor suppressor genes, is a common feature of natural compounds exhibiting anti-cancer properties. <i>Journal of Experimental and Clinical Cancer Research</i> , 2011, 30, 41.	3.5	97
285	Near-Neutrality, Robustness, and Epigenetics. <i>Genome Biology and Evolution</i> , 2011, 3, 1034-1038.	1.1	27
286	Small RNA-Induced Transcriptional Gene Regulation in Mammals. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 102, 11-46.	0.9	9
288	Mid-Range Inhomogeneity of Eukaryotic Genomes. <i>Scientific World Journal, The</i> , 2011, 11, 842-854.	0.8	5
289	Epigenetic regulation in cancer development. <i>Frontiers in Bioscience - Landmark</i> , 2011, 16, 2682.	3.0	17
290	Modeling regulatory motifs. , 0, , 126-147.		0
292	Epigenetic Silencing of Nucleolar rRNA Genes in Alzheimer's Disease. <i>PLoS ONE</i> , 2011, 6, e22585.	1.1	124
293	Integrated Epigenetics of Human Breast Cancer: Synoptic Investigation of Targeted Genes, MicroRNAs and Proteins upon Demethylation Treatment. <i>PLoS ONE</i> , 2011, 6, e27355.	1.1	46
294	Cell specific patterns of methylation in the human placenta. <i>Epigenetics</i> , 2011, 6, 368-379.	1.3	62
295	Interstrand Crosslink for Discrimination of Methylated Cytosines. <i>Chemistry Letters</i> , 2011, 40, 852-854.	0.7	0
296	c-JUN promotes BCR-ABL ⁺ induced lymphoid leukemia by inhibiting methylation of the 5' region of Cdk6. <i>Blood</i> , 2011, 117, 4065-4075.	0.6	34
297	Microbial and Plant Cell Synthesis of Secondary Metabolites and Strain Improvement. , 2011, , 121-156.		0

#	ARTICLE	IF	CITATIONS
298	DNA hypermethylation of the NOX5 gene in fetal ventricular septal defect. <i>Experimental and Therapeutic Medicine</i> , 2011, 2, 1011-1015.	0.8	27
299	Epigenetics of Early Child Development. <i>Frontiers in Psychiatry</i> , 2011, 2, 16.	1.3	136
300	Hypermethylation of Tumor Suppressor Genes Involved in Critical Regulatory Pathways for Developing a Blood-Based Test in Breast Cancer. <i>PLoS ONE</i> , 2011, 6, e16080.	1.1	131
301	Epigenetic control of development and expression of quantitative traits. <i>Reproduction, Fertility and Development</i> , 2011, 23, 64.	0.1	43
302	Epigenetic regulation of neurogenesis in the adult mammalian brain. <i>European Journal of Neuroscience</i> , 2011, 33, 1087-1093.	1.2	87
303	Virus-mediated efficient induction of epigenetic modifications of endogenous genes with phenotypic changes in plants. <i>Plant Journal</i> , 2011, 65, 156-168.	2.8	100
304	DNA methylation in insects: on the brink of the epigenomic era. <i>Insect Molecular Biology</i> , 2011, 20, 553-565.	1.0	211
305	Control of nuclear receptor function by local chromatin structure. <i>FEBS Journal</i> , 2011, 278, 2211-2230.	2.2	35
306	Structure and function of active chromatin and DNase I hypersensitive sites. <i>FEBS Journal</i> , 2011, 278, 2182-2210.	2.2	110
307	DNA methylation in oral squamous cell carcinoma: molecular mechanisms and clinical implications. <i>Oral Diseases</i> , 2011, 17, 771-778.	1.5	31
308	Cancer epigenetics reaches mainstream oncology. <i>Nature Medicine</i> , 2011, 17, 330-339.	15.2	1,102
309	TET1 and hydroxymethylcytosine in transcription and DNA methylation fidelity. <i>Nature</i> , 2011, 473, 343-348.	13.7	905
310	The epigenetic landscape of addiction. <i>Annals of the New York Academy of Sciences</i> , 2011, 1216, 99-113.	1.8	190
311	Unraveling the Glioma Epigenome—From Molecular Mechanisms to Novel Biomarkers and Therapeutic Targets. <i>Brain Pathology</i> , 2011, 21, 619-632.	2.1	38
312	Exposing the DNA methylome iceberg. <i>Trends in Biochemical Sciences</i> , 2011, 36, 381-7.	3.7	78
313	Insects as innovative models for functional studies of DNA methylation. <i>Trends in Genetics</i> , 2011, 27, 127-131.	2.9	188
314	Emerging patterns of epigenomic variation. <i>Trends in Genetics</i> , 2011, 27, 242-250.	2.9	33
315	Genomic and chromatin signals underlying transcription start-site selection. <i>Trends in Genetics</i> , 2011, 27, 475-485.	2.9	59

#	ARTICLE	IF	CITATIONS
316	Epigenetic alterations associated with cellular senescence: A barrier against tumorigenesis or a red carpet for cancer?. <i>Seminars in Cancer Biology</i> , 2011, 21, 360-366.	4.3	35
317	Methylation and demethylation of the Arabidopsis genome. <i>Current Opinion in Plant Biology</i> , 2011, 14, 137-141.	3.5	88
318	RNA-directed DNA methylation. <i>Current Opinion in Plant Biology</i> , 2011, 14, 142-147.	3.5	232
319	Methylation changes associated with early maturation stages in the Atlantic salmon. <i>BMC Genetics</i> , 2011, 12, 86.	2.7	71
320	High resolution profiling of human exon methylation by liquid hybridization capture-based bisulfite sequencing. <i>BMC Genomics</i> , 2011, 12, 597.	1.2	25
321	Adolescent idiopathic scoliosis (AIS), environment, exposome and epigenetics: a molecular perspective of postnatal normal spinal growth and the etiopathogenesis of AIS with consideration of a network approach and possible implications for medical therapy. <i>Scoliosis</i> , 2011, 6, 26.	0.4	56
322	Event extraction for DNA methylation. <i>Journal of Biomedical Semantics</i> , 2011, 2, S2.	0.9	11
323	Hypermethylation-modulated Downregulation of RASSF1A Expression Is Associated with the Progression of Esophageal Cancer. <i>Archives of Medical Research</i> , 2011, 42, 182-188.	1.5	13
324	DNA methylation systems and targets in plants. <i>FEBS Letters</i> , 2011, 585, 2008-2015.	1.3	73
325	The DNA methylome. <i>FEBS Letters</i> , 2011, 585, 1994-2000.	1.3	80
326	S-Adenosylmethionine-dependent alkylation reactions: When are radical reactions used?. <i>Bioorganic Chemistry</i> , 2011, 39, 161-170.	2.0	48
327	Snf2-family proteins: chromatin remodellers for any occasion. <i>Current Opinion in Chemical Biology</i> , 2011, 15, 649-656.	2.8	103
328	DNA hypermethylation as a chemotherapy target. <i>Cellular Signalling</i> , 2011, 23, 1082-1093.	1.7	91
329	Epigenetics and colorectal cancer. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2011, 8, 686-700.	8.2	577
330	Genomic mapping of 5-hydroxymethylcytosine in the human brain. <i>Nucleic Acids Research</i> , 2011, 39, 5015-5024.	6.5	344
331	Lysine Demethylases Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 8236-8250.	2.9	140
332	Epigenomics of human embryonic stem cells and induced pluripotent stem cells: insights into pluripotency and implications for disease. <i>Genome Medicine</i> , 2011, 3, 36.	3.6	49
333	Studying the epigenome using next generation sequencing. <i>Journal of Medical Genetics</i> , 2011, 48, 721-730.	1.5	108

#	ARTICLE	IF	CITATIONS
334	Epigenetic mechanisms in experience-driven memory formation and behavior. <i>Epigenomics</i> , 2011, 3, 649-664.	1.0	60
335	Tobacco-Smoking-Related Differential DNA Methylation: 27K Discovery and Replication. <i>American Journal of Human Genetics</i> , 2011, 88, 450-457.	2.6	582
336	Epigenetics and its implications for ecotoxicology. <i>Ecotoxicology</i> , 2011, 20, 607-624.	1.1	149
337	Expression of the dnmt3 genes in zebrafish development: similarity to Dnmt3a and Dnmt3b. <i>Development Genes and Evolution</i> , 2011, 220, 347-353.	0.4	31
338	Stable transmission of reversible modifications: maintenance of epigenetic information through the cell cycle. <i>Cellular and Molecular Life Sciences</i> , 2011, 68, 27-44.	2.4	55
339	Epigenetic aberrations during oncogenesis. <i>Cellular and Molecular Life Sciences</i> , 2011, 68, 1681-1702.	2.4	156
340	The optimal conditions for the estimation of DNA methylation levels using high throughput microarray derived DNA immunoprecipitation (MeDIP)-enrichment in human bloods. <i>Toxicology and Environmental Health Sciences</i> , 2011, 3, 185-192.	1.1	1
341	Network modelling of gene regulation. <i>Biophysical Reviews</i> , 2011, 3, 1-13.	1.5	4
342	Epigenetic mechanisms in virus-induced tumorigenesis. <i>Clinical Epigenetics</i> , 2011, 2, 233-247.	1.8	43
343	The struggle for life of the genome's selfish architects. <i>Biology Direct</i> , 2011, 6, 19.	1.9	198
344	Comprehensive profiling of zebrafish hepatic proximal promoter CpG island methylation and its modification during chemical carcinogenesis. <i>BMC Genomics</i> , 2011, 12, 3.	1.2	48
346	DNA Methylation and Nonsmall Cell Lung Cancer. <i>Anatomical Record</i> , 2011, 294, 1787-1795.	0.8	36
347	Fused-core silica column ultra-performance liquid chromatography-ion trap tandem mass spectrometry for determination of global DNA methylation status. <i>Analytical Biochemistry</i> , 2011, 409, 138-143.	1.1	15
348	A polymerase chain reaction-based method for constructing a linear vector with site-specific DNA methylation. <i>Analytical Biochemistry</i> , 2011, 416, 211-217.	1.1	11
349	Epigenetic mechanisms mediating vulnerability and resilience to psychiatric disorders. <i>Neuroscience and Biobehavioral Reviews</i> , 2011, 35, 1544-1551.	2.9	161
350	Multi-scale coding of genomic information: From DNA sequence to genome structure and function. <i>Physics Reports</i> , 2011, 498, 45-188.	10.3	108
351	Quantitative, high-resolution epigenetic profiling of CpG loci identifies associations with cord blood plasma homocysteine and birth weight in humans. <i>Epigenetics</i> , 2011, 6, 86-94.	1.3	123
352	Role of CpG context and content in evolutionary signatures of brain DNA methylation. <i>Epigenetics</i> , 2011, 6, 1308-1318.	1.3	30

#	ARTICLE	IF	CITATIONS
353	Epigenetic Mechanisms in Alzheimer's Disease. <i>Current Medicinal Chemistry</i> , 2011, 18, 1751-1756.	1.2	25
354	DNA methylation: A source of random variation in natural populations. <i>Epigenetics</i> , 2011, 6, 421-427.	1.3	97
355	The Redox Basis of Epigenetic Modifications: From Mechanisms to Functional Consequences. <i>Antioxidants and Redox Signaling</i> , 2011, 15, 551-589.	2.5	242
356	5-Aza-2â€²-deoxycytidine Activates Iron Uptake and Heme Biosynthesis by Increasing c-Myc Nuclear Localization and Binding to the E-boxes of Transferrin Receptor 1 (TfR1) and Ferrochelatase (Fech) Genes. <i>Journal of Biological Chemistry</i> , 2011, 286, 37196-37206.	1.6	19
357	The structural basis for selective binding of non-methylated CpG islands by the CFP1 CXXC domain. <i>Nature Communications</i> , 2011, 2, 227.	5.8	111
358	Defining pluripotent stem cells through quantitative proteomic analysis. <i>Expert Review of Proteomics</i> , 2011, 8, 29-42.	1.3	26
359	CpG Methylation in the Hexamerin 110 Gene in the European Honeybee, <i>Apis mellifera</i> . <i>Journal of Insect Science</i> , 2011, 11, 1-11.	0.6	21
360	Epigenetic factors and cardiac development. <i>Cardiovascular Research</i> , 2011, 91, 203-211.	1.8	63
361	Epigenetic Regulation of Gene Expression in Physiological and Pathological Brain Processes. <i>Physiological Reviews</i> , 2011, 91, 603-649.	13.1	315
362	Epigenetic regulation of cellular adhesion in cancer. <i>Carcinogenesis</i> , 2011, 32, 1414-1418.	1.3	16
363	BiQ Analyzer HT: locus-specific analysis of DNA methylation by high-throughput bisulfite sequencing. <i>Nucleic Acids Research</i> , 2011, 39, W551-W556.	6.5	114
364	Replication timing-related and gene body-specific methylation of active human genes. <i>Human Molecular Genetics</i> , 2011, 20, 670-680.	1.4	256
365	Integration of genomic and epigenomic DNA methylation data in common complex diseases by haplotype-specific methylation analysis. <i>Personalized Medicine</i> , 2011, 8, 243-251.	0.8	8
366	Tissue-Specific Differences in Cytosine Methylation and Their Association with Differential Gene Expression in Sorghum. <i>Plant Physiology</i> , 2011, 156, 1955-1966.	2.3	66
367	Functional aspects of cytidine-guanosine dinucleotides and their locations in genes. <i>Biomolecular Concepts</i> , 2011, 2, 391-405.	1.0	2
368	Methyl-Binding Domain Protein 2â€²-Dependent Proliferation and Survival of Breast Cancer Cells. <i>Molecular Cancer Research</i> , 2011, 9, 1152-1162.	1.5	40
369	Vascular Smooth Muscle Progenitor Cells. <i>Circulation Research</i> , 2011, 108, 365-377.	2.0	170
370	Epigenetic QTL Mapping in <i>Brassica napus</i> . <i>Genetics</i> , 2011, 189, 1093-1102.	1.2	71

#	ARTICLE	IF	CITATIONS
371	DNA methyltransferase 3b preferentially associates with condensed chromatin. <i>Nucleic Acids Research</i> , 2011, 39, 874-888.	6.5	34
372	Evidence for Widespread Genomic Methylation in the Migratory Locust, <i>Locusta migratoria</i> (Orthoptera: Acrididae). <i>PLoS ONE</i> , 2011, 6, e28167.	1.1	34
373	Conservation and divergence of DNA methylation in eukaryotes. <i>Epigenetics</i> , 2011, 6, 134-140.	1.3	65
374	Remodeling is at the heart of chromatin. <i>Epigenetics</i> , 2011, 6, 884-887.	1.3	4
375	Epigenetic Impacts on Neurodevelopment: Pathophysiological Mechanisms and Genetic Modes of Action. <i>Pediatric Research</i> , 2011, 69, 92R-100R.	1.1	62
376	Microarray coupled with methyl-CpG targeted transcriptional activation (MeTA-array) identifies hypermethylated genes containing the stringent criteria of CpG islands at high frequency. <i>Epigenetics</i> , 2011, 6, 752-759.	1.3	9
377	Placenta-specific Expression of the Interleukin-2 (IL-2) Receptor β Subunit from an Endogenous Retroviral Promoter. <i>Journal of Biological Chemistry</i> , 2011, 286, 35543-35552.	1.6	41
378	The Replication Focus Targeting Sequence (RFTS) Domain Is a DNA-competitive Inhibitor of Dnmt1. <i>Journal of Biological Chemistry</i> , 2011, 286, 15344-15351.	1.6	108
379	Expanded methyl-sensitive cut counting reveals hypomethylation as an epigenetic state that highlights functional sequences of the genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9715-9720.	3.3	28
380	Genome-wide DNA methylation in human heart failure. <i>Epigenomics</i> , 2011, 3, 103-109.	1.0	62
381	Histone modifications and methyl-CpG-binding domain protein levels at the TNFSF7 (CD70) promoter in SLE CD4+ T cells. <i>Lupus</i> , 2011, 20, 1365-1371.	0.8	74
382	Epigenetic suppression of the TGF-beta pathway revealed by transcriptome profiling in ovarian cancer. <i>Genome Research</i> , 2011, 21, 74-82.	2.4	78
383	Comparative Analyses of DNA Methylation and Sequence Evolution Using <i>Nasonia</i> Genomes. <i>Molecular Biology and Evolution</i> , 2011, 28, 3345-3354.	3.5	95
384	CpG Islands as a Putative Source for Animal miRNAs: Evolutionary and Functional Implications. <i>Molecular Biology and Evolution</i> , 2011, 28, 1545-1551.	3.5	4
385	DNA methylation status predicts cell type-specific enhancer activity. <i>EMBO Journal</i> , 2011, 30, 3028-3039.	3.5	203
386	Nucleosomes Containing Methylated DNA Stabilize DNA Methyltransferases 3A/3B and Ensure Faithful Epigenetic Inheritance. <i>PLoS Genetics</i> , 2011, 7, e1001286.	1.5	103
387	Detailed specificity analysis of antibodies binding to modified histone tails with peptide arrays. <i>Epigenetics</i> , 2011, 6, 256-263.	1.3	97
388	The RNA "Methyltransferase Misu (NSun2) Poises Epidermal Stem Cells to Differentiate. <i>PLoS Genetics</i> , 2011, 7, e1002403.	1.5	160

#	ARTICLE	IF	CITATIONS
389	Methylome analysis reveals Jak-STAT pathway deregulation in putative breast cancer stem cells. <i>Epigenetics</i> , 2011, 6, 428-439.	1.3	70
390	CHD1 Remodels Chromatin and Influences Transient DNA Methylation at the Clock Gene frequency. <i>PLoS Genetics</i> , 2011, 7, e1002166.	1.5	84
391	Replication Fork Polarity Gradients Revealed by Megabase-Sized U-Shaped Replication Timing Domains in Human Cell Lines. <i>PLoS Computational Biology</i> , 2012, 8, e1002443.	1.5	70
392	Deposition of Histone Variant H2A.Z within Gene Bodies Regulates Responsive Genes. <i>PLoS Genetics</i> , 2012, 8, e1002988.	1.5	329
393	Technical Considerations for Reduced Representation Bisulfite Sequencing with Multiplexed Libraries. <i>Journal of Biomedicine and Biotechnology</i> , 2012, 2012, 1-8.	3.0	60
394	Widespread occurrence of 5-methylcytosine in human coding and non-coding RNA. <i>Nucleic Acids Research</i> , 2012, 40, 5023-5033.	6.5	793
395	The Evolution of Invertebrate Gene Body Methylation. <i>Molecular Biology and Evolution</i> , 2012, 29, 1907-1916.	3.5	214
396	Characterization of NOL7 Gene Point Mutations, Promoter Methylation, and Protein Expression in Cervical Cancer. <i>International Journal of Gynecological Pathology</i> , 2012, 31, 15-24.	0.9	9
397	NCBI Epigenomics: What's new for 2013. <i>Nucleic Acids Research</i> , 2012, 41, D221-D225.	6.5	23
398	Recent Retrotransposon Insertions Are Methylated and Phylogenetically Clustered in Japonica Rice (<i>Oryza sativa</i> spp. japonica). <i>Molecular Biology and Evolution</i> , 2012, 29, 3193-3203.	3.5	22
399	Regulation and function of mammalian DNA methylation patterns: a genomic perspective. <i>Briefings in Functional Genomics</i> , 2012, 11, 240-250.	1.3	33
400	Light-regulated and cell-specific methylation of the maize PEPC promoter. <i>Journal of Experimental Botany</i> , 2012, 63, 1381-1390.	2.4	37
401	Polymorphism and Methylation of Four Genes Expressed in Salivary Glands of Russian Wheat Aphid (<i>Homoptera: Aphididae</i>). <i>Journal of Economic Entomology</i> , 2012, 105, 232-241.	0.8	11
402	DNA Methylation Rebalances Gene Dosage after Mammalian Gene Duplications. <i>Molecular Biology and Evolution</i> , 2012, 29, 133-144.	3.5	50
403	Normal early pregnancy. <i>Epigenetics</i> , 2012, 7, 729-734.	1.3	22
404	Developmental Epigenetics of the Murine Secondary Palate. <i>ILAR Journal</i> , 2012, 53, 240-252.	1.8	30
405	Characterization of CpG island DNA methylation of impairment-related genes in a rat model of cognitive aging. <i>Epigenetics</i> , 2012, 7, 1008-1019.	1.3	48
406	Human-specific CpG islands identify loci associated with human-specific traits and disease. <i>Epigenetics</i> , 2012, 7, 1188-1199.	1.3	38

#	ARTICLE	IF	CITATIONS
407	Mobility of DNA sequence recognition domains in DNA methyltransferases suggests epigenetics-driven adaptive evolution. <i>Mobile Genetic Elements</i> , 2012, 2, 292-296.	1.8	39
408	Epigenetics of drug abuse: predisposition or response. <i>Pharmacogenomics</i> , 2012, 13, 1149-1160.	0.6	104
410	Maternal dietary protein restriction and excess affects offspring gene expression and methylation of non-SMC subunits of condensin I in liver and skeletal muscle. <i>Epigenetics</i> , 2012, 7, 239-252.	1.3	63
411	Harnessing adult neurogenesis by cracking the epigenetic code. <i>Future Neurology</i> , 2012, 7, 65-79.	0.9	3
412	Intragenic DNA methylation: implications of this epigenetic mechanism for cancer research. <i>British Journal of Cancer</i> , 2012, 106, 248-253.	2.9	168
413	Genome-scale DNA methylation pattern profiling of human bone marrow mesenchymal stem cells in long-term culture. <i>Experimental and Molecular Medicine</i> , 2012, 44, 503.	3.2	49
414	Position-dependent correlations between DNA methylation and the evolutionary rates of mammalian coding exons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15841-15846.	3.3	40
415	Effect of high doses of folic acid supplementation in early pregnancy on child neurodevelopment at 18 months of age: the motherâ€“child cohort â€“Rheaâ€™ study in Crete, Greece. <i>Public Health Nutrition</i> , 2012, 15, 1728-1736.	1.1	62
416	Evaluation of single CpG sites as proxies of CpG island methylation states at the genome scale. <i>Nucleic Acids Research</i> , 2012, 40, 11490-11498.	6.5	36
417	Unique DNA methylome profiles in CpG island methylator phenotype colon cancers. <i>Genome Research</i> , 2012, 22, 283-291.	2.4	35
418	Characterization of <i>CbCyp51</i> from Field Isolates of <i>Cercospora beticola</i> . <i>Phytopathology</i> , 2012, 102, 298-305.	1.1	63
419	Gentechnische Methoden. , 2012, , .		9
420	Diet-Induced Epigenetic Changes and Cancer Prevention: A Mantra for Healthy Living. , 2012, , 283-326.		1
421	Epigenetic Mechanisms Underlying Developmental Plasticity in Horned Beetles. <i>Genetics Research International</i> , 2012, 2012, 1-14.	2.0	14
422	Epigenetic Alterations in Bladder Cancer and Their Potential Clinical Implications. <i>Advances in Urology</i> , 2012, 2012, 1-11.	0.6	24
423	Role of Microbiome in Regulating the HPA Axis and Its Relevance to Allergy. <i>Chemical Immunology and Allergy</i> , 2012, 98, 163-175.	1.7	40
424	The expanding role of epigenetics. <i>Global Cardiology Science & Practice</i> , 2012, 2012, 7.	0.3	12
425	Immune Related Genes Underpin the Evolution of Adaptive Immunity in Jawless Vertebrates. <i>Current Genomics</i> , 2012, 13, 86-94.	0.7	11

#	ARTICLE	IF	CITATIONS
427	Salt Stress Induced Variation in DNA Methylation Pattern and Its Influence on Gene Expression in Contrasting Rice Genotypes. <i>PLoS ONE</i> , 2012, 7, e40203.	1.1	231
428	Maternal nutritional status, C1 metabolism and offspring DNA methylation: a review of current evidence in human subjects. <i>Proceedings of the Nutrition Society</i> , 2012, 71, 154-165.	0.4	139
429	Epigenetic Regulation of Secondary Metabolite Biosynthetic Genes in Fungi. , 2012, , 57-69.		6
430	Active DNA Demethylation in Plants and Animals. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2012, 77, 161-173.	2.0	114
431	Epigenetics of Host-Pathogen Interactions: The Road Ahead and the Road Behind. <i>PLoS Pathogens</i> , 2012, 8, e1003007.	2.1	205
432	Understanding the Relationship Between Brain Gene Expression and Social Behavior: Lessons from the Honey Bee. <i>Annual Review of Genetics</i> , 2012, 46, 591-615.	3.2	166
433	A Perspective on Dietary Phytochemicals and Cancer Chemoprevention: Oxidative Stress, Nrf2, and Epigenomics. <i>Topics in Current Chemistry</i> , 2012, 329, 133-162.	4.0	113
434	DNA methylome analysis using short bisulfite sequencing data. <i>Nature Methods</i> , 2012, 9, 145-151.	9.0	313
435	DNA Methylation, H2A.Z, and the Regulation of Constitutive Expression. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2012, 77, 147-154.	2.0	47
436	Phosphorylation of RelA/p65 promotes DNMT-1 recruitment to chromatin and represses transcription of the tumor metastasis suppressor gene BRMS1. <i>Oncogene</i> , 2012, 31, 1143-1154.	2.6	84
437	Whole DNA methylome profiling in mice exposed to secondhand smoke. <i>Epigenetics</i> , 2012, 7, 1302-1314.	1.3	18
438	Gene organization inside replication domains in mammalian genomes. <i>Comptes Rendus - Mecanique</i> , 2012, 340, 745-757.	2.1	12
439	Birds do it, bees do it, worms and ciliates do it too: DNA methylation from unexpected corners of the tree of life. <i>Genome Biology</i> , 2012, 13, 174.	13.9	34
440	methylKit: a comprehensive R package for the analysis of genome-wide DNA methylation profiles. <i>Genome Biology</i> , 2012, 13, R87.	13.9	1,541
441	Functional annotation of the human brain methylome identifies tissue-specific epigenetic variation across brain and blood. <i>Genome Biology</i> , 2012, 13, R43.	13.9	585
442	Metabolic Memory and Chronic Diabetes Complications: Potential Role for Epigenetic Mechanisms. <i>Current Diabetes Reports</i> , 2012, 12, 551-559.	1.7	76
443	IDH1 mutations inhibit multiple α -ketoglutarate-dependent dioxygenase activities in astroglioma. <i>Journal of Neuro-Oncology</i> , 2012, 109, 253-260.	1.4	27
444	Root-Specific DNA Methylation in <i>Chloris virgata</i> , a Natural Alkaline-Resistant Halophyte, in Response to Salt and Alkaline Stresses. <i>Plant Molecular Biology Reporter</i> , 2012, 30, 1102-1109.	1.0	17

#	ARTICLE	IF	CITATIONS
445	Systematic assessment of reduced representation bisulfite sequencing to human blood samples: A promising method for large-sample-scale epigenomic studies. <i>Journal of Biotechnology</i> , 2012, 157, 1-6.	1.9	44
446	Robotic Liquid Handling and Automation in Epigenetics. <i>Journal of the Association for Laboratory Automation</i> , 2012, 17, 327-329.	2.8	11
447	Epigenetic Mechanisms of Human Imprinting Disorders. , 2012, , 253-271.		7
448	Epigenetic contributions in the development of rheumatoid arthritis. <i>Arthritis Research and Therapy</i> , 2012, 14, 227.	1.6	63
449	Heterogeneity and Randomness of DNA Methylation Patterns in Human Embryonic Stem Cells. <i>DNA and Cell Biology</i> , 2012, 31, 893-907.	0.9	9
450	Functional heterologous expression and purification of a mammalian methyl-CpG binding domain in suitable yield for DNA methylation profiling assays. <i>Protein Expression and Purification</i> , 2012, 82, 332-338.	0.6	4
451	Can the battle against tuberculosis gain from epigenetic research?. <i>Trends in Microbiology</i> , 2012, 20, 220-226.	3.5	35
452	Kin conflict in insect societies: a new epigenetic perspective. <i>Trends in Ecology and Evolution</i> , 2012, 27, 367-373.	4.2	43
453	Electrochemistry of Nucleic Acids. <i>Chemical Reviews</i> , 2012, 112, 3427-3481.	23.0	583
454	Development of second generation epigenetic agents. <i>MedChemComm</i> , 2012, 3, 135-161.	3.5	16
455	Zinc Finger Protein ZFP57 Requires Its Co-factor to Recruit DNA Methyltransferases and Maintains DNA Methylation Imprint in Embryonic Stem Cells via Its Transcriptional Repression Domain. <i>Journal of Biological Chemistry</i> , 2012, 287, 2107-2118.	1.6	153
456	RNA cytosine methylation by Dnmt2 and NSun2 promotes tRNA stability and protein synthesis. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 900-905.	3.6	488
457	Folate and DNA Methylation: A Review of Molecular Mechanisms and the Evidence for Folate's Role. <i>Advances in Nutrition</i> , 2012, 3, 21-38.	2.9	749
458	Genomics of DNA cytosine methylation in <i>Escherichia coli</i> reveals its role in stationary phase transcription. <i>Nature Communications</i> , 2012, 3, 886.	5.8	131
459	A DNA 3â€² Phosphatase Functions in Active DNA Demethylation in <i>Arabidopsis</i> . <i>Molecular Cell</i> , 2012, 45, 357-370.	4.5	81
460	Phenotypic diversity and epigenomic variation â€” The utility of mass spectrometric analysis of DNA methylation. <i>Journal of Proteomics</i> , 2012, 75, 3400-3409.	1.2	3
461	Epigenetic regulation of <i>ABCG2</i> gene is associated with susceptibility to xenobiotic exposure. <i>Journal of Proteomics</i> , 2012, 75, 3410-3418.	1.2	8
462	CpG methylation recruits sequence specific transcription factors essential for tissue specific gene expression. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 763-770.	0.9	89

#	ARTICLE	IF	CITATIONS
463	Live-attenuated measles virus vaccine confers cell contact loss and apoptosis of ovarian cancer cells via ROS-induced silencing of E-cadherin by methylation. <i>Cancer Letters</i> , 2012, 318, 14-25.	3.2	16
464	Electrochemical detection of 5-methylcytosine in bisulfite-treated DNA. <i>Electrochimica Acta</i> , 2012, 78, 75-81.	2.6	19
465	Primary style protein expression in the self-incompatible/compatible apricot by the 2D-DIGE technique. <i>Gene</i> , 2012, 503, 110-117.	1.0	11
466	Linking the DNA strand asymmetry to the spatio-temporal replication program. <i>European Physical Journal E</i> , 2012, 35, 92.	0.7	16
467	Linking the DNA strand asymmetry to the spatio-temporal replication program. <i>European Physical Journal E</i> , 2012, 35, 123.	0.7	13
468	Dynamic DNA cytosine methylation in the <i>Populus trichocarpa</i> genome: tissue-level variation and relationship to gene expression. <i>BMC Genomics</i> , 2012, 13, 27.	1.2	136
469	Single-base resolution maps of cultivated and wild rice methylomes and regulatory roles of DNA methylation in plant gene expression. <i>BMC Genomics</i> , 2012, 13, 300.	1.2	266
470	Genome-wide association between DNA methylation and alternative splicing in an invertebrate. <i>BMC Genomics</i> , 2012, 13, 480.	1.2	170
471	In planta assays involving epigenetically silenced genes reveal inhibition of cytosine methylation by genistein. <i>Plant Methods</i> , 2012, 8, 10.	1.9	20
473	Comparative cytogenetic study on two species of the genus <i>Entedon</i> Dalman, 1820 (Hymenoptera.) <i>Tj ETQq1 1 0.784314 rgBT /Over</i> <i>Comparative Cytogenetics</i> , 2012, 6, 79-92.	0.3	14
474	DNA Methylation in Plants: Relationship to Small RNAs and Histone Modifications, and Functions in Transposon Inactivation. <i>Plant and Cell Physiology</i> , 2012, 53, 766-784.	1.5	177
475	Structure-Based Mechanistic Insights into DNMT1-Mediated Maintenance DNA Methylation. <i>Science</i> , 2012, 335, 709-712.	6.0	283
476	Epigenetic Manifestation of Metabolic Syndrome and Dietary Management. <i>Antioxidants and Redox Signaling</i> , 2012, 17, 254-281.	2.5	14
477	DNA methylation in repetitive elements and post-traumatic stress disorder: a caseâ€“control study of US military service members. <i>Epigenomics</i> , 2012, 4, 29-40.	1.0	138
478	DNA methylation and mRNA expression profiles in bovine oocytes derived from prepubertal and adult donors. <i>Reproduction</i> , 2012, 144, 319-330.	1.1	32
479	From epigenetics to epigenomics and their implications in plant breeding. , 2012, , 207-226.		4
481	Global DNA hypomethylation in cancer: review of validated methods and clinical significance. <i>Clinical Chemistry and Laboratory Medicine</i> , 2012, 50, 1733-42.	1.4	85
482	Glue for Jumping Elements: Epigenetic Means for Controlling Transposable Elements in Plants. <i>Topics in Current Genetics</i> , 2012, , 125-145.	0.7	4

#	ARTICLE	IF	CITATIONS
483	Divergent Whole-Genome Methylation Maps of Human and Chimpanzee Brains Reveal Epigenetic Basis of Human Regulatory Evolution. <i>American Journal of Human Genetics</i> , 2012, 91, 455-465.	2.6	147
484	Impact of Methylation on the Physical Properties of DNA. <i>Biophysical Journal</i> , 2012, 102, 2140-2148.	0.2	118
485	Epigenetic regulation of stem cells differentiating along the neural lineage. <i>Current Opinion in Neurobiology</i> , 2012, 22, 762-767.	2.0	34
486	Genome-wide and Caste-Specific DNA Methylomes of the Ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Current Biology</i> , 2012, 22, 1755-1764.	1.8	361
487	Two Tunisian patients with Peters plus syndrome harbouring a novel splice site mutation in the B3GALT1 gene that modulates the mRNA secondary structure. <i>Gene</i> , 2012, 507, 68-73.	1.0	9
488	New primers for methylation-specific polymerase chain reaction enhance specificity of detecting STAT1 methylation. <i>Taiwanese Journal of Obstetrics and Gynecology</i> , 2012, 51, 43-49.	0.5	5
489	High-Throughput Sequencing of the Methylome Using Two-Base Encoding. <i>Methods in Molecular Biology</i> , 2012, 910, 71-86.	0.4	1
490	Epigenetics of Solid Cancer Stem Cells. <i>Methods in Molecular Biology</i> , 2012, 863, 15-31.	0.4	17
491	The Effect of c-Fos Demethylation on Sodium Fluoride-induced Apoptosis in L-02 Cells. <i>Biological Trace Element Research</i> , 2012, 149, 102-109.	1.9	21
492	Plant Transposable Elements. <i>Topics in Current Genetics</i> , 2012, , .	0.7	8
493	Enzymatic Control of Plasmonic Coupling and Surface Enhanced Raman Scattering Transduction for Sensitive Detection of DNA Demethylation. <i>Analytical Chemistry</i> , 2012, 84, 8602-8606.	3.2	30
495	Chromatin landscape and endocrine response in breast cancer. <i>Epigenomics</i> , 2012, 4, 675-683.	1.0	14
496	Functional Genomics. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	3
499	DNA methylation profiling identifies epigenetic dysregulation in pancreatic islets from type 2 diabetic patients. <i>EMBO Journal</i> , 2012, 31, 1405-1426.	3.5	355
500	DNA methylation in amphioxus: from ancestral functions to new roles in vertebrates. <i>Briefings in Functional Genomics</i> , 2012, 11, 142-155.	1.3	43
502	Cancer Epigenetics. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	5
503	The Nutrigenetics and Nutrigenomics of the Dietary Requirement for Choline. <i>Progress in Molecular Biology and Translational Science</i> , 2012, 108, 159-177.	0.9	16
504	Methylation of tumor suppressor microRNAs: lessons from lymphoid malignancies. <i>Expert Review of Molecular Diagnostics</i> , 2012, 12, 755-765.	1.5	14

#	ARTICLE	IF	CITATIONS
505	DNMT3A rs36012910 A>G polymorphism and gastric cancer susceptibility in a Chinese population. <i>Molecular Biology Reports</i> , 2012, 39, 10949-10955.	1.0	15
506	Effects of short-term high-fat overfeeding on genome-wide DNA methylation in the skeletal muscle of healthy young men. <i>Diabetologia</i> , 2012, 55, 3341-3349.	2.9	179
507	Epigenetics in Cardiovascular Biology. , 2012, , 331-340.		0
508	Biocommunication of Fungi. , 2012, , .		22
509	Chromatin Computation. <i>PLoS ONE</i> , 2012, 7, e35703.	1.1	16
510	Biased Gene Fractionation and Dominant Gene Expression among the Subgenomes of <i>Brassica rapa</i> . <i>PLoS ONE</i> , 2012, 7, e36442.	1.1	240
511	Is There a Relationship between DNA Methylation and Phenotypic Plasticity in Invertebrates?. <i>Frontiers in Physiology</i> , 2012, 2, 116.	1.3	132
512	A Cross-Platform Genome-Wide Comparison of the Relationship of Promoter DNA Methylation to Gene Expression. <i>Frontiers in Genetics</i> , 2012, 3, 12.	1.1	15
513	The Impact of Recent Alcohol Use on Genome Wide DNA Methylation Signatures. <i>Frontiers in Genetics</i> , 2012, 3, 54.	1.1	110
514	The Genetic and Epigenetic Journey of Embryonic Stem Cells into Mature Neural Cells. <i>Frontiers in Genetics</i> , 2012, 3, 81.	1.1	49
515	Biotic stress in plants: life lessons from your parents and grandparents. <i>Frontiers in Genetics</i> , 2012, 3, 256.	1.1	22
516	DNA methylation of the oxytocin receptor gene predicts neural response to ambiguous social stimuli. <i>Frontiers in Human Neuroscience</i> , 2012, 6, 280.	1.0	155
517	Quantitative, high-resolution CpG methylation assays on the pyrosequencing platform. , 0, , 223-234.		0
518	Epigenetic mechanisms in drug addiction and depression. , 2012, , 79-89.		2
519	Epigenetic Modulation of Gene Expression during Keratinocyte Differentiation. <i>Annals of Dermatology</i> , 2012, 24, 261.	0.3	6
520	Epileptogenesis: Can the Science of Epigenetics Give Us Answers?. <i>Epilepsy Currents</i> , 2012, 12, 105-110.	0.4	36
521	A unique regulatory phase of DNA methylation in the early mammalian embryo. <i>Nature</i> , 2012, 484, 339-344.	13.7	860
522	Stem cells: A view from the roots. <i>Biotechnology Journal</i> , 2012, 7, 704-722.	1.8	14

#	ARTICLE	IF	CITATIONS
523	The Involvement of 5-Hydroxymethylcytosine in Active DNA Demethylation in Mice1. <i>Biology of Reproduction</i> , 2012, 86, 104.	1.2	28
524	Tet family proteins and 5-hydroxymethylcytosine in development and disease. <i>Development (Cambridge)</i> , 2012, 139, 1895-1902.	1.2	316
525	Transcriptome and methylome interactions in rice hybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12040-12045.	3.3	203
526	Rescue of aging-associated decline in Dnmt3a2 expression restores cognitive abilities. <i>Nature Neuroscience</i> , 2012, 15, 1111-1113.	7.1	244
527	Transposable Elements as Tools for Reshaping the Genome: It Is a Huge World After All!. <i>Methods in Molecular Biology</i> , 2012, 859, 1-28.	0.4	23
528	Bisulfite sequencing of chromatin immunoprecipitated DNA (BisChIP-seq) directly informs methylation status of histone-modified DNA. <i>Genome Research</i> , 2012, 22, 1120-1127.	2.4	163
529	Mechanism and Stem Cell Activity of 5-Carboxycytosine Decarboxylation Determined by Isotope Tracing. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 6516-6520.	7.2	131
530	Heritable Transmission of Diabetic Metabolic Memory in Zebrafish Correlates With DNA Hypomethylation and Aberrant Gene Expression. <i>Diabetes</i> , 2012, 61, 485-491.	0.3	116
531	Epigenetic reprogramming in mouse pre-implantation development and primordial germ cells. <i>Development (Cambridge)</i> , 2012, 139, 15-31.	1.2	355
534	Structure and Function of Noncanonical Nucleobases. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 7110-7131.	7.2	159
535	Methylome analysis using MeDIP-seq with low DNA concentrations. <i>Nature Protocols</i> , 2012, 7, 617-636.	5.5	270
536	Epigenetic control on cell fate choice in neural stem cells. <i>Protein and Cell</i> , 2012, 3, 278-290.	4.8	38
537	Making alternative splicing decisions during epithelial-to-mesenchymal transition (EMT). <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 2515-2526.	2.4	56
538	Effects of exogenous nitric oxide on antioxidation and DNA methylation of <i>Dendrobium huoshanense</i> grown under drought stress. <i>Plant Cell, Tissue and Organ Culture</i> , 2012, 109, 307-314.	1.2	42
539	Genome-scale methylation analysis of Parkinson's disease patients' brains reveals DNA hypomethylation and increased mRNA expression of cytochrome P450 2E1. <i>Neurogenetics</i> , 2012, 13, 87-91.	0.7	122
540	DNA methylation regulates lineage-specifying genes in primary lymphatic and blood endothelial cells. <i>Angiogenesis</i> , 2012, 15, 317-329.	3.7	20
541	Shifting behaviour: epigenetic reprogramming in eusocial insects. <i>Current Opinion in Cell Biology</i> , 2012, 24, 367-373.	2.6	54
542	Factors responsible for the discrepancy between IL28B polymorphism prediction and the viral response to peginterferon plus ribavirin therapy in Japanese chronic hepatitis C patients. <i>Hepatology Research</i> , 2012, 42, 958-965.	1.8	7

#	ARTICLE	IF	CITATIONS
543	Epigenetic Mechanisms in the Actions of Endocrine-disrupting Chemicals: Gonadal Effects and Role in Female Reproduction. <i>Reproduction in Domestic Animals</i> , 2012, 47, 338-347.	0.6	46
544	Molecular alterations in hepatocarcinogenesis induced by dietary methyl deficiency. <i>Molecular Nutrition and Food Research</i> , 2012, 56, 116-125.	1.5	62
545	Epigenetic regulation of self-renewal and fate determination in neural stem cells. <i>Journal of Neuroscience Research</i> , 2012, 90, 529-539.	1.3	40
546	Coordinated changes in AHRR methylation in lymphoblasts and pulmonary macrophages from smokers. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2012, 159B, 141-151.	1.1	230
547	Hypermethylation in bladder cancer: biological pathways and translational applications. <i>Tumor Biology</i> , 2012, 33, 347-361.	0.8	51
548	TGF- β 2 signal transduction spreading to a wider field: a broad variety of mechanisms for context-dependent effects of TGF- β 2. <i>Cell and Tissue Research</i> , 2012, 347, 37-49.	1.5	88
549	Epigenetic down regulation of nerve growth factor during alcohol withdrawal. <i>Addiction Biology</i> , 2013, 18, 508-510.	1.4	58
550	HIV-1 transcription and latency: an update. <i>Retrovirology</i> , 2013, 10, 67.	0.9	271
551	MicroRNA-mediated regulation of target genes in several brain regions is correlated to both microRNA-targeting-specific promoter methylation and differential microRNA expression. <i>BioData Mining</i> , 2013, 6, 11.	2.2	15
552	DNA methylation of distal regulatory sites characterizes dysregulation of cancer genes. <i>Genome Biology</i> , 2013, 14, R21.	13.9	288
553	Redistribution of H3K27me3 upon DNA hypomethylation results in de-repression of Polycomb target genes. <i>Genome Biology</i> , 2013, 14, R25.	13.9	200
554	DNA methylation and transcriptional noise. <i>Epigenetics and Chromatin</i> , 2013, 6, 9.	1.8	115
555	A permissive chromatin structure is adopted prior to site-specific DNA demethylation of developmentally expressed genes involved in macronuclear differentiation. <i>Epigenetics and Chromatin</i> , 2013, 6, 5.	1.8	9
556	Identification and functional validation of HPV-mediated hypermethylation in head and neck squamous cell carcinoma. <i>Genome Medicine</i> , 2013, 5, 15.	3.6	118
557	Cytosine methylation at CG and CNG sites is differential during the development of triploid black poplar. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2013, 22, 414-424.	0.9	3
558	DNA unmethylome profiling by covalent capture of CpG sites. <i>Nature Communications</i> , 2013, 4, 2190.	5.8	53
560	PPAR β -induced PARylation promotes local DNA demethylation by production of 5-hydroxymethylcytosine. <i>Nature Communications</i> , 2013, 4, 2262.	5.8	97
561	Emerging Intelligent Computing Technology and Applications. <i>Communications in Computer and Information Science</i> , 2013, , .	0.4	1

#	ARTICLE	IF	CITATIONS
562	DNA methylation and methylcytosine oxidation in cell fate decisions. <i>Current Opinion in Cell Biology</i> , 2013, 25, 152-161.	2.6	82
563	Toxicological evaluation of microcystins in aquatic fish species: Current knowledge and future directions. <i>Aquatic Toxicology</i> , 2013, 142-143, 1-16.	1.9	67
564	Genome-wide methylation profiling of the bronchial mucosa of asthmatics: relationship to atopy. <i>BMC Medical Genetics</i> , 2013, 14, 39.	2.1	38
565	Promoter hypomethylation, especially around the E26 transformation-specific motif, and increased expression of poly (ADP-ribose) polymerase 1 in BRCA-mutated serous ovarian cancer. <i>BMC Cancer</i> , 2013, 13, 90.	1.1	18
566	Increased 5-Methylcytosine and Decreased 5-Hydroxymethylcytosine Levels are Associated with Reduced Striatal A2AR Levels in Huntington's Disease. <i>NeuroMolecular Medicine</i> , 2013, 15, 295-309.	1.8	129
567	DNA methylation regulates associative reward learning. <i>Nature Neuroscience</i> , 2013, 16, 1445-1452.	7.1	197
568	Evidence of a conserved functional role for DNA methylation in termites. <i>Insect Molecular Biology</i> , 2013, 22, 143-154.	1.0	36
569	The correlation of genome size and DNA methylation rate in metazoans. <i>Theory in Biosciences</i> , 2013, 132, 47-60.	0.6	43
570	Epigenomic association analysis identifies smoking-related DNA methylation sites in African Americans. <i>Human Genetics</i> , 2013, 132, 1027-1037.	1.8	153
571	Active DNA Demethylation and 5-Hydroxymethylcytosine. , 2013, , 69-83.		0
572	Epigenetic Cancer Prevention Mechanisms in Skin Cancer. <i>AAPS Journal</i> , 2013, 15, 1064-1071.	2.2	27
573	Emerging Concepts in Neuro-Oncology. , 2013, , .		0
574	Nuclear calcium signalling in the regulation of brain function. <i>Nature Reviews Neuroscience</i> , 2013, 14, 593-608.	4.9	295
575	Combining genomic and proteomic approaches for epigenetics research. <i>Epigenomics</i> , 2013, 5, 439-452.	1.0	31
576	Differential androgen receptor expression and DNA methylation state in striatum song nucleus Area X between wild and domesticated songbird strains. <i>European Journal of Neuroscience</i> , 2013, 38, 2600-2610.	1.2	22
577	Characterization of the DNA methylome and its interindividual variation in human peripheral blood monocytes. <i>Epigenomics</i> , 2013, 5, 255-269.	1.0	19
578	Treatment implications of the altered cytokine-insulin axis in neurodegenerative disease. <i>Biochemical Pharmacology</i> , 2013, 86, 862-871.	2.0	21
579	DNA methylation alterations of upland cotton (<i>Gossypium hirsutum</i>) in response to cold stress. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 2445-2453.	1.0	37

#	ARTICLE	IF	CITATIONS
580	Epigenomic Alterations in Localized and Advanced Prostate Cancer. <i>Neoplasia</i> , 2013, 15, 373-IN5.	2.3	69
581	Genotoxicity of tobacco smoke-derived aromatic amines and bladder cancer: current state of knowledge and future research directions. <i>FASEB Journal</i> , 2013, 27, 2090-2100.	0.2	50
582	Genomic insights into cancer-associated aberrant CpG island hypermethylation. <i>Briefings in Functional Genomics</i> , 2013, 12, 174-190.	1.3	105
583	Excision of 8-oxoguanine from methylated CpG dinucleotides by human 8-oxoguanine DNA glycosylase. <i>FEBS Letters</i> , 2013, 587, 3129-3134.	1.3	18
584	Micro- and nanoscale devices for the investigation of epigenetics and chromatin dynamics. <i>Nature Nanotechnology</i> , 2013, 8, 709-718.	15.6	57
585	The DNA methylation landscape of small cell lung cancer suggests a differentiation defect of neuroendocrine cells. <i>Oncogene</i> , 2013, 32, 3559-3568.	2.6	67
586	Targeted DNA demethylation and activation of endogenous genes using programmable TALE-TET1 fusion proteins. <i>Nature Biotechnology</i> , 2013, 31, 1137-1142.	9.4	433
587	Epigenetics and Cancer. , 2013, , .		5
588	Cell and Molecular Biology of Breast Cancer. , 2013, , .		10
589	Insights into the role of DNA methylation in diatoms by genome-wide profiling in <i>Phaeodactylum tricornutum</i> . <i>Nature Communications</i> , 2013, 4, 2091.	5.8	113
590	Estimating absolute methylation levels at single-CpG resolution from methylation enrichment and restriction enzyme sequencing methods. <i>Genome Research</i> , 2013, 23, 1541-1553.	2.4	138
591	Systems approaches to human autoimmune diseases. <i>Current Opinion in Immunology</i> , 2013, 25, 598-605.	2.4	15
592	Epigenetics of Inflammatory Bowel Disease. , 2013, , 171-187.		0
593	Molecular Genetics of Inflammatory Bowel Disease. , 2013, , .		0
594	Epigenetics, Autism Spectrum, and Neurodevelopmental Disorders. <i>Neurotherapeutics</i> , 2013, 10, 742-756.	2.1	100
596	Effect of Prenatal Programming on Heifer Development. <i>Veterinary Clinics of North America - Food Animal Practice</i> , 2013, 29, 517-536.	0.5	16
597	The functional genetic link of NLGN4X knockdown and neurodevelopment in neural stem cells. <i>Human Molecular Genetics</i> , 2013, 22, 3749-3760.	1.4	37
598	Epigenetic Mechanisms of Neurodegeneration in Huntington's Disease. <i>Neurotherapeutics</i> , 2013, 10, 664-676.	2.1	77

#	ARTICLE	IF	CITATIONS
599	Epigenetic changes: a common theme in acute myelogenous leukemogenesis. <i>Journal of Hematology and Oncology</i> , 2013, 6, 57.	6.9	55
600	Systems biology approach to stage-wise characterization of epigenetic genes in lung adenocarcinoma. <i>BMC Systems Biology</i> , 2013, 7, 141.	3.0	49
601	Identical sets of methylated and nonmethylated genes in <i>Ciona intestinalis</i> sperm and muscle cells. <i>Epigenetics and Chromatin</i> , 2013, 6, 38.	1.8	29
602	Environmental Epigenomics in Health and Disease. <i>Epigenetics and Human Health</i> , 2013, , .	0.2	3
603	Chromatin Structure and Gene Expression: Function Follows Form. <i>Epigenetics and Human Health</i> , 2013, , 189-205.	0.2	0
604	An epigenetic framework for neurodevelopmental disorders: From pathogenesis to potential therapy. <i>Neuropharmacology</i> , 2013, 68, 2-82.	2.0	190
605	Epigenetics, fragile X syndrome and transcriptional therapy. <i>American Journal of Medical Genetics, Part A</i> , 2013, 161, 2797-2808.	0.7	31
606	Characterizing 5-methylcytosine in the mammalian epitranscriptome. <i>Genome Biology</i> , 2013, 14, 215.	13.9	204
607	Automated selection of differentially methylated regions in microarray data. , 2013, , .		0
608	The "early life" origins of obesity-related health disorders: New discoveries regarding the intergenerational transmission of developmentally programmed traits in the global cardiometabolic health crisis. <i>American Journal of Physical Anthropology</i> , 2013, 152, 79-93.	2.1	46
609	Epigenetics and Psychostimulant Addiction. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2013, 3, a012047-a012047.	2.9	61
610	Integrated analysis of genome-wide DNA methylation and gene expression profiles in molecular subtypes of breast cancer. <i>Nucleic Acids Research</i> , 2013, 41, 8464-8474.	6.5	57
611	SPARC and DNA methylation: Possible diagnostic and therapeutic implications in gastrointestinal cancers. <i>Cancer Letters</i> , 2013, 328, 10-17.	3.2	28
612	Mammalian cells acquire epigenetic hallmarks of human cancer during immortalization. <i>Nucleic Acids Research</i> , 2013, 41, 182-195.	6.5	42
613	Megabase Replication Domains Along the Human Genome: Relation to Chromatin Structure and Genome Organisation. <i>Sub-Cellular Biochemistry</i> , 2013, 61, 57-80.	1.0	15
614	Consumption of soybean, soy foods, soy isoflavones and breast cancer incidence: Differences between Chinese women and women in Western countries and possible mechanisms. <i>Food Science and Human Wellness</i> , 2013, 2, 146-161.	2.2	190
615	Dynamics of 5-Hydroxymethylcytosine and Chromatin Marks in Mammalian Neurogenesis. <i>Cell Reports</i> , 2013, 3, 291-300.	2.9	385
616	Electrochemical strategy for sensing DNA methylation and DNA methyltransferase activity. <i>Analytica Chimica Acta</i> , 2013, 768, 76-81.	2.6	55

#	ARTICLE	IF	CITATIONS
617	Epigenetic changes in the progression of Alzheimer's disease. <i>Mechanisms of Ageing and Development</i> , 2013, 134, 486-495.	2.2	157
618	NSun2-Mediated Cytosine-5 Methylation of Vault Noncoding RNA Determines Its Processing into Regulatory Small RNAs. <i>Cell Reports</i> , 2013, 4, 255-261.	2.9	448
619	Epstein-Barr virus interactions with the Bcl-2 protein family and apoptosis in human tumor cells. <i>Journal of Zhejiang University: Science B</i> , 2013, 14, 8-24.	1.3	28
620	Variations in genomic DNA methylation during the long-term in vitro proliferation of oil palm embryogenic suspension cultures. <i>Plant Cell Reports</i> , 2013, 32, 359-368.	2.8	73
621	Label-Free Real-Time Detection of DNA Methylation Based on Quartz Crystal Microbalance Measurement. <i>Analytical Chemistry</i> , 2013, 85, 2096-2101.	3.2	52
622	Cigarette Smoke Condensate Induces Differential Expression and Promoter Methylation Profiles of Critical Genes Involved in Lung Cancer in NL-20 Lung Cells In Vitro. <i>International Journal of Toxicology</i> , 2013, 32, 23-31.	0.6	24
623	Genome-wide DNA Methylation Analysis Using Massively Parallel Sequencing Technologies. <i>Seminars in Hematology</i> , 2013, 50, 70-77.	1.8	11
624	Antiepileptic drugs and the fetal epigenome. <i>Epilepsia</i> , 2013, 54, e16-9.	2.6	10
625	Methylome of DNase I sensitive chromatin in <i>Populus trichocarpa</i> shoot apical meristematic cells: a simplified approach revealing characteristics of gene-body DNA methylation in open chromatin state. <i>New Phytologist</i> , 2013, 197, 416-430.	3.5	44
626	Epigenetics in Sports. <i>Sports Medicine</i> , 2013, 43, 93-110.	3.1	53
627	Next-Generation Sequencing: From Understanding Biology to Personalized Medicine. <i>Biology</i> , 2013, 2, 378-398.	1.3	35
628	Epigenetics and Brain Cancer. , 2013, , 21-40.		0
629	Epigenetic flexibility in metabolic regulation: disease cause and prevention?. <i>Trends in Cell Biology</i> , 2013, 23, 203-209.	3.6	127
630	Epigenetic medicine and fetal alcohol spectrum disorders. <i>Epigenomics</i> , 2013, 5, 73-86.	1.0	45
631	Epigenetic Regulation of Vascular Smooth Muscle Cell Function in Atherosclerosis. <i>Current Atherosclerosis Reports</i> , 2013, 15, 319.	2.0	34
633	Functions of DNA Methylation and Hydroxymethylation in Mammalian Development. <i>Current Topics in Developmental Biology</i> , 2013, 104, 47-83.	1.0	133
634	Epigenetics: Setting Up Lifetime Production of Beef Cows by Managing Nutrition. <i>Annual Review of Animal Biosciences</i> , 2013, 1, 339-363.	3.6	27
635	Reactive Oxygen Species, Kinase Signaling, and Redox Regulation of Epigenetics. , 2013, , 309-342.		0

#	ARTICLE	IF	CITATIONS
636	Hypermethylation and Post-Transcriptional Regulation of DNA Methyltransferases in the Ovarian Carcinomas of the Laying Hen. PLoS ONE, 2013, 8, e61658.	1.1	24
637	Developmental and environmental epigenetic programming of the endocrine pancreas: consequences for type 2 diabetes. Cellular and Molecular Life Sciences, 2013, 70, 1575-1595.	2.4	39
638	Challenges for the application of DNA methylation biomarkers in molecular diagnostic testing for cancer. Expert Review of Molecular Diagnostics, 2013, 13, 283-294.	1.5	22
639	DNA methylation: the future of crime scene investigation?. Molecular Biology Reports, 2013, 40, 4349-4360.	1.0	14
640	Multimerization of the Dnmt3a DNA Methyltransferase and Its Functional Implications. Progress in Molecular Biology and Translational Science, 2013, 117, 445-464.	0.9	16
642	First evidence of DNA methylation in insect <i>Tribolium castaneum</i> . Epigenetics, 2013, 8, 534-541.	1.3	61
643	Epigenetics and MicroRNAs in Renal Cancer. , 2013, , 63-84.		0
644	Comparison of epigenetic profiles of human oral epithelial cells from HIV-positive (on HAART) and HIV-negative subjects. Epigenetics, 2013, 8, 703-709.	1.3	16
645	Cellular, molecular, and epigenetic mechanisms in non-associative conditioning: Implications for pain and memory. Neurobiology of Learning and Memory, 2013, 105, 133-150.	1.0	93
646	Epigenetics: a new mechanism of regulation of heart failure?. Basic Research in Cardiology, 2013, 108, 361.	2.5	63
647	On the potential role of active DNA demethylation in establishing epigenetic states associated with neural plasticity and memory. Neurobiology of Learning and Memory, 2013, 105, 125-132.	1.0	36
648	Combination therapy: Histone deacetylase inhibitors and platinum-based chemotherapeutics for cancer. Cancer Letters, 2013, 329, 1-8.	3.2	87
651	Consumption of Purple Sweet Potato Affects Post-Translational Modification of Plasma Proteins in Hamsters. Journal of Agricultural and Food Chemistry, 2013, 61, 12450-12458.	2.4	9
652	The Function of Intragenic DNA Methylation: Insights from Insect Epigenomes. Integrative and Comparative Biology, 2013, 53, 319-328.	0.9	96
653	Ibandronate increases the expression of the pro-apoptotic gene FAS by epigenetic mechanisms in tumor cells. Biochemical Pharmacology, 2013, 85, 173-185.	2.0	23
654	DNA sequence variation and methylation in an arsenic tolerant earthworm population. Soil Biology and Biochemistry, 2013, 57, 524-532.	4.2	68
655	DNA 5-Methylcytosine Demethylation Activities of the Mammalian DNA Methyltransferases. Journal of Biological Chemistry, 2013, 288, 9084-9091.	1.6	95
656	Oxidative Stress and Chromatin Remodeling in Chronic Obstructive Pulmonary Disease and Smoking-Related Diseases. Antioxidants and Redox Signaling, 2013, 18, 1956-1971.	2.5	153

#	ARTICLE	IF	CITATIONS
657	Resetting epigenetic signatures to induce somatic cell reprogramming. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 1413-1424.	2.4	6
658	SNAT2 expression and regulation in human growth-restricted placentas. <i>Pediatric Research</i> , 2013, 74, 104-110.	1.1	38
659	Modeling of epigenome dynamics identifies transcription factors that mediate Polycomb targeting. <i>Genome Research</i> , 2013, 23, 60-73.	2.4	108
660	Gene × environment interactions in the prediction of response to antidepressant treatment. <i>International Journal of Neuropsychopharmacology</i> , 2013, 16, 701-711.	1.0	27
661	Origins of Shared Genetic Variation in African Cichlids. <i>Molecular Biology and Evolution</i> , 2013, 30, 906-917.	3.5	86
662	Crystal structures of isoorotate decarboxylases reveal a novel catalytic mechanism of 5-carboxyl-uracil decarboxylation and shed light on the search for DNA decarboxylase. <i>Cell Research</i> , 2013, 23, 1296-1309.	5.7	50
663	Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. <i>Genome Research</i> , 2013, 23, 1522-1540.	2.4	162
664	Designing DNA interstrand lock for locus-specific methylation detection in a nanopore. <i>Scientific Reports</i> , 2013, 3, 2381.	1.6	29
665	RNA-Mediated Epigenetic Heredity Requires the Cytosine Methyltransferase Dnmt2. <i>PLoS Genetics</i> , 2013, 9, e1003498.	1.5	173
666	Epigenetic Mechanisms in Penile Carcinoma. <i>International Journal of Molecular Sciences</i> , 2013, 14, 10791-10808.	1.8	17
667	Function and Evolution of DNA Methylation in <i>Nasonia vitripennis</i> . <i>PLoS Genetics</i> , 2013, 9, e1003872.	1.5	162
668	DNA Methylation Impacts Gene Expression and Ensures Hypoxic Survival of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003419.	2.1	132
669	Repressive Epigenetic Changes at the <i>mGlu2</i> Promoter in Frontal Cortex of 5-HT _{2A} Knockout Mice. <i>Molecular Pharmacology</i> , 2013, 83, 1166-1175.	1.0	33
670	Ecological Epigenetics: An Introduction to the Symposium. <i>Integrative and Comparative Biology</i> , 2013, 53, 307-318.	0.9	19
671	Human Genome Replication Proceeds through Four Chromatin States. <i>PLoS Computational Biology</i> , 2013, 9, e1003233.	1.5	54
672	Convergent Transcription Induces Dynamic DNA Methylation at <i>disiRNA</i> Loci. <i>PLoS Genetics</i> , 2013, 9, e1003761.	1.5	35
673	TET2 and TET3 regulate GlcNAcylation and H3K4 methylation through OGT and SET1/COMPASS. <i>EMBO Journal</i> , 2013, 32, 645-655.	3.5	411
674	Methylated DNA and microRNA in Body Fluids as Biomarkers for Cancer Detection. <i>International Journal of Molecular Sciences</i> , 2013, 14, 10307-10331.	1.8	37

#	ARTICLE	IF	CITATIONS
675	Large, Male Germ Cell-Specific Hypomethylated DNA Domains With Unique Genomic and Epigenomic Features on the Mouse X Chromosome. <i>DNA Research</i> , 2013, 20, 549-565.	1.5	10
676	DNMT gene expression and methylome in Marek's disease resistant and susceptible chickens prior to and following infection by MDV. <i>Epigenetics</i> , 2013, 8, 431-444.	1.3	50
677	DNA methylation analysis of murine hematopoietic side population cells during aging. <i>Epigenetics</i> , 2013, 8, 1114-1122.	1.3	41
678	The mysterious presence of a 5-methylcytosine oxidase in the <i>Drosophila</i> genome. <i>Cell Cycle</i> , 2013, 12, 3357-3365.	1.3	44
679	Alterations of DNA methylome in human bladder cancer. <i>Epigenetics</i> , 2013, 8, 1013-1022.	1.3	55
680	Evolution of a contagious cancer: epigenetic variation in Devil Facial Tumour Disease. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20121720.	1.2	18
681	Developmentally Programmed CpG Island Methylation Confers Tissue- and Cell-Type-Specific Transcriptional Activation. <i>Molecular and Cellular Biology</i> , 2013, 33, 1845-1858.	1.1	44
682	CpG_MPs: identification of CpG methylation patterns of genomic regions from high-throughput bisulfite sequencing data. <i>Nucleic Acids Research</i> , 2013, 41, e4-e4.	6.5	48
683	Regulation of GTP-binding Protein ($G_{i\pm s}$) Expression in Human Myometrial Cells. <i>Journal of Biological Chemistry</i> , 2013, 288, 6704-6716.	1.6	6
684	Meeting the methodological challenges in molecular mapping of the embryonic epigenome. <i>Molecular Human Reproduction</i> , 2013, 19, 809-827.	1.3	11
685	Ecological Epigenetics: Beyond MS-AFLP. <i>Integrative and Comparative Biology</i> , 2013, 53, 340-350.	0.9	128
687	TET Proteins and 5-Methylcytosine Oxidation in the Immune System. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2013, 78, 1-10.	2.0	28
688	Reversible DNA methylation regulates seasonal photoperiodic time measurement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16651-16656.	3.3	153
689	SWI/SNF in cardiac progenitor cell differentiation. <i>Journal of Cellular Biochemistry</i> , 2013, 114, 2437-2445.	1.2	13
690	Genome-wide analysis of DNA methylation changes induced by gestational arsenic exposure in liver tumors. <i>Cancer Science</i> , 2013, 104, 1575-1585.	1.7	22
692	RNA interference knockdown of DNA methyl-transferase 3 affects gene alternative splicing in the honey bee. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12750-12755.	3.3	237
693	Activation-induced cytidine deaminase (AID) is necessary for the epithelial-mesenchymal transition in mammary epithelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2977-86.	3.3	67
694	Mapping the zebrafish brain methylome using reduced representation bisulfite sequencing. <i>Epigenetics</i> , 2013, 8, 979-989.	1.3	67

#	ARTICLE	IF	CITATIONS
695	Epigenetic effects of green tea polyphenols in cancer. <i>Epigenomics</i> , 2013, 5, 729-741.	1.0	96
696	Epigenetic regulation of the human genome: coherence between promoter activity and large-scale chromatin environment. <i>Frontiers in Life Science: Frontiers of Interdisciplinary Research in the Life Sciences</i> , 2013, 7, 44-62.	1.1	8
697	DNA methylation dynamics during the mammalian life cycle. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20110328.	1.8	262
698	Probing DNA shape and methylation state on a genomic scale with DNase I. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6376-6381.	3.3	151
700	On how mammalian transcription factors recognize methylated DNA. <i>Epigenetics</i> , 2013, 8, 131-137.	1.3	85
701	<i>Helicobacter pylori</i> CagA: From Pathogenic Mechanisms to Its Use as an Anti-Cancer Vaccine. <i>Frontiers in Immunology</i> , 2013, 4, 328.	2.2	62
702	Retroelements: molecular features and implications for disease. <i>Genes and Genetic Systems</i> , 2013, 88, 31-43.	0.2	5
703	DNA Methylation in Cancer: A Gene Silencing Mechanism and the Clinical Potential of Its Biomarkers. <i>Tohoku Journal of Experimental Medicine</i> , 2013, 229, 173-185.	0.5	72
704	Promoter Methylation Profiles between Human Lung Adenocarcinoma Multidrug Resistant A549/Cisplatin (A549/DDP) Cells and Its Progenitor A549 Cells. <i>Biological and Pharmaceutical Bulletin</i> , 2013, 36, 1310-1316.	0.6	28
705	Gene-Environment Interactions in Major Depressive Disorder. <i>Canadian Journal of Psychiatry</i> , 2013, 58, 76-83.	0.9	94
706	Changes in Methylation Patterns of <i>Kiss1</i> and <i>Kiss1r</i> Gene Promoters across Puberty. <i>Genetics & Epigenetics</i> , 2013, 5, GEG.S12897.	2.5	23
707	Aberrant DNA methylation profile of chronic and transformed classic Philadelphia-negative myeloproliferative neoplasms. <i>Haematologica</i> , 2013, 98, 1414-1420.	1.7	46
708	Regulation and Function of DNA and Histone Methylations. <i>Current Pharmaceutical Design</i> , 2013, 19, 719-733.	0.9	8
709	Detection of differentially methylated gene promoters in failing and nonfailing human left ventricle myocardium using computation analysis. <i>Physiological Genomics</i> , 2013, 45, 597-605.	1.0	56
710	Interaction-based evolution: how natural selection and nonrandom mutation work together. <i>Biology Direct</i> , 2013, 8, 24.	1.9	29
711	Acetaldehyde and parkinsonism: role of CYP450 2E1. <i>Frontiers in Behavioral Neuroscience</i> , 2013, 7, 71.	1.0	24
713	Genomewide DNA Methylation Analysis Identifies Novel Methylated Genes in Non-Small-Cell Lung Carcinomas. <i>Journal of Thoracic Oncology</i> , 2013, 8, 562-573.	0.5	31
714	Histone Acetylation: From Code to Web and Router Via Intrinsically Disordered Regions. <i>Current Pharmaceutical Design</i> , 2013, 19, 5019-5042.	0.9	19

#	ARTICLE	IF	CITATIONS
715	Epigenetic Modifications Unlock the Milk Protein Gene Loci during Mouse Mammary Gland Development and Differentiation. PLoS ONE, 2013, 8, e53270.	1.1	50
716	DNA Methylation of Specific CpG Sites in the Promoter Region Regulates the Transcription of the Mouse Oxytocin Receptor. PLoS ONE, 2013, 8, e56869.	1.1	85
717	Efficient Deamination of 5-Methylcytidine and 5-Substituted Cytidine Residues in DNA by Human APOBEC3A Cytidine Deaminase. PLoS ONE, 2013, 8, e63461.	1.1	43
718	Gastric Inhibitory Polypeptide Receptor Methylation in Newly Diagnosed, Drug-Naïve Patients with Type 2 Diabetes: A Case-Control Study. PLoS ONE, 2013, 8, e75474.	1.1	13
719	Accurate monitoring of promoter gene methylation with high-resolution melting polymerase chain reaction using the ABCB1 gene as a model. Genetics and Molecular Research, 2013, 12, 714-722.	0.3	8
720	DNA Methyltransferase-1 Inhibitors as Epigenetic Therapy for Cancer. Current Cancer Drug Targets, 2013, 13, 379-399.	0.8	130
721	Maternal Diet during Pregnancy Induces Gene Expression and DNA Methylation Changes in Fetal Tissues in Sheep. Frontiers in Genetics, 2013, 4, 49.	1.1	95
722	Cigarette smoking and DNA methylation. Frontiers in Genetics, 2013, 4, 132.	1.1	317
723	Genetics and epigenetics of arrhythmia and heart failure. Frontiers in Genetics, 2013, 4, 219.	1.1	59
724	Insights into Chromatin Structure and Dynamics in Plants. Biology, 2013, 2, 1378-1410.	1.3	33
725	Rapid Collection of Biospecimens by Automated Identification of Patients Eligible for Pharmacoepigenetic Studies. Journal of Personalized Medicine, 2013, 3, 263-274.	1.1	3
726	Personalized treatment strategies in glioblastoma: MGMT promoter methylation status. OncoTargets and Therapy, 2013, 6, 1363.	1.0	127
728	Epigenetic Regulation of Neural Differentiation from Embryonic Stem Cells. , 0, , .		0
729	Epigenetic Mechanisms of the Vascular Endothelium. , 2014, , .		1
730	DNA methylation, microRNAs, and their crosstalk as potential biomarkers in hepatocellular carcinoma. World Journal of Gastroenterology, 2014, 20, 7894.	1.4	74
731	A Novel Method for Identification and Quantification of Consistently Differentially Methylated Regions. PLoS ONE, 2014, 9, e97513.	1.1	4
732	Genome-wide DNA Methylation Profiles of Small Intestine and Liver in Fast-growing and Slow-growing Weaning Piglets. Asian-Australasian Journal of Animal Sciences, 2014, 27, 1532-1539.	2.4	6
733	Causes and Consequences of Age-Related Changes in DNA Methylation: A Role for ROS?. Biology, 2014, 3, 403-425.	1.3	41

#	ARTICLE	IF	CITATIONS
734	Structure and Function of Human DNA Methyltransferases. , 2014, , .		0
735	Chromatin Structure and Modification. , 2014, , 113-123.		0
736	Cooperation between phenotypic plasticity and genetic mutations can account for the cumulative selection in evolution. Biophysics (Nagoya-shi, Japan), 2014, 10, 99-108.	0.4	12
737	Network-based analysis identifies epigenetic biomarkers of esophageal squamous cell carcinoma progression. Bioinformatics, 2014, 30, 3054-3061.	1.8	15
738	Cytogenetic evidences of genome rearrangement and differential epigenetic chromatin modification in the sea lamprey (<i>Petromyzon marinus</i>). Genetica, 2014, 142, 545-554.	0.5	18
739	PD_NGSAtlas: a reference database combining next-generation sequencing epigenomic and transcriptomic data for psychiatric disorders. BMC Medical Genomics, 2014, 7, 71.	0.7	9
740	Systematic mapping of occluded genes by cell fusion reveals prevalence and stability of <i>cis</i> -mediated silencing in somatic cells. Genome Research, 2014, 24, 267-280.	2.4	12
741	Fundamental diversity of human CpG islands at multiple biological levels. Epigenetics, 2014, 9, 483-491.	1.3	28
742	Conserved and Divergent Patterns of DNA Methylation in Higher Vertebrates. Genome Biology and Evolution, 2014, 6, 2998-3014.	1.1	27
743	Methylation of the <i>Sf</i> locus in almond is associated with <i>S</i> -RNase loss of function. Plant Molecular Biology, 2014, 86, 681-689.	2.0	37
744	Prenatal stress-induced programming of genome-wide promoter DNA methylation in 5-HTT-deficient mice. Translational Psychiatry, 2014, 4, e473-e473.	2.4	44
745	Differential methylation in CN-AML preferentially targets non-CGI regions and is dictated by <i>DNMT3A</i> mutational status and associated with predominant hypomethylation of HOX genes. Epigenetics, 2014, 9, 1108-1119.	1.3	74
746	The imprinted gene <i>LRRTM1</i> mediates schizotypy and handedness in a nonclinical population. Journal of Human Genetics, 2014, 59, 332-336.	1.1	42
747	Prenatal maternal immune activation causes epigenetic differences in adolescent mouse brain. Translational Psychiatry, 2014, 4, e434-e434.	2.4	88
748	Epigenetics and Cardiovascular Disease. , 2014, , 747-782.		0
749	Evolution of DNA Methylation Patterns in the Brassicaceae is Driven by Differences in Genome Organization. PLoS Genetics, 2014, 10, e1004785.	1.5	184
750	Genome-wide profiling of DNA methylation and gene expression in <i>Crassostrea gigas</i> male gametes. Frontiers in Physiology, 2014, 5, 224.	1.3	92
751	Methylome Diversification through Changes in DNA Methyltransferase Sequence Specificity. PLoS Genetics, 2014, 10, e1004272.	1.5	92

#	ARTICLE	IF	CITATIONS
752	Independently specified <i>Atoh1</i> domains define novel developmental compartments in rhombomere 1. <i>Development (Cambridge)</i> , 2014, 141, 389-398.	1.2	33
753	Interactions between E-Cadherin and MicroRNA Deregulation in Head and Neck Cancers: The Potential Interplay. <i>BioMed Research International</i> , 2014, 2014, 1-8.	0.9	24
754	TET2 Inhibits Differentiation of Embryonic Stem Cells but Does Not Overcome Methylation-Induced Gene Silencing. <i>Bone Marrow Research</i> , 2014, 2014, 1-9.	1.7	2
755	Grand challenges in evolutionary and population genetics: the importance of integrating epigenetics, genomics, modeling, and experimentation. <i>Frontiers in Genetics</i> , 2014, 5, 197.	1.1	40
756	<i>Trichinella spiralis</i> , potential model nematode for epigenetics and its implication in metazoan parasitism. <i>Frontiers in Physiology</i> , 2014, 4, 410.	1.3	13
757	MODMatcher: Multi-Omics Data Matcher for Integrative Genomic Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003790.	1.5	35
758	Epigenetic Modifications and Type 2 Diabetes in Humans. <i>Frontiers in Diabetes</i> , 2014, , 102-110.	0.4	1
759	Elucidating the molecular bases of epigenetic inheritance in non-model invertebrates: the case of the root-knot nematode <i>Meloidogyne incognita</i> . <i>Frontiers in Physiology</i> , 2014, 5, 211.	1.3	24
760	Epigenetic features in the oyster <i>Crassostrea gigas</i> suggestive of functionally relevant promoter DNA methylation in invertebrates. <i>Frontiers in Physiology</i> , 2014, 5, 129.	1.3	44
761	Epigenetic mechanisms in Alzheimer's disease. <i>Degenerative Neurological and Neuromuscular Disease</i> , 2014, 4, 85.	0.7	8
762	Shotgun Bisulfite Sequencing of the <i>Betula platyphylla</i> Genome Reveals the Tree's DNA Methylation Patterning. <i>International Journal of Molecular Sciences</i> , 2014, 15, 22874-22886.	1.8	15
763	<i>GCK</i> Gene-Body Hypomethylation Is Associated with the Risk of Coronary Heart Disease. <i>BioMed Research International</i> , 2014, 2014, 1-7.	0.9	32
764	Epigenetic regulation and cancer (Review). <i>Oncology Reports</i> , 2014, 31, 523-532.	1.2	114
765	Exploring the molecular causes of hepatitis B virus vaccination response: an approach with epigenomic and transcriptomic data. <i>BMC Medical Genomics</i> , 2014, 7, 12.	0.7	21
766	DNMT3A: the DioNysian MonsTer of acute myeloid leukaemia. <i>Therapeutic Advances in Hematology</i> , 2014, 5, 187-196.	1.1	11
767	DNA methylation and demethylation: A pathway to gametogenesis and development. <i>Molecular Reproduction and Development</i> , 2014, 81, 113-125.	1.0	38
768	Epigenetic regulation in neural crest development. <i>Developmental Biology</i> , 2014, 396, 159-168.	0.9	73
769	Epigenetic modifiers of islet function and mass. <i>Trends in Endocrinology and Metabolism</i> , 2014, 25, 628-636.	3.1	32

#	ARTICLE	IF	CITATIONS
770	Stark sexual display divergence among jumping spider populations in the face of gene flow. <i>Molecular Ecology</i> , 2014, 23, 5208-5223.	2.0	9
771	Fetal Alcohol Programming of Hypothalamic Proopiomelanocortin System by Epigenetic Mechanisms and Later Life Vulnerability to Stress. <i>Alcoholism: Clinical and Experimental Research</i> , 2014, 38, 2323-2330.	1.4	26
772	DNA methylation functions as a critical regulator of Kir4.1 expression during CNS development. <i>Glia</i> , 2014, 62, 411-427.	2.5	50
773	Altered CpG methylation in sporadic Alzheimer's disease is associated with APP and MAPT dysregulation. <i>Human Molecular Genetics</i> , 2014, 23, 648-656.	1.4	126
774	Masterpiece of epigenetic engineering – how <i>Toxoplasma gondii</i> reprogrammes host brains to change fear to sexual attraction. <i>Molecular Ecology</i> , 2014, 23, 5934-5936.	2.0	26
776	The DNA Methylation Signature of Smoking: An Archetype for the Identification of Biomarkers for Behavioral Illness. <i>Nebraska Symposium on Motivation</i> , 2014, 61, 109-127.	0.9	26
777	Whole genome sequencing and methylome analysis of the wild guinea pig. <i>BMC Genomics</i> , 2014, 15, 1036.	1.2	14
778	Genome-wide and single-base resolution DNA methylomes of the Pacific oyster <i>Crassostrea gigas</i> provide insight into the evolution of invertebrate CpG methylation. <i>BMC Genomics</i> , 2014, 15, 1119.	1.2	110
779	The effects of perinatal testosterone exposure on the DNA methylome of the mouse brain are late-emerging. <i>Biology of Sex Differences</i> , 2014, 5, 8.	1.8	106
780	Epigenetics of chronic pain after thoracic surgery. <i>Current Opinion in Anaesthesiology</i> , 2014, 27, 1-5.	0.9	20
781	PGC7 suppresses TET3 for protecting DNA methylation. <i>Nucleic Acids Research</i> , 2014, 42, 2893-2905.	6.5	52
782	Methylsorb: A simple method for quantifying DNA methylation using DNA-gold affinity interactions. , 2014, , .		2
783	Differential Methylation during Maize Leaf Growth Targets Developmentally Regulated Genes. <i>Plant Physiology</i> , 2014, 164, 1350-1364.	2.3	84
784	Sex-dependent activity of <i>de novo</i> methyltransferase 3 (<i>Tudmt3</i>) in the two-spotted mite, <i>Tetranychus urticae</i> ... <i>Insect Molecular Biology</i> , 2014, 23, 743-753.	1.0	7
785	DNA Methylation of the TNF- α Promoter Region in Peripheral Blood Monocytes and the Cortex of Human Alzheimer's Disease Patients. <i>Dementia and Geriatric Cognitive Disorders</i> , 2014, 38, 10-15.	0.7	27
786	EpimiR: a database of curated mutual regulation between miRNAs and epigenetic modifications. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau023.	1.4	55
787	The Epigenetic Landscape of Acute Myeloid Leukemia. <i>Advances in Hematology</i> , 2014, 2014, 1-15.	0.6	76
788	Epigenetic Dynamics: Role of Epimarks and Underlying Machinery in Plants Exposed to Abiotic Stress. <i>International Journal of Genomics</i> , 2014, 2014, 1-10.	0.8	26

#	ARTICLE	IF	CITATIONS
789	Genome-Wide and Gene-Specific Epigenomic Platforms for Hepatocellular Carcinoma Biomarker Development Trials. <i>Gastroenterology Research and Practice</i> , 2014, 2014, 1-9.	0.7	12
790	Gene Expression during Imidacloprid-Induced Hormesis in Green Peach Aphid. <i>Dose-Response</i> , 2014, 12, dose-response.1.	0.7	22
791	DNA Methylation, Epigenetics, and Evolution in Vertebrates: Facts and Challenges. <i>International Journal of Evolutionary Biology</i> , 2014, 2014, 1-7.	1.0	84
792	Epigenetic Regulation of a Brain-specific Glycosyltransferase N-Acetylglucosaminyltransferase-IX (GnT-IX) by Specific Chromatin Modifiers. <i>Journal of Biological Chemistry</i> , 2014, 289, 11253-11261.	1.6	44
793	Genome-wide alteration of 5-hydroxymethylcytosine in a mouse model of fragile X-associated tremor/ataxia syndrome. <i>Human Molecular Genetics</i> , 2014, 23, 1095-1107.	1.4	52
794	Epigenetics, Inflammation, and Aging. , 2014, , 85-101.		4
795	TET enzymatic oxidation of 5-methylcytosine, 5-hydroxymethylcytosine and 5-formylcytosine. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2014, 764-765, 18-35.	0.9	45
796	Brain region-specific methylation in the promoter of the murine oxytocin receptor gene is involved in its expression regulation. <i>Psychoneuroendocrinology</i> , 2014, 39, 121-131.	1.3	52
797	DNA memories of early social life. <i>Neuroscience</i> , 2014, 264, 64-75.	1.1	59
798	Cytosine modifications in neurodevelopment and diseases. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 405-418.	2.4	34
799	Delivery of epidrugs. <i>Drug Discovery Today</i> , 2014, 19, 1337-1352.	3.2	17
800	Gene expression regulation mediated through reversible m6A RNA methylation. <i>Nature Reviews Genetics</i> , 2014, 15, 293-306.	7.7	1,401
801	Molecular inversion probe-based SPR biosensing for specific, label-free and real-time detection of regional DNA methylation. <i>Chemical Communications</i> , 2014, 50, 3585-3588.	2.2	78
802	The effect of smoking on DNA methylation of peripheral blood mononuclear cells from African American women. <i>BMC Genomics</i> , 2014, 15, 151.	1.2	193
803	Genome-wide methylation changes are associated with muscle fiber density and drip loss in male three-yellow chickens. <i>Molecular Biology Reports</i> , 2014, 41, 3509-3516.	1.0	7
804	Single-base resolution of mouse offspring brain methylome reveals epigenome modifications caused by gestational folic acid. <i>Epigenetics and Chromatin</i> , 2014, 7, 3.	1.8	57
805	Differential expression of histone H3 genes and selective association of the variant H3.7 with a specific sequence class in <i>Stylonychia macronuclear</i> development. <i>Epigenetics and Chromatin</i> , 2014, 7, 4.	1.8	17
806	Epigenetic alterations in osteosarcoma: promising targets. <i>Molecular Biology Reports</i> , 2014, 41, 3303-3315.	1.0	29

#	ARTICLE	IF	CITATIONS
807	A TET Homologue Protein from <i>Coprinopsis cinerea</i> (CcTET) That Biochemically Converts 5-Methylcytosine to 5-Hydroxymethylcytosine, 5-Formylcytosine, and 5-Carboxylcytosine. <i>Journal of the American Chemical Society</i> , 2014, 136, 4801-4804.	6.6	56
808	Control of cerebral size and thickness. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 3199-3218.	2.4	14
809	Epigenetic Signaling in Psychiatric Disorders. <i>Journal of Molecular Biology</i> , 2014, 426, 3389-3412.	2.0	135
810	The CHH motif in sugar beet satellite DNA: a modulator for cytosine methylation. <i>Plant Journal</i> , 2014, 78, 937-950.	2.8	17
811	Design, Synthesis and Biological Evaluation of 4-Amino-N-(4-aminophenyl)benzamide Analogues of Quinoline-Based SGLT2 as Inhibitors of DNA Methylation. <i>ChemMedChem</i> , 2014, 9, 590-601.	1.6	49
812	Patterns of DNA Methylation in Animals: An Ecotoxicological Perspective. <i>Integrative and Comparative Biology</i> , 2014, 54, 77-86.	0.9	97
813	Genome methylation in <i>D. melanogaster</i> is found at specific short motifs and is independent of DNMT2 activity. <i>Genome Research</i> , 2014, 24, 821-830.	2.4	113
814	Structural Basis for Hydroxymethylcytosine Recognition by the SRA Domain of UHRF2. <i>Molecular Cell</i> , 2014, 54, 879-886.	4.5	92
815	Comparative epigenetic analyses reveal distinct patterns of oncogenic pathways activation in breast cancer subtypes. <i>Human Molecular Genetics</i> , 2014, 23, 5378-5393.	1.4	31
816	Functional Analysis of DNA and Chromatin. <i>Methods in Molecular Biology</i> , 2014, , .	0.4	2
817	Purification, characterization, sequencing and molecular cloning of a novel cysteine methyltransferase that regulates trehalose-6-phosphate synthase from <i>Saccharomyces cerevisiae</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 1861-1871.	1.1	6
818	Epigenetic regulation of the RHOX homeobox gene cluster and its association with human male infertility. <i>Human Molecular Genetics</i> , 2014, 23, 12-23.	1.4	45
819	PRDM14 promotes active DNA demethylation through the Ten-eleven translocation (TET)-mediated base excision repair pathway in embryonic stem cells. <i>Development (Cambridge)</i> , 2014, 141, 269-280.	1.2	113
820	Epigenetic regulation of the ABCB1 gene in drug-sensitive and drug-resistant lymphoid tumour cell lines obtained from canine patients. <i>Veterinary Journal</i> , 2014, 199, 103-109.	0.6	37
821	Methamphetamine Downregulates Striatal Glutamate Receptors via Diverse Epigenetic Mechanisms. <i>Biological Psychiatry</i> , 2014, 76, 47-56.	0.7	109
822	Comprehensive DNA methylation and hydroxymethylation analysis in the human brain and its implication in mental disorders. <i>Neuropharmacology</i> , 2014, 80, 133-139.	2.0	84
823	5-Hydroxymethylcytosine-Mediated DNA Demethylation in Stem Cells and Development. <i>Stem Cells and Development</i> , 2014, 23, 923-930.	1.1	23
824	Large replication skew domains delimit GC-poor gene deserts in human. <i>Computational Biology and Chemistry</i> , 2014, 53, 153-165.	1.1	5

#	ARTICLE	IF	CITATIONS
825	Quantification of 5-methylcytosine, 5-hydroxymethylcytosine and 5-carboxylcytosine from the blood of cancer patients by an enzyme-based immunoassay. <i>Analytica Chimica Acta</i> , 2014, 852, 212-217.	2.6	57
826	Epigenetic primer for diagnostic applications: a window into personalized medicine. <i>Personalized Medicine</i> , 2014, 11, 323-337.	0.8	2
827	Aberrant methylation of tRNA links cellular stress to neurodevelopmental disorders. <i>EMBO Journal</i> , 2014, 33, 2020-2039.	3.5	490
828	Drought resistance and DNA methylation of interspecific hybrids between <i>Fraxinus mandshurica</i> and <i>Fraxinus americana</i> . <i>Trees - Structure and Function</i> , 2014, 28, 1679-1692.	0.9	17
829	Targeting components of epigenome by small molecules. <i>Archives of Pharmacal Research</i> , 2014, 37, 1367-1374.	2.7	10
830	Epigenetics and Ocular Diseases: From Basic Biology to Clinical Study. <i>Journal of Cellular Physiology</i> , 2014, 229, 825-833.	2.0	23
831	Fine-scale population epigenetic structure in relation to gastrointestinal parasite load in red grouse (<i>Lagopus lagopus scotica</i>). <i>Molecular Ecology</i> , 2014, 23, 4256-4273.	2.0	51
832	Discovery of a Bacterial 5-Methylcytosine Deaminase. <i>Biochemistry</i> , 2014, 53, 7426-7435.	1.2	11
833	Is DNA methylation modulated by wounding-induced oxidative burst in maize?. <i>Plant Physiology and Biochemistry</i> , 2014, 82, 202-208.	2.8	13
834	Detection of single methylated cytosine using junction-forming DNA probes. <i>Analyst, The</i> , 2014, 139, 2122-2126.	1.7	4
835	Nutrient-driven O-GlcNAc cycling “think globally but act locally”. <i>Journal of Cell Science</i> , 2014, 127, 1857-67.	1.2	51
836	Modulation of Neurogenesis by Targeting Epigenetic Enzymes Using Small Molecules: An Overview. <i>ACS Chemical Neuroscience</i> , 2014, 5, 1164-1177.	1.7	14
837	Genetic, Epigenetic, and Environmental Contributions to Neural Tube Closure. <i>Annual Review of Genetics</i> , 2014, 48, 583-611.	3.2	192
839	Dissecting the dynamic changes of 5-hydroxymethylcytosine in T-cell development and differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3306-15.	3.3	139
840	Now you see it: Genome methylation makes a comeback in <i>Drosophila</i> . <i>BioEssays</i> , 2014, 36, 1138-1144.	1.2	23
841	Epigenetic Regulation of Macrophage Polarization by DNA Methyltransferase 3b. <i>Molecular Endocrinology</i> , 2014, 28, 565-574.	3.7	170
842	DNA methylation and microRNA biomarkers for noninvasive detection of gastric and colorectal cancer. <i>Biochemical and Biophysical Research Communications</i> , 2014, 455, 43-57.	1.0	139
843	A signal-on fluorescent assay for DNA methyltransferase activity using a methylation-resistant endonuclease. <i>Analyst, The</i> , 2014, 139, 2674.	1.7	8

#	ARTICLE	IF	CITATIONS
844	Epigenetic inheritance and genome regulation: is DNA methylation linked to ploidy in haplodiploid insects?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140411.	1.2	36
845	eMethylsorb: electrochemical quantification of DNA methylation at CpG resolution using DNA-gold affinity interactions. <i>Chemical Communications</i> , 2014, 50, 13153-13156.	2.2	68
846	Alzheimer's disease and epigenetic diet. <i>Neurochemistry International</i> , 2014, 78, 105-116.	1.9	57
847	DNA methylation dynamics of the human preimplantation embryo. <i>Nature</i> , 2014, 511, 611-615.	13.7	488
848	An epigenetic window into the past?. <i>Science</i> , 2014, 345, 511-512.	6.0	41
849	CpG methylation in the 5'-flanking region of LGP2 gene lacks association with resistance/susceptibility to GCRV but contributes to the differential expression between muscle and spleen tissues in grass carp, <i>Ctenopharyngodon idella</i> . <i>Fish and Shellfish Immunology</i> , 2014, 40, 154-163.	1.6	13
850	Epigenetics and Evolution. <i>Integrative and Comparative Biology</i> , 2014, 54, 31-42.	0.9	61
851	Evolutionary conservation of the eumetazoan gene regulatory landscape. <i>Genome Research</i> , 2014, 24, 639-650.	2.4	143
852	Epigenetic Modification at Notch Responsive Promoters Blunts Efficacy of Inducing Notch Pathway Reactivation After Myocardial Infarction. <i>Circulation Research</i> , 2014, 115, 636-649.	2.0	56
853	Connections between TET proteins and aberrant DNA modification in cancer. <i>Trends in Genetics</i> , 2014, 30, 464-474.	2.9	221
854	Irradiation-induced hippocampal neurogenesis impairment is associated with epigenetic regulation of bdnf gene transcription. <i>Brain Research</i> , 2014, 1577, 77-88.	1.1	46
855	Expanding the roles of chromatin insulators in nuclear architecture, chromatin organization and genome function. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 4089-4113.	2.4	22
856	DNA methylation in obesity and type 2 diabetes. <i>Annals of Medicine</i> , 2014, 46, 103-113.	1.5	70
857	Transcriptional and epigenetic networks of helper T and innate lymphoid cells. <i>Immunological Reviews</i> , 2014, 261, 23-49.	2.8	76
858	An integrated platform for bovine DNA methylome analysis suitable for small samples. <i>BMC Genomics</i> , 2014, 15, 451.	1.2	33
859	Bis-class: a new classification tool of methylation status using bayes classifier and local methylation information. <i>BMC Genomics</i> , 2014, 15, 608.	1.2	12
860	Marked methylation changes in intestinal genes during the perinatal period of preterm neonates. <i>BMC Genomics</i> , 2014, 15, 716.	1.2	65
861	Methylation plotter: a web tool for dynamic visualization of DNA methylation data. <i>Source Code for Biology and Medicine</i> , 2014, 9, 11.	1.7	53

#	ARTICLE	IF	CITATIONS
862	Whole-genome bisulfite sequencing of multiple individuals reveals complementary roles of promoter and gene body methylation in transcriptional regulation. <i>Genome Biology</i> , 2014, 15, 408.	3.8	173
863	Non-exhaustive DNA methylation-mediated transposon silencing in the black truffle genome, a complex fungal genome with massive repeat element content. <i>Genome Biology</i> , 2014, 15, 411.	3.8	67
864	Methylsorb: A Simple Method for Quantifying DNA Methylation Using DNA-Gold Affinity Interactions. <i>Analytical Chemistry</i> , 2014, 86, 10179-10185.	3.2	59
865	5-hydroxymethylcytosine. <i>Cancer Biology and Therapy</i> , 2014, 15, 10-15.	1.5	44
866	Determination of global DNA methylation level by capillary electrophoresis using octyl-modified quaternized cellulose as an electrolyte additive. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 2771-2777.	1.9	8
867	Plant systems biology: insights, advances and challenges. <i>Planta</i> , 2014, 240, 33-54.	1.6	66
868	Hypermethylation of the enolase gene (ENO2) in autism. <i>European Journal of Pediatrics</i> , 2014, 173, 1233-1244.	1.3	31
869	The interplay of DNA methylation over time with Th2 pathway genetic variants on asthma risk and temporal asthma transition. <i>Clinical Epigenetics</i> , 2014, 6, 8.	1.8	47
870	DNA methylation profiles at birth and child ADHD symptoms. <i>Journal of Psychiatric Research</i> , 2014, 49, 51-59.	1.5	93
871	Understanding posttraumatic stress disorder: insights from the methylome. <i>Genes, Brain and Behavior</i> , 2014, 13, 52-68.	1.1	44
872	Differential impact of cumulative SES risk on methylation of protein-protein interaction pathways as a function of SLC6A4 genetic variation in African American young adults. <i>Biological Psychology</i> , 2014, 96, 28-34.	1.1	31
873	Imprinted loci in domestic livestock species as epigenomic targets for artificial selection of complex traits. <i>Animal Genetics</i> , 2014, 45, 25-39.	0.6	21
874	Accelerated chromatin biochemistry using DNA-barcoded nucleosome libraries. <i>Nature Methods</i> , 2014, 11, 834-840.	9.0	129
875	Effects of cytosine methylation on transcription factor binding sites. <i>BMC Genomics</i> , 2014, 15, 119.	1.2	214
876	DNA methylation profiling in the thalamus and hippocampus of postnatal malnourished mice, including effects related to long-term potentiation. <i>BMC Neuroscience</i> , 2014, 15, 31.	0.8	10
877	Whole DNA methylome profiling in lung cancer cells before and after epithelial-to-mesenchymal transition. <i>Diagnostic Pathology</i> , 2014, 9, 66.	0.9	19
878	Genetic Labeling of Neurons in Mouse Brain. <i>Cold Spring Harbor Protocols</i> , 2014, 2014, pdb.top080374.	0.2	10
879	Epigenetics of human melanoma: promises and challenges. <i>Journal of Molecular Cell Biology</i> , 2014, 6, 356-367.	1.5	36

#	ARTICLE	IF	CITATIONS
880	Unmasking risk loci: <scp>DNA</scp> methylation illuminates the biology of cancer predisposition. <i>BioEssays</i> , 2014, 36, 184-190.	1.2	16
881	The emerging role of epigenetics in cardiovascular disease. <i>Therapeutic Advances in Chronic Disease</i> , 2014, 5, 178-187.	1.1	107
882	Natural compounds in epigenetics: A current view. <i>Food and Chemical Toxicology</i> , 2014, 73, 71-83.	1.8	35
883	From development to diseases: The role of 5hmC in brain. <i>Genomics</i> , 2014, 104, 347-351.	1.3	87
884	Integrating Early Life Experience, Gene Expression, Brain Development, and Emergent Phenotypes. <i>Advances in Genetics</i> , 2014, 86, 277-307.	0.8	52
885	Maternal Epigenetic Inheritance and Stress During Gestation. , 2014, , 197-219.		3
886	Dnmt1-Independent CG Methylation Contributes to Nucleosome Positioning in Diverse Eukaryotes. <i>Cell</i> , 2014, 156, 1286-1297.	13.5	188
887	Non-toxic dose chidamide synergistically enhances platinum-induced DNA damage responses and apoptosis in Non-Small-Cell lung cancer cells. <i>Biomedicine and Pharmacotherapy</i> , 2014, 68, 483-491.	2.5	56
888	Effects of lanthanum on POD expression and DNA methylation of purple pepper under salt stress. <i>Journal of Rare Earths</i> , 2014, 32, 467-475.	2.5	9
889	A new strategy for methylated DNA detection based on photoelectrochemical immunosensor using Bi2S3 nanorods, methyl bonding domain protein and anti-his tag antibody. <i>Biosensors and Bioelectronics</i> , 2014, 51, 103-108.	5.3	94
890	MeCP2: the long trip from a chromatin protein to neurological disorders. <i>Trends in Molecular Medicine</i> , 2014, 20, 487-498.	3.5	90
891	Large hypomethylated domains serve as strong repressive machinery for key developmental genes in vertebrates. <i>Development (Cambridge)</i> , 2014, 141, 2568-2580.	1.2	41
892	Loss of the Polycomb Mark from Bivalent Promoters Leads to Activation of Cancer-Promoting Genes in Colorectal Tumors. <i>Cancer Research</i> , 2014, 74, 3617-3629.	0.4	43
893	Network-guided regression for detecting associations between DNA methylation and gene expression. <i>Bioinformatics</i> , 2014, 30, 2693-2701.	1.8	13
894	Unlocking epigenetic codes in neurogenesis. <i>Genes and Development</i> , 2014, 28, 1253-1271.	2.7	79
895	DNA methylation and evolution of duplicate genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5932-5937.	3.3	88
896	Epigenomics and the control of fate, form and function in social insects. <i>Current Opinion in Insect Science</i> , 2014, 1, 31-38.	2.2	23
897	Evolutionary insights into DNA methylation in insects. <i>Current Opinion in Insect Science</i> , 2014, 1, 25-30.	2.2	82

#	ARTICLE	IF	CITATIONS
898	Nucleic Acid Oxidation in DNA Damage Repair and Epigenetics. <i>Chemical Reviews</i> , 2014, 114, 4602-4620.	23.0	79
899	Epigenetic targeting of the Nanog pathway and signaling networks during chemical carcinogenesis. <i>Carcinogenesis</i> , 2014, 35, 1726-1736.	1.3	22
900	Expression and methylation of DNA repair genes in lens epithelium cells of age-related cataract. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2014, 766-767, 31-36.	0.4	36
901	Hunting for Darwin's gemmules and Lamarck's fluid: Transgenerational signaling and histone methylation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 1440-1453.	0.9	12
902	Environmental stressors and the epigenome. <i>Drug Discovery Today: Technologies</i> , 2014, 12, e3-e8.	4.0	20
903	Role of BDNF epigenetics in activity-dependent neuronal plasticity. <i>Neuropharmacology</i> , 2014, 76, 709-718.	2.0	150
904	Epigenetics in human gliomas. <i>Cancer Letters</i> , 2014, 342, 185-192.	3.2	48
905	Epigenetic Modifications in Alzheimer's Disease: Cause or Effect?. <i>Journal of Alzheimer's Disease</i> , 2014, 43, 1169-1173.	1.2	27
906	Multivariate Boosting for Integrative Analysis of High-Dimensional Cancer Genomic Data. <i>Cancer Informatics</i> , 2014, 13s7, CIN.S16353.	0.9	2
907	Sequence-selective Modification of DNA Cytosine by Using Junction-forming DNA Probes and Its Application to the Detection of Single Cytosine Methylation. <i>Analytical Sciences</i> , 2014, 30, 371-376.	0.8	2
908	FKBP5 and CRHR1 polymorphisms moderate the stressâ€“physical health association in a national sample.. <i>Health Psychology</i> , 2014, 33, 1046-1056.	1.3	22
909	Epigenetic alterations in acute myeloid leukemias. <i>FEBS Journal</i> , 2015, 282, 1786-1800.	2.2	36
910	Chromatin dynamics of plant telomeres and ribosomal genes. <i>Plant Journal</i> , 2015, 83, 18-37.	2.8	52
911	<scp>DNA</scp> Methylation: Hemodialysis Versus Hemodiafiltration. <i>Therapeutic Apheresis and Dialysis</i> , 2015, 19, 119-124.	0.4	9
912	CellMethy: Identification of a focal concordantly methylated pattern of CpGs revealed wide differences between normal and cancer tissues. <i>Scientific Reports</i> , 2015, 5, 18037.	1.6	5
913	Epigenetic Mechanisms Involved in Huntington's Disease Pathogenesis. <i>Journal of Huntington's Disease</i> , 2015, 4, 1-15.	0.9	38
914	Upcoming Meetings Related to Huntington's Disease. <i>Journal of Huntington's Disease</i> , 2015, 4, 107-107.	0.9	25
915	<i>Carcinogenesis.</i> , 2015, , 1135-1172.		0

#	ARTICLE	IF	CITATIONS
916	Stress increases DNA methylation of the neuronal PAS domain 4 (Npas4) gene. <i>NeuroReport</i> , 2015, 26, 827-832.	0.6	13
917	Adult porcine genome-wide DNA methylation patterns support pigs as a biomedical model. <i>BMC Genomics</i> , 2015, 16, 743.	1.2	96
918	Molecular basis for the substrate specificity and catalytic mechanism of thymine-7-hydroxylase in fungi. <i>Nucleic Acids Research</i> , 2015, 43, gkv979.	6.5	9
919	Genome-wide analysis of DNA methylation in pigs using reduced representation bisulfite sequencing. <i>DNA Research</i> , 2015, 22, 343-355.	1.5	72
920	Expression of Placental Members of the Human Growth Hormone Gene Family Is Increased in Response to Sequential Inhibition of DNA Methylation and Histone Deacetylation. <i>BioResearch Open Access</i> , 2015, 4, 446-456.	2.6	3
921	Cigarette smoke condensate and individual constituents modulate DNA methyltransferase expression in human liver cells. <i>SAGE Open Medicine</i> , 2015, 3, 205031211557831.	0.7	4
922	Genome-wide DNA methylome variation in two genetically distinct chicken lines using MethylC-seq. <i>BMC Genomics</i> , 2015, 16, 851.	1.2	39
923	Low temperature-induced DNA hypermethylation attenuates expression of RhAG, an AGAMOUS homolog, and increases petal number in rose (<i>Rosa hybrida</i>). <i>BMC Plant Biology</i> , 2015, 15, 237.	1.6	57
924	DNA methylation analysis of phenotype specific stratified Indian population. <i>Journal of Translational Medicine</i> , 2015, 13, 151.	1.8	43
925	A Review of Epigenetic Markers of Tobacco and Alcohol Consumption. <i>Behavioral Sciences and the Law</i> , 2015, 33, 675-690.	0.6	10
926	Gene Expression Signatures Based on Variability can Robustly Predict Tumor Progression and Prognosis. <i>Cancer Informatics</i> , 2015, 14, CIN.S23862.	0.9	21
927	H2A.Z mediates different aspects of chromatin function and modulates flowering responses in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2015, 83, 96-109.	2.8	59
928	Genome-wide screen of promoter methylation analysis of ES cells and ES derived epidermal-like cells. <i>Cell Biochemistry and Function</i> , 2015, 33, 398-406.	1.4	2
929	Epigenetics/Programming in the HPA Axis. , 2015, 6, 87-110.		54
930	Global histone post-translational modifications and cancer: Biomarkers for diagnosis, prognosis and treatment?. <i>World Journal of Biological Chemistry</i> , 2015, 6, 333.	1.7	92
931	Methylation profile of SNRPN gene and its correlation with weight and chronological age. <i>Genetics and Molecular Research</i> , 2015, 14, 13791-13798.	0.3	7
932	Comparative Aspects of Molecular Mechanisms of Drug Resistance through ABC Transporters and Other Related Molecules in Canine Lymphoma. <i>Veterinary Sciences</i> , 2015, 2, 185-205.	0.6	9
933	Functions of TET Proteins in Hematopoietic Transformation. <i>Molecules and Cells</i> , 2015, 38, 925-935.	1.0	21

#	ARTICLE	IF	CITATIONS
934	Epigenetic Modifications: Therapeutic Potential in Cancer. <i>Brazilian Archives of Biology and Technology</i> , 2015, 58, 526-539.	0.5	3
935	Current and Future Prospects for Epigenetic Biomarkers of Substance Use Disorders. <i>Genes</i> , 2015, 6, 991-1022.	1.0	70
936	Increased Histone Deacetylase Activity Involved in the Suppressed Invasion of Cancer Cells Survived from ALA-Mediated Photodynamic Treatment. <i>International Journal of Molecular Sciences</i> , 2015, 16, 23994-24010.	1.8	11
937	Overexpression of the Heterochromatinization Factor BAHD1 in HEK293 Cells Differentially Reshapes the DNA Methylome on Autosomes and X Chromosome. <i>Frontiers in Genetics</i> , 2015, 6, 339.	1.1	23
938	In Utero Exposure to Diethylstilbestrol and Blood DNA Methylation in Women Ages 40â€“59 Years from the Sister Study. <i>PLoS ONE</i> , 2015, 10, e0118757.	1.1	16
939	CHR729 Is a CHD3 Protein That Controls Seedling Development in Rice. <i>PLoS ONE</i> , 2015, 10, e0138934.	1.1	38
940	Genome-Wide Epigenetic Regulation of Gene Transcription in Maize Seeds. <i>PLoS ONE</i> , 2015, 10, e0139582.	1.1	28
941	Fetal Alcohol Exposure Reduces Dopamine Receptor D2 and Increases Pituitary Weight and Prolactin Production via Epigenetic Mechanisms. <i>PLoS ONE</i> , 2015, 10, e0140699.	1.1	31
942	Single Base-Resolution Methylome of the Dizygotic Sheep. <i>PLoS ONE</i> , 2015, 10, e0142034.	1.1	5
943	Epigenetic Control of Cell Division and Cell Differentiation in the Root Apex. <i>Frontiers in Plant Science</i> , 2015, 6, 1178.	1.7	42
944	Effect of 50â€“Hz Extremely Low-Frequency Electromagnetic Fields on the DNA Methylation and DNA Methyltransferases in Mouse Spermatocyte-Derived Cell Line GC-2. <i>BioMed Research International</i> , 2015, 2015, 1-10.	0.9	23
946	DNA Methylation: A Possible Target for Current and Future Studies on Cancer?. <i>Epigenetic Diagnosis & Therapy</i> , 2015, 1, 5-13.	0.1	0
947	Base-resolution methylation patterns accurately predict transcription factor bindings in vivo. <i>Nucleic Acids Research</i> , 2015, 43, 2757-2766.	6.5	46
948	Transcriptional Activity and DNA Methylation Dynamics of the Gal4/UAS System in Zebrafish. <i>Marine Biotechnology</i> , 2015, 17, 593-603.	1.1	14
949	High-Throughput Sequencing-Based Mapping of Cytosine Modifications. , 2015, , 39-53.		5
950	Engineering of a Histone-Recognition Domain in Dnmt3a Alters the Epigenetic Landscape and Phenotypic Features of Mouse ESCs. <i>Molecular Cell</i> , 2015, 59, 89-103.	4.5	76
951	DNA methyltransferases have an essential role in female fecundity inÂbrown planthopper, Nilaparvata lugens. <i>Biochemical and Biophysical Research Communications</i> , 2015, 464, 83-88.	1.0	43
952	Building up and knocking down: An emerging role for epigenetics and proteasomal degradation in systems consolidation. <i>Neuroscience</i> , 2015, 300, 39-52.	1.1	15

#	ARTICLE	IF	CITATIONS
953	Epigenetic Mechanisms of Psychostimulant-Induced Addiction. <i>International Review of Neurobiology</i> , 2015, 120, 85-105.	0.9	25
954	De novo identification of differentially methylated regions in the human genome. <i>Epigenetics and Chromatin</i> , 2015, 8, 6.	1.8	684
955	Oxidative DNA demethylation mediated by Tet enzymes. <i>National Science Review</i> , 2015, 2, 318-328.	4.6	29
956	Effects of non-CpG site methylation on DNA thermal stability: a fluorescence study. <i>Nucleic Acids Research</i> , 2015, 43, 10722-10733.	6.5	22
957	Changes in global DNA methylation intensity and DNMT1 transcription during the aging process of scallop <i>Chlamys farreri</i> . <i>Journal of Ocean University of China</i> , 2015, 14, 685-690.	0.6	15
958	Racial differences in genome-wide methylation profiling and gene expression in breast tissues from healthy women. <i>Epigenetics</i> , 2015, 10, 1177-1187.	1.3	49
959	Genetic Polymorphism of DNA Methyltransferase 3A rs1550117 A>G and Risk of Cancer: A Meta-analysis. <i>Journal of Investigative Surgery</i> , 2015, 28, 346-353.	0.6	10
960	Plasmonic coupling-dependent SERS of gold nanoparticles anchored on methylated DNA and detection of global DNA methylation in SERS-based platforms. <i>Journal of Optics (United Kingdom)</i> , 2015, 17, 114022.	1.0	9
961	Structural impact of complete CpG methylation within target DNA on specific complex formation of the inducible transcription factor Egr1. <i>FEBS Letters</i> , 2015, 589, 1748-1753.	1.3	39
962	Neuroepigenetics: Desoxyribonucleic acid methylation in Alzheimer's disease and other dementias. <i>Medicina Clínica (English Edition)</i> , 2015, 144, 457-464.	0.1	2
963	Systems biology meets -omic technologies: novel approaches to biomarker discovery and companion diagnostic development. <i>Expert Review of Molecular Diagnostics</i> , 2015, 15, 255-265.	1.5	18
964	Vision from next generation sequencing: Multi-dimensional genome-wide analysis for producing gene regulatory networks underlying retinal development, aging and disease. <i>Progress in Retinal and Eye Research</i> , 2015, 46, 1-30.	7.3	50
965	Current Perspectives on Epigenetic Modifications by Dietary Chemopreventive and Herbal Phytochemicals. <i>Current Pharmacology Reports</i> , 2015, 1, 245-257.	1.5	42
966	Regulation of CD4 and CD8 Coreceptor Expression and CD4 Versus CD8 Lineage Decisions. <i>Advances in Immunology</i> , 2015, 125, 1-40.	1.1	23
967	Epigenetics in Social Insects. <i>Advances in Insect Physiology</i> , 2015, 48, 227-269.	1.1	15
968	Expression of DNMT1 in neural stem/precursor cells is critical for survival of newly generated neurons in the adult hippocampus. <i>Neuroscience Research</i> , 2015, 95, 1-11.	1.0	40
969	Molecular mechanisms of synaptic remodeling in alcoholism. <i>Neuroscience Letters</i> , 2015, 601, 11-19.	1.0	61
970	The Tet1 and histone methylation expression pattern in dairy goat testis. <i>Theriogenology</i> , 2015, 83, 1154-1161.	0.9	11

#	ARTICLE	IF	CITATIONS
971	Thymic stromal lymphopoietin (TSLP) secretion from human nasal epithelium is a function of TSLP genotype. <i>Mucosal Immunology</i> , 2015, 8, 993-999.	2.7	31
972	Role of Hippocampus Mitogen-Activated Protein Kinase Phosphatase-1 mRNA Expression and DNA Methylation in the Depression of the Rats with Chronic Unpredicted Stress. <i>Cellular and Molecular Neurobiology</i> , 2015, 35, 473-482.	1.7	7
973	Transposable element-driven transcript diversification and its relevance to genetic disorders. <i>Gene</i> , 2015, 558, 187-194.	1.0	21
974	Epidaurus: aggregation and integration analysis of prostate cancer epigenome. <i>Nucleic Acids Research</i> , 2015, 43, e7-e7.	6.5	10
975	Methylation of microRNA genes regulates gene expression in bisexual flower development in andromonoecious poplar. <i>Journal of Experimental Botany</i> , 2015, 66, 1891-1905.	2.4	55
976	Function and information content of DNA methylation. <i>Nature</i> , 2015, 517, 321-326.	13.7	1,656
977	Clinical impact of molecular biomarkers in gliomas. <i>Journal of Clinical Neuroscience</i> , 2015, 22, 437-444.	0.8	57
978	Genomic profiling of DNA methyltransferases reveals a role for DNMT3B in genic methylation. <i>Nature</i> , 2015, 520, 243-247.	13.7	566
979	DNA methylation analysis of human myoblasts during in vitro myogenic differentiation: de novo methylation of promoters of muscle-related genes and its involvement in transcriptional down-regulation. <i>Human Molecular Genetics</i> , 2015, 24, 410-423.	1.4	44
980	Anion exchange chromatography for the determination of 5-methyl-2â€²-deoxycytidine: application to cisplatin-sensitive and cisplatin-resistant ovarian cancer cell lines. <i>Analytical and Bioanalytical Chemistry</i> , 2015, 407, 2423-2431.	1.9	9
981	Reconfiguration of DNA methylation in aging. <i>Mechanisms of Ageing and Development</i> , 2015, 151, 60-70.	2.2	227
982	Principles of Epigenetic Treatment. , 2015, , 443-465.		0
983	Chromosome 7 gain and DNA hypermethylation at the HOXA10 locus are associated with expression of a stem cell related HOX-signature in glioblastoma. <i>Genome Biology</i> , 2015, 16, 16.	3.8	82
984	CpG signalling, H2A.Z/H3 acetylation and microRNA-mediated deferred self-attenuation orchestrate foetal NOS3 expression. <i>Clinical Epigenetics</i> , 2015, 7, 9.	1.8	21
985	Genome-wide profiling of DNA methylation provides insights into epigenetic regulation of fungal development in a plant pathogenic fungus, <i>Magnaporthe oryzae</i> . <i>Scientific Reports</i> , 2015, 5, 8567.	1.6	115
986	Epigenetic remodeling in B-cell acute lymphoblastic leukemia occurs in two tracks and employs embryonic stem cell-like signatures. <i>Nucleic Acids Research</i> , 2015, 43, 2590-2602.	6.5	42
987	Involvement of DNA methylation in the control of cell growth during heat stress in tobacco BY-2 cells. <i>Protoplasma</i> , 2015, 252, 1451-1459.	1.0	29
988	Phosphorylation of TET Proteins Is Regulated via O-GlcNAcylation by the O-Linked N-Acetylglucosamine Transferase (OGT). <i>Journal of Biological Chemistry</i> , 2015, 290, 4801-4812.	1.6	102

#	ARTICLE	IF	CITATIONS
989	The Osteological Paradox 20 Years Later: Past Perspectives, Future Directions. <i>Journal of Archaeological Research</i> , 2015, 23, 397-450.	1.4	208
990	Omics in Aquatic Ecotoxicology. , 2015, , 183-203.		6
991	Augmenting Antitumor Immune Responses with Epigenetic Modifying Agents. <i>Frontiers in Immunology</i> , 2015, 6, 29.	2.2	139
992	The epigenetics of aging and neurodegeneration. <i>Progress in Neurobiology</i> , 2015, 131, 21-64.	2.8	334
993	IUGR with infantile overnutrition programs an insulin-resistant phenotype through DNA methylation of peroxisome proliferator-activated receptor- γ coactivator-1 α in rats. <i>Pediatric Research</i> , 2015, 77, 625-632.	1.1	19
994	DNA Methylation and Hydroxymethylation in Cancer. , 2015, , 9-30.		4
995	Epigenetic aberrations in acute myeloid leukemia: Early key events during leukemogenesis. <i>Experimental Hematology</i> , 2015, 43, 609-624.	0.2	47
996	RNA N ⁶ -methyladenosine methylation in post-transcriptional gene expression regulation. <i>Genes and Development</i> , 2015, 29, 1343-1355.	2.7	727
997	DNA-bare gold affinity interactions: mechanism and applications in biosensing. <i>Analytical Methods</i> , 2015, 7, 7042-7054.	1.3	131
998	Metabolic Syndrome and Complications of Pregnancy. , 2015, , .		2
999	Parallel Epigenomic and Transcriptomic Responses to Viral Infection in Honey Bees (<i>Apis mellifera</i>). <i>PLoS Pathogens</i> , 2015, 11, e1004713.	2.1	145
1000	The Potential Role of DNA Methylation in Abdominal Aortic Aneurysms. <i>International Journal of Molecular Sciences</i> , 2015, 16, 11259-11275.	1.8	27
1001	Epigenetic Profile of Human Adventitial Progenitor Cells Correlates With Therapeutic Outcomes in a Mouse Model of Limb Ischemia. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 675-688.	1.1	38
1002	Pediatric cancer epigenome and the influence of folate. <i>Epigenomics</i> , 2015, 7, 961-973.	1.0	18
1003	The regulatory mechanisms of intragenic DNA methylation. <i>Epigenomics</i> , 2015, 7, 527-531.	1.0	26
1004	Does DNA methylation regulate metamorphosis? The case of the sea lamprey (<i>Petromyzon marinus</i>) as an example. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2015, 185, 42-46.	0.7	29
1005	Experimental heart failure modelled by the cardiomyocyte-specific loss of an epigenome modifier, DNMT3B. <i>Journal of Molecular and Cellular Cardiology</i> , 2015, 82, 174-183.	0.9	45
1006	Transcription-Dependent Generation of a Specialized Chromatin Structure at the TCR β Locus. <i>Journal of Immunology</i> , 2015, 194, 3432-3443.	0.4	10

#	ARTICLE	IF	CITATIONS
1007	Epigenetics of the failing heart. <i>Heart Failure Reviews</i> , 2015, 20, 435-459.	1.7	16
1008	Mutation and Expression of a Methyl-Binding Protein 6 (MBD6) in Gastric and Colorectal Cancers. <i>Pathology and Oncology Research</i> , 2015, 21, 857-858.	0.9	4
1009	Extensive reprogramming of cytosine methylation in <i>Oryza</i> allotetraploids. <i>Genes and Genomics</i> , 2015, 37, 517-524.	0.5	4
1010	The Epigenetic Effects of Prenatal Cadmium Exposure. <i>Current Environmental Health Reports</i> , 2015, 2, 195-203.	3.2	69
1011	Analyses of random BAC clone sequences of Japanese cedar, <i>Cryptomeria japonica</i> . <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	4
1012	DNA Methylation and Chromatin Organization in Insects: Insights from the Ant <i>Camponotus floridanus</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 931-942.	1.1	30
1013	<i>Mecp2</i> regulates neural cell differentiation by suppressing the <i>Id1</i> to <i>Her2</i> axis in zebrafish. <i>Journal of Cell Science</i> , 2015, 128, 2340-2350.	1.2	47
1014	The hypomethylating agent Decitabine causes a paradoxical increase in 5-hydroxymethylcytosine in human leukemia cells. <i>Scientific Reports</i> , 2015, 5, 9281.	1.6	30
1015	DNA methylation and hydroxymethylation in stem cells. <i>Cell Biochemistry and Function</i> , 2015, 33, 161-173.	1.4	43
1016	The alternative role of DNA methylation in splicing regulation. <i>Trends in Genetics</i> , 2015, 31, 274-280.	2.9	458
1017	The role of DNA methylation: a challenge for the DOHaD paradigm in going beyond the historical debate. <i>Journal of Developmental Origins of Health and Disease</i> , 2015, 6, 2-4.	0.7	8
1018	Developmental exposure to 2,3,7,8-tetrachlorodibenzo-p-dioxin alters DNA methyltransferase (<i>dnmt</i>) expression in zebrafish (<i>Danio rerio</i>). <i>Toxicology and Applied Pharmacology</i> , 2015, 284, 142-151.	1.3	60
1019	Reading the unique DNA methylation landscape of the brain: Non-CpG methylation, hydroxymethylation, and MeCP2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6800-6806.	3.3	205
1020	Alterations in global DNA methylation and hydroxymethylation are not detected in Alzheimer's disease. <i>Neuropathology and Applied Neurobiology</i> , 2015, 41, 497-506.	1.8	78
1021	DNA Methylation in Memory Formation. <i>Neuroscientist</i> , 2015, 21, 475-489.	2.6	71
1022	MeCP2 binds to non-CG methylated DNA as neurons mature, influencing transcription and the timing of onset for Rett syndrome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5509-5514.	3.3	256
1024	GC skew is a conserved property of unmethylated CpG island promoters across vertebrates. <i>Nucleic Acids Research</i> , 2015, 43, gkv811.	6.5	45
1025	DNA N6-methyladenine: a new epigenetic mark in eukaryotes?. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 705-710.	16.1	228

#	ARTICLE	IF	CITATIONS
1026	Mutant DNA methylation regulators endow hematopoietic stem cells with the preleukemic stem cell property, a requisite of leukemia initiation and relapse. <i>Frontiers of Medicine</i> , 2015, 9, 412-420.	1.5	10
1027	Conservation of tRNA and rRNA 5-methylcytosine in the kingdom Plantae. <i>BMC Plant Biology</i> , 2015, 15, 199.	1.6	98
1028	Epigenetic alterations and decreasing insecticide sensitivity of the Asian tiger mosquito <i>Aedes albopictus</i> . <i>Ecotoxicology and Environmental Safety</i> , 2015, 122, 45-53.	2.9	51
1029	Priming effect of menadione sodium bisulphite against salinity stress in <i>Arabidopsis</i> involves epigenetic changes in genes controlling proline metabolism. <i>Environmental and Experimental Botany</i> , 2015, 120, 23-30.	2.0	32
1030	<scp>CB</scp>1â€œreceptor knockout neonatal mice are protected against ethanolâ€œinduced impairments of <scp>DNMT</scp>1, <scp>DNMT</scp>3A, and <scp>DNA</scp> methylation. <i>Journal of Neurochemistry</i> , 2015, 132, 429-442.	2.1	75
1031	Organellar Genomes of Flowering Plants. , 2015, , 179-204.		5
1032	Recent advances in genomics and transcriptomics of cnidarians. <i>Marine Genomics</i> , 2015, 24, 131-138.	0.4	22
1033	Changepoint detection in base-resolution methylome data reveals a robust signature of methylated domain landscape. <i>BMC Genomics</i> , 2015, 16, 594.	1.2	8
1034	Transposable elements, mRNA expression level and strand-specificity of small RNAs are associated with non-additive inheritance of gene expression in hybrid plants. <i>BMC Plant Biology</i> , 2015, 15, 168.	1.6	17
1035	Expression level and immunolocalization of de novo methyltransferase 3 protein (TuDNMT3) in adult females and males of the two-spotted spider mite, <i>Tetranychus urticae</i> . <i>Experimental and Applied Acarology</i> , 2015, 67, 381-392.	0.7	1
1036	SINE transcription by RNA polymerase III is suppressed by histone methylation but not by DNA methylation. <i>Nature Communications</i> , 2015, 6, 6569.	5.8	80
1037	Modeling of replicates variances for detecting RNA methylation site in MERIP-SEQ data. , 2015, , .		0
1038	Genome-wide epigenetic and proteomic analysis reveals altered Notch signaling in EPC dysfunction. <i>Physiological Reports</i> , 2015, 3, e12358.	0.7	12
1039	The potential of DNA modifications as biomarkers and therapeutic targets in oncology. <i>Expert Review of Molecular Diagnostics</i> , 2015, 15, 1325-1337.	1.5	26
1040	Arginine methyltransferases mediate an epigenetic ovarian response to endometriosis. <i>Reproduction</i> , 2015, 150, 297-310.	1.1	23
1041	Lung Cancer Biomarkers. <i>Advances in Clinical Chemistry</i> , 2015, 72, 107-170.	1.8	92
1042	Genome-wide analysis of DNA methylation in the sexual stage of the insect pathogenic fungus <i>Cordyceps militaris</i> . <i>Fungal Biology</i> , 2015, 119, 1246-1254.	1.1	39
1043	Charting oxidized methylcytosines at base resolution. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 656-661.	3.6	62

#	ARTICLE	IF	CITATIONS
1044	Effects of sleeping with reduced carbohydrate availability on acute training responses. <i>Journal of Applied Physiology</i> , 2015, 119, 643-655.	1.2	82
1046	Integrative Genomic Approaches to Studying Epigenetic Mechanisms of Phenotypic Plasticity in the Aphid. <i>True Bugs (Heteroptera) of the Neotropics</i> , 2015, , 95-117.	1.2	2
1047	Neighborhood crime and depressive symptoms among African American women: Genetic moderation and epigenetic mediation of effects. <i>Social Science and Medicine</i> , 2015, 146, 120-128.	1.8	47
1048	Epigenetics and miRNA during bacteria-induced host immune responses. <i>Epigenomics</i> , 2015, 7, 1197-1212.	1.0	18
1049	Epigenetic gene expression—an introduction. , 2015, , 1-19.		2
1050	Presence of DNA methyltransferase activity and CpC methylation in <i>Drosophila melanogaster</i> . <i>Molecular Biology Reports</i> , 2015, 42, 1615-1621.	1.0	24
1051	Transcriptional Regulatory Events Initiated by <i>Ascl1</i> and <i>Neurog2</i> During Neuronal Differentiation of P19 Embryonic Carcinoma Cells. <i>Journal of Molecular Neuroscience</i> , 2015, 55, 684-705.	1.1	11
1052	Dynamic changes in the cardiac methylome during postnatal development. <i>FASEB Journal</i> , 2015, 29, 1329-1343.	0.2	56
1053	Human DNA methyltransferase gene-transformed yeasts display an inducible flocculation inhibited by 5-aza-2'-deoxycytidine. <i>Biochemical and Biophysical Research Communications</i> , 2015, 456, 689-694.	1.0	12
1054	Development and application of the adverse outcome pathway framework for understanding and predicting chronic toxicity: I. Challenges and research needs in ecotoxicology. <i>Chemosphere</i> , 2015, 120, 764-777.	4.2	167
1055	The role of mutations in epigenetic regulators in myeloid malignancies. <i>Immunological Reviews</i> , 2015, 263, 22-35.	2.8	46
1056	Whole-genome DNA methylation patterns and complex associations with gene structure and expression during flower development in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2015, 81, 268-281.	2.8	76
1057	DNA Methylation and Its Implications and Accessibility for Neuropsychiatric Therapeutics. <i>Annual Review of Pharmacology and Toxicology</i> , 2015, 55, 591-611.	4.2	63
1059	Reversible Inhibitors of LSD1 as Therapeutic Agents in Acute Myeloid Leukemia: Clinical Significance and Progress to Date. <i>Medicinal Research Reviews</i> , 2015, 35, 586-618.	5.0	120
1060	Epigenetic Regulation of Memory by Acetylation and Methylation of Chromatin: Implications in Neurological Disorders, Aging, and Addiction. <i>NeuroMolecular Medicine</i> , 2015, 17, 97-110.	1.8	46
1062	DNA Methylation in Social Insects: How Epigenetics Can Control Behavior and Longevity. <i>Annual Review of Entomology</i> , 2015, 60, 435-452.	5.7	156
1063	Transcription of Inflammatory Genes: Long Noncoding RNA and Beyond. <i>Journal of Interferon and Cytokine Research</i> , 2015, 35, 79-88.	0.5	29
1064	Cocaine triggers epigenetic alterations in the corticostriatal circuit. <i>Brain Research</i> , 2015, 1628, 50-59.	1.1	33

#	ARTICLE	IF	CITATIONS
1065	Intrauterine growth restriction inhibits expression of eukaryotic elongation factor 2 kinase, a regulator of protein translation. <i>Physiological Genomics</i> , 2016, 48, 616-625.	1.0	1
1066	Epigenetic Mechanisms in Depression. , 2016, , 181-207.		0
1067	Potential role of S-adenosylmethionine in osteosarcoma development. <i>OncoTargets and Therapy</i> , 2016, 9, 3653.	1.0	2
1068	DNA Methyltransferase Activity Assays: Advances and Challenges. <i>Theranostics</i> , 2016, 6, 369-391.	4.6	54
1069	Targeting New Candidate Genes by Small Molecules Approaching Neurodegenerative Diseases. <i>International Journal of Molecular Sciences</i> , 2016, 17, 26.	1.8	7
1070	Relationship Between the Altered Expression and Epigenetics of <i>GSTM3</i> and Age-Related Cataract. , 2016, 57, 4721.		28
1071	Stem Cell Epigenetics in Medical Therapy. , 2016, , 877-887.		0
1072	Prospective Advances in Medical Epigenetics. , 2016, , 891-910.		0
1073	Epigenetic Regulations of GABAergic Neurotransmission: Relevance for Neurological Disorders and Epigenetic Therapy. <i>Medical Epigenetics</i> , 2016, 4, 1-19.	262.3	6,201
1074	DNA methylation array analysis identifies breast cancer associated <i>RPTOR</i> , <i>MGRN1</i> and <i>RAPSN</i> hypomethylation in peripheral blood DNA. <i>Oncotarget</i> , 2016, 7, 64191-64202.	0.8	33
1075	DNA Methylation and Chromatin Remodeling: The Blueprint of Cancer Epigenetics. <i>Scientifica</i> , 2016, 2016, 1-11.	0.6	26
1076	The Involvement of Epigenetic Mechanisms in HPV-induced Cervical Cancer. , 0, , .		2
1077	Changes in methylation of genomic DNA from chicken immune organs in response to H5N1 influenza virus infection. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	14
1078	Sequenom MassARRAY Technology for the Analysis of DNA Methylation. , 2016, , 137-153.		1
1079	Modulation of Epigenetics by Environmental Toxic Molecules. <i>Advances in Molecular Toxicology</i> , 2016, 10, 361-389.	0.4	6
1080	Epigenetics in Schistosomes: What We Know and What We Need Know. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 149.	1.8	15
1081	Emerging Molecular and Biological Functions of MBD2, a Reader of DNA Methylation. <i>Frontiers in Genetics</i> , 2016, 7, 93.	1.1	61
1082	Using <i>Nematostella vectensis</i> to Study the Interactions between Genome, Epigenome, and Bacteria in a Changing Environment. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	21

#	ARTICLE	IF	CITATIONS
1083	Epigenome: A Biomarker or Screening Tool to Evaluate Health Impact of Cumulative Exposure to Chemical and Non-Chemical Stressors. <i>Biosensors</i> , 2016, 6, 12.	2.3	4
1084	The Future is The Past: Methylation QTLs in Schizophrenia. <i>Genes</i> , 2016, 7, 104.	1.0	26
1085	Molecular Mechanisms of p53 Deregulation in Cancer: An Overview in Multiple Myeloma. <i>International Journal of Molecular Sciences</i> , 2016, 17, 2003.	1.8	59
1086	Transgenerational Epigenetic Contributions to Stress Responses: Fact or Fiction?. <i>PLoS Biology</i> , 2016, 14, e1002426.	2.6	70
1087	System-Wide Associations between DNA-Methylation, Gene Expression, and Humoral Immune Response to Influenza Vaccination. <i>PLoS ONE</i> , 2016, 11, e0152034.	1.1	53
1088	Novel Insights into Insect-Microbe Interactions—Role of Epigenomics and Small RNAs. <i>Frontiers in Plant Science</i> , 2016, 7, 1164.	1.7	23
1089	An S-adenosyl Methionine Synthetase (SAMS) Gene from <i>Andropogon virginicus</i> L. Confers Aluminum Stress Tolerance and Facilitates Epigenetic Gene Regulation in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1627.	1.7	30
1090	Flax (<i>Linum usitatissimum</i> L.). , 2016, , 157-194.		52
1091	Liganded Thyroid Hormone Receptors Transactivate the DNA Methyltransferase 3a Gene in Mouse Neuronal Cells. <i>Endocrinology</i> , 2016, 157, 3647-3657.	1.4	36
1092	The concerted impact of domestication and transposon insertions on methylation patterns between dogs and grey wolves. <i>Molecular Ecology</i> , 2016, 25, 1838-1855.	2.0	73
1093	6-Substituted 2-Aminopurine-2-Deoxyribonucleoside 5-Triphosphates that Trace Cytosine Methylation. <i>ChemBioChem</i> , 2016, 17, 1532-1540.	1.3	7
1094	Intra- and inter-individual differences in human sperm DNA methylation. <i>Andrology</i> , 2016, 4, 832-842.	1.9	15
1095	The caste- and sex-specific DNA methylome of the termite <i>Zootermopsis nevadensis</i> . <i>Scientific Reports</i> , 2016, 6, 37110.	1.6	139
1096	Luminal B breast cancer subtype displays a dicotomic epigenetic pattern. <i>SpringerPlus</i> , 2016, 5, 623.	1.2	11
1097	TEA: the epigenome platform for <i>Arabidopsis</i> methylome study. <i>BMC Genomics</i> , 2016, 17, 1027.	1.2	3
1098	Determination of DNA Methylation and Hydroxymethylation Levels in Biological Samples by Field-Amplified Sample Injection-Capillary Zone Electrophoresis with UV Detection. <i>Chromatographia</i> , 2016, 79, 1649-1658.	0.7	1
1099	Evaluation of Possible Proximate Mechanisms Underlying the Kinship Theory of Intragenomic Conflict in Social Insects. <i>Integrative and Comparative Biology</i> , 2016, 56, 1206-1214.	0.9	7
1100	Genome-wide DNA methylation profiles changes associated with constant heat stress in pigs as measured by bisulfite sequencing. <i>Scientific Reports</i> , 2016, 6, 27507.	1.6	80

#	ARTICLE	IF	CITATIONS
1101	Evolution of DNA Methylation across Insects. <i>Molecular Biology and Evolution</i> , 2017, 34, msw264.	3.5	246
1102	Global DNA methylation variations after short-term heat shock treatment in cultured microspores of <i>Brassica napus</i> cv. Topas. <i>Scientific Reports</i> , 2016, 6, 38401.	1.6	58
1103	Developmental and Thyroid Hormone Regulation of the DNA Methyltransferase 3a Gene in <i>Xenopus</i> Tadpoles. <i>Endocrinology</i> , 2016, 157, 4961-4972.	1.4	18
1104	The DmtA methyltransferase contributes to <i>Aspergillus flavus</i> conidiation, sclerotial production, aflatoxin biosynthesis and virulence. <i>Scientific Reports</i> , 2016, 6, 23259.	1.6	99
1105	Divergent DNA Methylation Provides Insights into the Evolution of Duplicate Genes in Zebrafish. G3: Genes, Genomes, Genetics, 2016, 6, 3581-3591.	0.8	12
1107	Clinical Epigenetics and Epigenomics. <i>Translational Bioinformatics</i> , 2016, , 269-293.	0.0	0
1108	BsRADseq: screening DNA methylation in natural populations of non-model species. <i>Molecular Ecology</i> , 2016, 25, 1697-1713.	2.0	96
1109	A simple and novel method for the quantitative detection of 5-hydroxymethylcytosine using carbon nanotube field-effect transistors. <i>Nano Research</i> , 2016, 9, 1701-1708.	5.8	8
1110	Microfluidic Chromatin Immunoprecipitation for Analysis of Epigenomic Regulations. , 2016, , 349-363.		2
1111	AP endonuclease 1 prevents the extension of a T/G mismatch by DNA polymerase β to prevent mutations in CpGs during base excision repair. <i>DNA Repair</i> , 2016, 43, 89-97.	1.3	6
1112	DNA methylation in hematopoietic development and disease. <i>Experimental Hematology</i> , 2016, 44, 783-790.	0.2	18
1113	Don't worry; be informed about the epigenetics of anxiety. <i>Pharmacology Biochemistry and Behavior</i> , 2016, 146-147, 60-72.	1.3	32
1114	The SNF2 family ATPase LSH promotes cell-autonomous de novo DNA methylation in somatic cells. <i>Nucleic Acids Research</i> , 2016, 44, 7592-7604.	6.5	24
1115	Microfluidic Methods for Molecular Biology. , 2016, , .		4
1116	The genome-wide DNA sequence specificity of the anti-tumour drug bleomycin in human cells. <i>Molecular Biology Reports</i> , 2016, 43, 639-651.	1.0	9
1117	Epigenetic Control of Genes Involved in Cancer Initiation and Progression. , 2016, , 1-26.		0
1118	Evolutionary Transition of Promoter and Gene Body DNA Methylation across Invertebrate-Vertebrate Boundary. <i>Molecular Biology and Evolution</i> , 2016, 33, 1019-1028.	3.5	98
1120	Tagging methyl-CpG-binding domain proteins reveals different spatiotemporal expression and supports distinct functions. <i>Epigenomics</i> , 2016, 8, 455-473.	1.0	25

#	ARTICLE	IF	CITATIONS
1121	The role of global and regional DNA methylation and histone modifications in glycemic traits and type 2 diabetes: A systematic review. <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2016, 26, 553-566.	1.1	61
1122	Detecting 5-methylcytosine using an enzyme-free DNA strand exchange reaction without pretreatment under physiological conditions. <i>Chemical Communications</i> , 2016, 52, 6833-6836.	2.2	5
1123	Evolution of Epigenetic Regulation in Vertebrate Genomes. <i>Trends in Genetics</i> , 2016, 32, 269-283.	2.9	86
1124	Current Trends in Wildlife Research. <i>Wildlife Research Monographs</i> , 2016, , .	0.4	4
1125	High-Throughput DNA Sequencing and the Next Generation of Molecular Markers in Wildlife Research. <i>Wildlife Research Monographs</i> , 2016, , 201-223.	0.4	4
1126	Type 3 iodothyronine deiodinase in neonatal goats: molecular cloning, expression, localization, and methylation signature. <i>Functional and Integrative Genomics</i> , 2016, 16, 419-428.	1.4	2
1127	DNA Methylation Biphasically Regulates 3T3-L1 Preadipocyte Differentiation. <i>Molecular Endocrinology</i> , 2016, 30, 677-687.	3.7	35
1128	Presymptomatic Alterations in Amino Acid Metabolism and DNA Methylation in the Cerebellum of a Murine Model of Niemann-Pick Type C Disease. <i>American Journal of Pathology</i> , 2016, 186, 1582-1597.	1.9	23
1129	Enhancer, epigenetics, and human disease. <i>Current Opinion in Genetics and Development</i> , 2016, 36, 27-33.	1.5	19
1130	Nongenomic regulation of gene expression. <i>Current Opinion in Pediatrics</i> , 2016, 28, 521-528.	1.0	2
1131	N 6-Methyladenosine (m6A) Methylation in mRNA with A Dynamic and Reversible Epigenetic Modification. <i>Molecular Biotechnology</i> , 2016, 58, 450-459.	1.3	101
1132	Zebrafish Discoveries in Cancer Epigenetics. <i>Advances in Experimental Medicine and Biology</i> , 2016, 916, 169-197.	0.8	10
1133	Structure-Guided Optimization of DNA Methyltransferase Inhibitors. , 2016, , 53-73.		6
1134	Expression of genes encoding subunits A and B of succinate dehydrogenase in germinating maize seeds is regulated by methylation of their promoters. <i>Journal of Plant Physiology</i> , 2016, 205, 33-40.	1.6	23
1135	Mitochondrial health, the epigenome and healthspan. <i>Clinical Science</i> , 2016, 130, 1285-1305.	1.8	57
1136	The canine X chromosome is a sink for canine endogenous retrovirus transposition. <i>Gene Reports</i> , 2016, 4, 169-176.	0.4	1
1137	Nonmodal scutes patterns in the Loggerhead Sea Turtle (<i>Caretta caretta</i>): a possible epigenetic effect?. <i>Canadian Journal of Zoology</i> , 2016, 94, 379-383.	0.4	25
1138	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. <i>Genome Biology</i> , 2016, 17, 191.	3.8	120

#	ARTICLE	IF	CITATIONS
1139	Integrated analysis of DNA methylation profiles and gene expression profiles to identify genes associated with pilocytic astrocytomas. <i>Molecular Medicine Reports</i> , 2016, 13, 3491-3497.	1.1	10
1140	Epigenetics, Energy Balance, and Cancer. <i>Energy Balance and Cancer</i> , 2016, , .	0.2	2
1141	Epigenetic Effects of Gut Microbiota on Obesity and Gastrointestinal Cancers. <i>Energy Balance and Cancer</i> , 2016, , 167-189.	0.2	1
1142	EpiRADseq: scalable analysis of genomewide patterns of methylation using next-generation sequencing. <i>Methods in Ecology and Evolution</i> , 2016, 7, 60-69.	2.2	74
1143	Energy Balance, Epigenetics, and Prostate Cancer. <i>Energy Balance and Cancer</i> , 2016, , 235-250.	0.2	0
1145	Bisulfite Sequence Analyses Using CyVerse Discovery Environment: From Mapping to DMRs. <i>Current Protocols in Plant Biology</i> , 2016, 1, 510-529.	2.8	4
1146	TGFB2 and BCL2L11 methylation in male laryngeal cancer patients. <i>Oncology Letters</i> , 2016, 12, 2999-3003.	0.8	3
1147	Integrated analysis of gene expression and methylation profiles of 48 candidate genes in breast cancer patients. <i>Breast Cancer Research and Treatment</i> , 2016, 160, 371-383.	1.1	33
1148	DNA methylation-regulated microRNA pathways in ovarian serous cystadenocarcinoma: A meta-analysis. <i>Computational Biology and Chemistry</i> , 2016, 65, 154-164.	1.1	12
1149	BioVLAB-mCpG-SNP- EXPRESS : A system for multi-level and multi-perspective analysis and exploration of DNA methylation, sequence variation (SNPs), and gene expression from multi-omics data. <i>Methods</i> , 2016, 111, 64-71.	1.9	5
1150	Transcription factors as readers and effectors of DNA methylation. <i>Nature Reviews Genetics</i> , 2016, 17, 551-565.	7.7	482
1151	Detection of differentially methylated regions in whole genome bisulfite sequencing data using local Getis-Ord statistics. <i>Bioinformatics</i> , 2016, 32, 3396-3404.	1.8	27
1152	Chemical Modulation of Cell Fate in Stem Cell Therapeutics and Regenerative Medicine. <i>Cell Chemical Biology</i> , 2016, 23, 893-916.	2.5	43
1153	Deciphering the epitranscriptome: A green perspective. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 822-835.	4.1	36
1154	DNA methylation in Parkinson's disease. <i>Journal of Neurochemistry</i> , 2016, 139, 108-120.	2.1	78
1155	Epigenetic mutagen as histone modulator can be detected by yeast flocculation. <i>Mutagenesis</i> , 2016, 31, 687-693.	1.0	8
1156	Epigenetics and Applications in Plants. , 2016, , 255-270.		0
1157	Genome-wide methylation profile following prenatal and postnatal dietary omega-3 fatty acid supplementation in pigs. <i>Animal Genetics</i> , 2016, 47, 658-671.	0.6	26

#	ARTICLE	IF	CITATIONS
1158	Molecular characterization and expression analysis of Patched 1 gene in the half-smooth tongue sole (<i>Cynoglossus semilaevis</i>). <i>Acta Oceanologica Sinica</i> , 2016, 35, 19-28.	0.4	4
1159	Ocean acidification influences host <scp>DNA</scp> methylation and phenotypic plasticity in environmentally susceptible corals. <i>Evolutionary Applications</i> , 2016, 9, 1165-1178.	1.5	196
1160	NRL-Regulated Transcriptome Dynamics of Developing Rod Photoreceptors. <i>Cell Reports</i> , 2016, 17, 2460-2473.	2.9	104
1161	DNA methylation: a permissive mark in memory formation and maintenance. <i>Learning and Memory</i> , 2016, 23, 587-593.	0.5	54
1162	Nucleus-selective Chemical Proteomics Using Hoechst-tagged Reactive Molecules. <i>Chemistry Letters</i> , 2016, 45, 265-267.	0.7	20
1163	A single day of 5-azacytidine exposure during development induces neurodegeneration in neonatal mice and neurobehavioral deficits in adult mice. <i>Physiology and Behavior</i> , 2016, 167, 16-27.	1.0	9
1164	Allosteric control of mammalian DNA methyltransferases â€“ a new regulatory paradigm. <i>Nucleic Acids Research</i> , 2016, 44, 8556-8575.	6.5	156
1165	Towards DNA methylation detection using biosensors. <i>Analyst, The</i> , 2016, 141, 5922-5943.	1.7	40
1166	Epigenetic regulation of skeletal muscle metabolism. <i>Clinical Science</i> , 2016, 130, 1051-1063.	1.8	33
1167	Novel features of telomere biology revealed by the absence of telomeric DNA methylation. <i>Genome Research</i> , 2016, 26, 1047-1056.	2.4	18
1168	New hope: the emerging role of 5-hydroxymethylcytosine in mental health and disease. <i>Epigenomics</i> , 2016, 8, 981-991.	1.0	20
1169	ALKBH1-Mediated tRNA Demethylation Regulates Translation. <i>Cell</i> , 2016, 167, 816-828.e16.	13.5	366
1170	DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. <i>Cell Stem Cell</i> , 2016, 19, 808-822.	5.2	216
1171	DNMT1-PPAR β pathway in macrophages regulates chronic inflammation and atherosclerosis development in mice. <i>Scientific Reports</i> , 2016, 6, 30053.	1.6	103
1172	The Modification of Tet1 in Male Germline Stem Cells and Interact with PCNA, HDAC1 to promote their Self-renewal and Proliferation. <i>Scientific Reports</i> , 2016, 6, 37414.	1.6	20
1173	DNA Labeling Using DNA Methyltransferases. <i>Advances in Experimental Medicine and Biology</i> , 2016, 945, 511-535.	0.8	5
1174	Mapping epigenetic changes to the host cell genome induced by <i>Burkholderia pseudomallei</i> reveals pathogen-specific and pathogen-generic signatures of infection. <i>Scientific Reports</i> , 2016, 6, 30861.	1.6	24
1175	Enzymology of Mammalian DNA Methyltransferases. <i>Advances in Experimental Medicine and Biology</i> , 2016, 945, 87-122.	0.8	49

#	ARTICLE	IF	CITATIONS
1176	DNA Methylation and Gene Regulation in Honeybees: From Genome-Wide Analyses to Obligatory Epialleles. <i>Advances in Experimental Medicine and Biology</i> , 2016, 945, 193-211.	0.8	19
1177	Characterization of eukaryotic DNA N6-methyladenine by a highly sensitive restriction enzyme-assisted sequencing. <i>Nature Communications</i> , 2016, 7, 11301.	5.8	93
1178	Dynamic DNA methylation regulates neuronal intrinsic membrane excitability. <i>Science Signaling</i> , 2016, 9, ra83.	1.6	64
1179	Epigenetic Landmarks During Somatic Reprogramming. <i>IUBMB Life</i> , 2016, 68, 854-857.	1.5	2
1180	Genome-wide methylation analysis identified sexually dimorphic methylated regions in hybrid tilapia. <i>Scientific Reports</i> , 2016, 6, 35903.	1.6	71
1181	Gene Body Methylation and Transcriptional Regulation: Statistical Modelling and More. , 2016, , 212-230.		0
1182	Induction of autophagy improves embryo viability in cloned mouse embryos. <i>Scientific Reports</i> , 2016, 5, 17829.	1.6	26
1183	Inhibiting DNA methylation switches adipogenesis to osteoblastogenesis by activating Wnt10a. <i>Scientific Reports</i> , 2016, 6, 25283.	1.6	53
1184	Integrating Epigenomics into the Understanding of Biomedical Insight. <i>Bioinformatics and Biology Insights</i> , 2016, 10, BBI.S38427.	1.0	22
1185	Comparison of pre-processing methodologies for Illumina 450k methylation array data in familial analyses. <i>Clinical Epigenetics</i> , 2016, 8, 75.	1.8	10
1186	Identification of time-dependent biomarkers and effects of exposure to volatile organic compounds using high-throughput analysis. <i>Environmental Toxicology</i> , 2016, 31, 1563-1570.	2.1	9
1187	ALS and FTD: an epigenetic perspective. <i>Acta Neuropathologica</i> , 2016, 132, 487-502.	3.9	60
1188	Hypermethylation of p15 gene associated with an inferior poor long-term outcome in childhood acute lymphoblastic leukemia. <i>Journal of Cancer Research and Clinical Oncology</i> , 2016, 142, 497-504.	1.2	14
1189	Field Guidelines for Genetic Experimental Designs in High-Throughput Sequencing. , 2016, , .		6
1190	The Role of Endogenous Versus Exogenous DNA Damage in Risk Assessment. , 2016, , 83-102.		0
1191	Genome-Wide Analysis of DNA Methylation Patterns by High-Throughput Sequencing. , 2016, , 197-221.		5
1192	From Genome-Wide Association Study to Phenome-Wide Association Study: New Paradigms in Obesity Research. <i>Progress in Molecular Biology and Translational Science</i> , 2016, 140, 185-231.	0.9	10
1193	Sex differences in DNA methylation and expression in zebrafish brain: a test of an extended "male sex drive" hypothesis. <i>Gene</i> , 2016, 590, 307-316.	1.0	30

#	ARTICLE	IF	CITATIONS
1194	Gene expression, oocyte nuclear maturation and developmental competence of bovine oocytes and embryos produced after <i>in vivo</i> and <i>in vitro</i> heat shock. <i>Zygote</i> , 2016, 24, 748-759.	0.5	20
1195	The importance of trans-generational effects in Lepidoptera. <i>Environmental Epigenetics</i> , 2016, 62, 489-499.	0.9	33
1196	The interplay between DNA methylation, folate and neurocognitive development. <i>Epigenomics</i> , 2016, 8, 863-879.	1.0	64
1197	The dynamic changes of DNA methylation in primordial germ cell differentiation. <i>Gene</i> , 2016, 591, 305-312.	1.0	12
1198	Methylation Analysis of the BMP2 Gene Promoter Region in Patients With Pulmonary Arterial Hypertension. <i>Archivos De Bronconeumologia</i> , 2016, 52, 293-298.	0.4	9
1199	Distinct genomic and epigenomic features demarcate hypomethylated blocks in colon cancer. <i>BMC Cancer</i> , 2016, 16, 88.	1.1	1
1200	Role of ND10 nuclear bodies in the chromatin repression of HSV-1. <i>Virology Journal</i> , 2016, 13, 62.	1.4	25
1201	Integrative DNA methylome analysis of pan-cancer biomarkers in cancer discordant monozygotic twin-pairs. <i>Clinical Epigenetics</i> , 2016, 8, 7.	1.8	32
1202	A primary role of TET proteins in establishment and maintenance of <i>De Novo</i> bivalency at CpG islands. <i>Nucleic Acids Research</i> , 2016, 44, 8682-8692.	6.5	49
1203	MECP2, a multi-talented modulator of chromatin architecture. <i>Briefings in Functional Genomics</i> , 2016, 15, elw023.	1.3	59
1205	Alternative migratory locust phenotypes are associated with differences in the expression of genes encoding the methylation machinery. <i>Insect Molecular Biology</i> , 2016, 25, 105-115.	1.0	22
1206	Novel Epigenetic Regulation of Alpha-Synuclein Expression in Down Syndrome. <i>Molecular Neurobiology</i> , 2016, 53, 155-162.	1.9	10
1207	DNA methylation signatures of mood stabilizers and antipsychotics in bipolar disorder. <i>Epigenomics</i> , 2016, 8, 197-208.	1.0	70
1208	Single-Cell Genomics and Epigenomics. <i>Series in Bioengineering</i> , 2016, , 257-301.	0.3	2
1209	Altered Mitochondrial DNA Methylation Pattern in Alzheimer Disease-Related Pathology and in Parkinson Disease. <i>American Journal of Pathology</i> , 2016, 186, 385-397.	1.9	150
1210	Serine Metabolism Supports the Methionine Cycle and DNA/RNA Methylation through De Novo ATP Synthesis in Cancer Cells. <i>Molecular Cell</i> , 2016, 61, 210-221.	4.5	320
1211	Essentials of Single-Cell Analysis. <i>Series in Bioengineering</i> , 2016, , .	0.3	29
1212	Lin28A Binds Active Promoters and Recruits Tet1 to Regulate Gene Expression. <i>Molecular Cell</i> , 2016, 61, 153-160.	4.5	74

#	ARTICLE	IF	CITATIONS
1213	Promoter targeted bisulfite sequencing reveals DNA methylation profiles associated with low sperm motility in asthenozoospermia. <i>Human Reproduction</i> , 2016, 31, 24-33.	0.4	47
1214	Breeding animals for quality products: not only genetics. <i>Reproduction, Fertility and Development</i> , 2016, 28, 94.	0.1	29
1215	TET1 contributes to neurogenesis onset time during fetal brain development in mice. <i>Biochemical and Biophysical Research Communications</i> , 2016, 471, 437-443.	1.0	16
1216	epiGBS: reference-free reduced representation bisulfite sequencing. <i>Nature Methods</i> , 2016, 13, 322-324.	9.0	122
1217	Epigenetics, the Environment, and Children's Health Across Lifespans. , 2016, , .		7
1218	Enrichment analysis of Alu elements with different spatial chromatin proximity in the human genome. <i>Protein and Cell</i> , 2016, 7, 250-266.	4.8	23
1219	Effects of rumen-protected methionine and choline supplementation on the preimplantation embryo in Holstein cows. <i>Theriogenology</i> , 2016, 85, 1669-1679.	0.9	39
1220	Abnormal DNA methylation in the lumbar spinal cord following chronic constriction injury in rats. <i>Neuroscience Letters</i> , 2016, 610, 1-5.	1.0	36
1221	Análisis de la metilación de la región promotora del gen BMPR2 en pacientes con hipertensión arterial pulmonar. <i>Archivos De Bronconeumología</i> , 2016, 52, 293-298.	0.4	13
1222	Drugging the methylome: DNA methylation and memory. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2016, 51, 185-194.	2.3	20
1223	Epigenetics and Development. , 2016, , 353-359.		1
1224	Focussing reduced representation CpG sequencing through judicious restriction enzyme choice. <i>Genomics</i> , 2016, 107, 109-119.	1.3	8
1225	Re-patterning of H3K27me3, H3K4me3 and DNA methylation during fibroblast conversion into induced cardiomyocytes. <i>Stem Cell Research</i> , 2016, 16, 507-518.	0.3	99
1226	Clinical potential of DNA methylation in organ transplantation. <i>Journal of Heart and Lung Transplantation</i> , 2016, 35, 843-850.	0.3	26
1227	Stable methylation of a non-coding RNA gene regulates gene expression in response to abiotic stress in <i>Populus simonii</i> . <i>Journal of Experimental Botany</i> , 2016, 67, 1477-1492.	2.4	57
1228	Effects of DNA Methylation and Chromatin State on Rates of Molecular Evolution in Insects. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 357-363.	0.8	37
1229	Evaluation of 5-methylcytosine and 5-hydroxymethylcytosine as potential biomarkers for characterisation of chemical allergens. <i>Toxicology</i> , 2016, 340, 17-26.	2.0	4
1230	Hypermethylation of gene promoters in peripheral blood leukocytes in humans long term after radiation exposure. <i>Environmental Research</i> , 2016, 146, 10-17.	3.7	20

#	ARTICLE	IF	CITATIONS
1231	Association analysis of toluene exposure time with high-throughput mRNA expressions and methylation patterns using in vivo samples. <i>Environmental Research</i> , 2016, 146, 59-64.	3.7	12
1232	Scalable Cloud-Based Data Analysis Software Systems for Big Data from Next Generation Sequencing. <i>Studies in Big Data</i> , 2016, , 263-283.	0.8	4
1233	Regulation of maintenance DNA methylation via histone ubiquitylation. <i>Journal of Biochemistry</i> , 2016, 159, 9-15.	0.9	26
1234	Dnmt3a2: a hub for enhancing cognitive functions. <i>Molecular Psychiatry</i> , 2016, 21, 1130-1136.	4.1	41
1235	Clinical Relevance of Prognostic and Predictive Molecular Markers in Gliomas. <i>Advances and Technical Standards in Neurosurgery</i> , 2016, , 91-108.	0.2	37
1236	Whole-genome bisulfite sequencing maps from multiple human tissues reveal novel CpG islands associated with tissue-specific regulation. <i>Human Molecular Genetics</i> , 2016, 25, 69-82.	1.4	44
1237	Modulation of DNA methylation machineries in Japanese rice fish (<i>Oryzias latipes</i>) embryogenesis by ethanol and 5-azacytidine. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2016, 179, 174-183.	1.3	9
1238	Genome-wide CpG island methylation and intergenic demethylation propensities vary among different tumor sites. <i>Nucleic Acids Research</i> , 2016, 44, 1105-1117.	6.5	44
1239	Prenatal Diagnosis Innovation: Genome Sequencing of Maternal Plasma. <i>Annual Review of Medicine</i> , 2016, 67, 419-432.	5.0	97
1240	Correspondence of DNA Methylation Between Blood and Brain Tissue and Its Application to Schizophrenia Research. <i>Schizophrenia Bulletin</i> , 2016, 42, 406-414.	2.3	227
1241	Dietary polyphenols and chromatin remodeling. <i>Critical Reviews in Food Science and Nutrition</i> , 2017, 57, 2589-2599.	5.4	61
1242	Expression Profiling of DNA Methylation and Transcriptional Repression Associated Genes in Lens Epithelium Cells of Age-Related Cataract. <i>Cellular and Molecular Neurobiology</i> , 2017, 37, 537-543.	1.7	18
1243	Epigenetic regulation of bone cells. <i>Connective Tissue Research</i> , 2017, 58, 76-89.	1.1	27
1244	Insights into microbial cryptic gene activation and strain improvement: principle, application and technical aspects. <i>Journal of Antibiotics</i> , 2017, 70, 25-40.	1.0	97
1245	Methylation specific targeting of a chromatin remodeling complex from sponges to humans. <i>Scientific Reports</i> , 2017, 7, 40674.	1.6	22
1246	Mutual regulation of microRNAs and DNA methylation in human cancers. <i>Epigenetics</i> , 2017, 12, 187-197.	1.3	116
1247	Transcriptome-Wide Mapping of RNA 5-Methylcytosine in Arabidopsis mRNAs and Noncoding RNAs. <i>Plant Cell</i> , 2017, 29, 445-460.	3.1	196
1248	Formation and repair of oxidatively generated damage in cellular DNA. <i>Free Radical Biology and Medicine</i> , 2017, 107, 13-34.	1.3	240

#	ARTICLE	IF	CITATIONS
1249	HIV Latency: Should We Shock or Lock?. <i>Trends in Immunology</i> , 2017, 38, 217-228.	2.9	146
1250	Somatic mutations in cancer: Stochastic versus predictable. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2017, 814, 37-46.	0.9	16
1251	Contributions of polyunsaturated fatty acids (PUFA) on cerebral neurobiology: an integrated omics approach with epigenomic focus. <i>Journal of Nutritional Biochemistry</i> , 2017, 42, 84-94.	1.9	15
1252	Molecular characterization of HOXC8 gene and methylation status analysis of its exon 1 associated with the length of cashmere fiber in Liaoning cashmere goat. <i>Genetica</i> , 2017, 145, 115-126.	0.5	21
1253	Heterogeneous pattern of DNA methylation in developmentally important genes correlates with its chromatin conformation. <i>BMC Molecular Biology</i> , 2017, 18, 1.	3.0	11
1254	Distal CpG islands can serve as alternative promoters to transcribe genes with silenced proximal promoters. <i>Genome Research</i> , 2017, 27, 553-566.	2.4	32
1255	Differential DNA methylation may contribute to temporal and spatial regulation of gene expression and the development of mycelia and conidia in entomopathogenic fungus <i>Metarhizium robertsii</i> . <i>Fungal Biology</i> , 2017, 121, 293-303.	1.1	37
1256	An endoparasitoid wasp influences host DNA methylation. <i>Scientific Reports</i> , 2017, 7, 43287.	1.6	23
1257	Use of human methylation arrays for epigenome research in the common marmoset (<i>Callithrix jacchus</i>). <i>Epigenetics</i> , 2017, 10, 1040-1048.	1.0	3
1258	Dynamics and Context-Dependent Roles of DNA Methylation. <i>Journal of Molecular Biology</i> , 2017, 429, 1459-1475.	2.0	126
1259	DNA methyltransferases contribute to the fungal development, stress tolerance and virulence of the entomopathogenic fungus <i>Metarhizium robertsii</i> . <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 4215-4226.	1.7	40
1260	CRHR1 promoter hypomethylation: An epigenetic readout of panic disorder?. <i>European Neuropsychopharmacology</i> , 2017, 27, 360-371.	0.3	46
1261	RhMKK9, a rose MAP KINASE KINASE gene, is involved in rehydration-triggered ethylene production in rose gynoceia. <i>BMC Plant Biology</i> , 2017, 17, 51.	1.6	26
1263	Totipotency in the mouse. <i>Journal of Molecular Medicine</i> , 2017, 95, 687-694.	1.7	18
1264	A cytosine methyltransferase ortholog dmtA is involved in the sensitivity of <i>Aspergillus flavus</i> to environmental stresses. <i>Fungal Biology</i> , 2017, 121, 501-514.	1.1	24
1265	Epigenetic control of gene expression: Potential implications for cancer treatment. <i>Critical Reviews in Oncology/Hematology</i> , 2017, 111, 166-172.	2.0	113
1266	DNA Methylation and Tag SNPs of the BDNF Gene in Conversion of Amnesic Mild Cognitive Impairment into Alzheimer's Disease: A Cross-Sectional Cohort Study. <i>Journal of Alzheimer's Disease</i> , 2017, 58, 263-274.	1.2	36
1267	Epigenome-wide Association of DNA Methylation in Whole Blood With Bone Mineral Density. <i>Journal of Bone and Mineral Research</i> , 2017, 32, 1644-1650.	3.1	49

#	ARTICLE	IF	CITATIONS
1268	Metamorphosis and transition between developmental stages in European eel (<i>Anguilla anguilla</i> , L.) involve epigenetic changes in DNA methylation patterns. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 22, 139-145.	0.4	7
1269	DeepCpG: accurate prediction of single-cell DNA methylation states using deep learning. <i>Genome Biology</i> , 2017, 18, 67.	3.8	361
1270	Essential role of long non-coding RNAs in de novo chromatin modifications: the genomic address code hypothesis. <i>Biophysical Reviews</i> , 2017, 9, 73-77.	1.5	14
1271	Advances in Vision Research, Volume I. <i>Essentials in Ophthalmology</i> , 2017, , .	0.0	0
1272	Obesogenic diet intake during pregnancy programs aberrant synaptic plasticity and addiction-like behavior to a palatable food in offspring. <i>Behavioural Brain Research</i> , 2017, 330, 46-55.	1.2	26
1273	Genome-wide DNA Methylation Analysis Reveals <i>GABBR2</i> as a Novel Epigenetic Target for <i>EGFR</i> 19 Deletion Lung Adenocarcinoma with Induction Erlotinib Treatment. <i>Clinical Cancer Research</i> , 2017, 23, 5003-5014.	3.2	16
1274	DNA damage, DNA susceptibility to oxidation and glutathione redox status in patients with Alzheimer's disease treated with and without memantine. <i>Journal of the Neurological Sciences</i> , 2017, 378, 158-162.	0.3	14
1275	5-Formylcytosine does not change the global structure of DNA. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 544-552.	3.6	44
1276	Functional relevance of miRNAs in premature ageing. <i>Mechanisms of Ageing and Development</i> , 2017, 168, 10-19.	2.2	11
1277	A highly efficient fluorescence-based switch-on detection method of 5-formyluracil in DNA. <i>Nano Research</i> , 2017, 10, 2449-2458.	5.8	27
1278	Independent validation of body fluid-specific CpG markers and construction of a robust multiplex assay. <i>Forensic Science International: Genetics</i> , 2017, 29, 261-268.	1.6	27
1279	Epigenetic Characterization of Satellite DNA in Sugar Beet (<i>Beta vulgaris</i>). <i>RNA Technologies</i> , 2017, , 445-462.	0.2	1
1280	The chemistries and consequences of DNA and RNA methylation and demethylation. <i>RNA Biology</i> , 2017, 14, 1099-1107.	1.5	105
1282	Deregulation of α -synuclein in Parkinson's disease: Insight from epigenetic structure and transcriptional regulation of SNCA. <i>Progress in Neurobiology</i> , 2017, 154, 21-36.	2.8	55
1284	Epigenetic Study in Asian Eye Diseases. <i>Essentials in Ophthalmology</i> , 2017, , 487-496.	0.0	0
1285	Epigenetics and Liver Fibrosis. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2017, 4, 125-134.	2.3	88
1286	Concerted Divergence after Gene Duplication in Polycomb Repressive Complexes. <i>Plant Physiology</i> , 2017, 174, 1192-1204.	2.3	11
1287	DNA Methylation and Hydroxymethylation Profile of CD34+ Enriched Cell Products Intended for Autologous CD34+ Cell Transplantation. <i>DNA and Cell Biology</i> , 2017, 36, 737-746.	0.9	0

#	ARTICLE	IF	CITATIONS
1288	Strand-specific CpG hemimethylation, a novel epigenetic modification functional for genomic imprinting. <i>Nucleic Acids Research</i> , 2017, 45, 8822-8834.	6.5	11
1289	MeDIP-seq and nCpG analyses illuminate sexually dimorphic methylation of gonadal development genes with high historic methylation in turtle hatchlings with temperature-dependent sex determination. <i>Epigenetics and Chromatin</i> , 2017, 10, 28.	1.8	27
1290	Hypermethylated CpG sites in the <i>MTR</i> gene promoter in preterm placenta. <i>Epigenomics</i> , 2017, 9, 985-996.	1.0	13
1291	A refined DNA methylation detection method using <i>Msp</i> I coupled quantitative PCR. <i>Analytical Biochemistry</i> , 2017, 533, 1-9.	1.1	12
1293	Epigenetics of Huntington's Disease. <i>Advances in Experimental Medicine and Biology</i> , 2017, 978, 277-299.	0.8	50
1294	Technologies for Deciphering Epigenomic DNA Patterns. <i>Advances in Experimental Medicine and Biology</i> , 2017, 978, 477-488.	0.8	0
1295	MeCP2, A Modulator of Neuronal Chromatin Organization Involved in Rett Syndrome. <i>Advances in Experimental Medicine and Biology</i> , 2017, 978, 3-21.	0.8	13
1296	Genetics and developmental biology of cooperation. <i>Molecular Ecology</i> , 2017, 26, 4364-4377.	2.0	32
1297	Human DNA (cytosine-5)-methyltransferases: a functional and structural perspective for epigenetic cancer therapy. <i>Biochimie</i> , 2017, 139, 137-147.	1.3	13
1298	Active DNA Demethylation in Neurodevelopment. , 2017, , 43-59.		1
1299	Epigenetics in natural animal populations. <i>Journal of Evolutionary Biology</i> , 2017, 30, 1612-1632.	0.8	112
1300	Mephedrone exposure in adolescent rats alters the rewarding effect of morphine in adults. <i>European Journal of Pharmacology</i> , 2017, 810, 63-69.	1.7	10
1301	Widespread 5-methylcytosine in the genomes of avian Coccidia and other apicomplexan parasites detected by an ELISA-based method. <i>Parasitology Research</i> , 2017, 116, 1573-1579.	0.6	7
1302	Histone Modifications Pattern Associated With a State of Mesenchymal Stem Cell Cultures Derived From Amniotic Fluid of Normal and Fetus-Affected Gestations. <i>Journal of Cellular Biochemistry</i> , 2017, 118, 3744-3755.	1.2	4
1303	Epigenetics and Its Role in Human Cancer. <i>Translational Medicine Research</i> , 2017, , 249-267.	0.0	3
1304	Large-scale gene network analysis reveals the significance of extracellular matrix pathway and homeobox genes in acute myeloid leukemia: an introduction to the Pigengene package and its applications. <i>BMC Medical Genomics</i> , 2017, 10, 16.	0.7	34
1305	Transient and permanent changes in DNA methylation patterns in inorganic arsenic-mediated epithelial-to-mesenchymal transition. <i>Toxicology and Applied Pharmacology</i> , 2017, 331, 6-17.	1.3	25
1306	Modeling complex patterns of differential DNA methylation that associate with gene expression changes. <i>Nucleic Acids Research</i> , 2017, 45, 5100-5111.	6.5	46

#	ARTICLE	IF	CITATIONS
1307	Therapeutic benefits of the methyl donor S-adenosylmethionine on nerve injury-induced mechanical hypersensitivity and cognitive impairment in mice. <i>Pain</i> , 2017, 158, 802-810.	2.0	45
1308	Septin 9_i2 is downregulated in tumors, impairs cancer cell migration and alters subnuclear actin filaments. <i>Scientific Reports</i> , 2017, 7, 44976.	1.6	55
1310	Simplification, Innateness, and the Absorption of Meaning from Context: How Novelty Arises from Gradual Network Evolution. <i>Evolutionary Biology</i> , 2017, 44, 145-189.	0.5	11
1311	Exercise and the Skeletal Muscle Epigenome. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2017, 7, a029876.	2.9	34
1312	Tissue-specific methylation profile in obese patients with type 2 diabetes before and after Roux-en-Y gastric bypass. <i>Diabetology and Metabolic Syndrome</i> , 2017, 9, 15.	1.2	17
1313	Oral Biology. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	2
1314	Circannual and circadian rhythms of hypothalamic DNA methyltransferase and histone deacetylase expression in male Siberian hamsters (<i>Phodopus sungorus</i>). <i>General and Comparative Endocrinology</i> , 2017, 243, 130-137.	0.8	29
1315	Tools and Strategies for Analysis of Genome-Wide and Gene-Specific DNA Methylation Patterns. <i>Methods in Molecular Biology</i> , 2017, 1537, 249-277.	0.4	67
1316	Generating Multiple Base-Resolution DNA Methylomes Using Reduced Representation Bisulfite Sequencing. <i>Methods in Molecular Biology</i> , 2017, 1537, 279-298.	0.4	15
1317	Dual Effects of a RETN Single Nucleotide Polymorphism (SNP) at 420 on Plasma Resistin: Genotype and DNA Methylation. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2017, 102, 884-892.	1.8	12
1318	Analyzing Targeted Nucleosome Position and Occupancy in Cancer, Obesity, and Diabetes. <i>Methods in Pharmacology and Toxicology</i> , 2017, , 51-62.	0.1	0
1319	The epigenetic landscape of <i>Alu</i> repeats delineates the structural and functional genomic architecture of colon cancer cells. <i>Genome Research</i> , 2017, 27, 118-132.	2.4	51
1320	Evolution of bird genomes—a transposon's-eye view. <i>Annals of the New York Academy of Sciences</i> , 2017, 1389, 164-185.	1.8	114
1321	Epigenetic regulation of immune checkpoints: another target for cancer immunotherapy?. <i>Immunotherapy</i> , 2017, 9, 99-108.	1.0	24
1323	Insights into Epigenome Evolution from Animal and Plant Methylomes. <i>Genome Biology and Evolution</i> , 2017, 9, 3189-3201.	1.1	35
1324	Functional role of DNA methylation at the FLO1 promoter in budding yeast. <i>FEMS Microbiology Letters</i> , 2017, 364, .	0.7	7
1325	Screening the key genes of hepatocellular adenoma via microarray analysis of DNA expression and methylation profiles. <i>Oncology Letters</i> , 2017, 14, 3975-3980.	0.8	5
1326	Prostaglandin E2 Leads to the Acquisition of DNMT3A-Dependent Tolerogenic Functions in Human Myeloid-Derived Suppressor Cells. <i>Cell Reports</i> , 2017, 21, 154-167.	2.9	116

#	ARTICLE	IF	CITATIONS
1327	Molecular Control of HIV and SIV Latency. <i>Current Topics in Microbiology and Immunology</i> , 2017, 417, 1-22.	0.7	11
1328	Maternal Nutrition and Cognition. , 2017, , 29-42.		0
1329	Increased cytosine methylation at promoter of the NB-LRR class R gene RCY1 correlated with compromised resistance to cucumber mosaic virus in EMS-generated src mutants of <i>Arabidopsis thaliana</i> . <i>Physiological and Molecular Plant Pathology</i> , 2017, 100, 151-162.	1.3	5
1330	Analysis of the expression level and methylation of tumor protein p53, phosphatase and tensin homolog and mutS homolog 2 in N-methyl-N-nitrosourea-induced thymic lymphoma in C57BL/6 mice. <i>Oncology Letters</i> , 2017, 14, 4339-4348.	0.8	6
1331	The construction of intrahepatic cholangiocarcinoma model in zebrafish. <i>Scientific Reports</i> , 2017, 7, 13419.	1.6	12
1332	Genome-wide DNA methylomes from discrete developmental stages reveal the predominance of non-CpG methylation in <i>Tribolium castaneum</i> . <i>DNA Research</i> , 2017, 24, 445-457.	1.5	36
1333	5-hydroxymethylcytosine accumulation in postmitotic neurons results in functional demethylation of expressed genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7812-E7821.	3.3	122
1334	Roles of RNA methylation by means of N6-methyladenosine (m6A) in human cancers. <i>Cancer Letters</i> , 2017, 408, 112-120.	3.2	223
1335	Rapid adaptive responses to climate change in corals. <i>Nature Climate Change</i> , 2017, 7, 627-636.	8.1	327
1336	Single tube gene synthesis by phosphoramidate chemical ligation. <i>Chemical Communications</i> , 2017, 53, 10700-10702.	2.2	19
1337	Transcriptome sequencing and estimation of DNA methylation level in the subsocial wood-feeding cockroach <i>Cryptocercus punctulatus</i> (Blattodea: Cryptocercidae). <i>Applied Entomology and Zoology</i> , 2017, 52, 643-651.	0.6	9
1338	The Molecular Basis of DNA Methylation. <i>Cancer Drug Discovery and Development</i> , 2017, , 19-51.	0.2	2
1339	Characterization of a core region in the A2UCOE that confers effective anti-silencing activity. <i>Scientific Reports</i> , 2017, 7, 10213.	1.6	9
1340	Correlation between the methylation of the FUT1 promoter region and FUT1 expression in the duodenum of piglets from newborn to weaning. <i>3 Biotech</i> , 2017, 7, 247.	1.1	9
1341	Recruitment of histone modifications to assist mRNA dosage maintenance after degeneration of cytosine DNA methylation during animal evolution. <i>Genome Research</i> , 2017, 27, 1513-1524.	2.4	8
1342	Connecting the Dots Between Fatty Acids, Mitochondrial Function, and DNA Methylation in Atherosclerosis. <i>Current Atherosclerosis Reports</i> , 2017, 19, 36.	2.0	3
1343	Detect differentially methylated regions using non-homogeneous hidden Markov model for methylation array data. <i>Bioinformatics</i> , 2017, 33, 3701-3708.	1.8	10
1344	Intraspecific DNA methylation polymorphism in the non-edible oilseed plant castor bean. <i>Plant Diversity</i> , 2017, 39, 300-307.	1.8	9

#	ARTICLE	IF	CITATIONS
1345	Dynamics of RNA Polymerase II Pausing and Bivalent Histone H3 Methylation during Neuronal Differentiation in Brain Development. <i>Cell Reports</i> , 2017, 20, 1307-1318.	2.9	47
1346	Genomic plasticity between human and mycobacterial DNA: A review. <i>Tuberculosis</i> , 2017, 107, 38-47.	0.8	11
1347	Perkinsus infection is associated with alterations in the level of global DNA methylation of gills and gastrointestinal tract of the oyster <i>Crassostrea gasar</i> . <i>Journal of Invertebrate Pathology</i> , 2017, 149, 76-81.	1.5	13
1348	Oxytocin and Anxiety Disorders. <i>Current Topics in Behavioral Neurosciences</i> , 2017, 35, 467-498.	0.8	43
1349	A multiplex microplatform for the detection of multiple DNA methylation events using goldâ€DNA affinity. <i>Analyst, The</i> , 2017, 142, 3573-3578.	1.7	10
1350	Measuring quantitative effects of methylation on transcription factorâ€DNA binding affinity. <i>Science Advances</i> , 2017, 3, eaao1799.	4.7	62
1351	CpG and methylation-dependent DNA binding and dynamics of the methylcytosine binding domain 2 protein at the single-molecule level. <i>Nucleic Acids Research</i> , 2017, 45, 9164-9177.	6.5	25
1352	LINE-1 hypomethylation is not a common event in preneoplastic stages of gastric carcinogenesis. <i>Scientific Reports</i> , 2017, 7, 4828.	1.6	12
1353	5-Aminolevulinic acid improves DNA damage and DNA Methylation changes in deltamethrin-exposed <i>Phaseolus vulgaris</i> seedlings. <i>Plant Physiology and Biochemistry</i> , 2017, 118, 267-273.	2.8	14
1354	Multiple network algorithm for epigenetic modules via the integration of genome-wide DNA methylation and gene expression data. <i>BMC Bioinformatics</i> , 2017, 18, 72.	1.2	52
1355	Mitochondrial Genomic Backgrounds Affect Nuclear DNA Methylation and Gene Expression. <i>Cancer Research</i> , 2017, 77, 6202-6214.	0.4	51
1356	Functional redundancy between <i>Apc</i> and <i>Apc2</i> regulates tissue homeostasis and prevents tumorigenesis in murine mammary epithelium. <i>Oncogene</i> , 2017, 36, 1793-1803.	2.6	25
1357	Antibiotic dialogues: induction of silent biosynthetic gene clusters by exogenous small molecules. <i>FEMS Microbiology Reviews</i> , 2017, 41, 19-33.	3.9	160
1358	Epigenetic impacts of endocrine disruptors in the brain. <i>Frontiers in Neuroendocrinology</i> , 2017, 44, 1-26.	2.5	66
1359	Exercise-induced epigenetic regulations in inflammatory related cells. <i>Journal of Applied Biomedicine</i> , 2017, 15, 63-70.	0.6	4
1360	Epigenetic Regulation of SNAP25 Prevents Progressive Glutamate Excitotoxicity in Hypoxic CA3 Neurons. <i>Molecular Neurobiology</i> , 2017, 54, 6133-6147.	1.9	18
1361	No evidence that DNA methylation is associated with the regulation of fertility in the adult honey bee <i>Apis mellifera</i> (Hymenoptera: Apidae) worker ovary. <i>Austral Entomology</i> , 2017, 56, 115-121.	0.8	1
1362	5â€Hydroxymethylcytosine marks postmitotic neural cells in the adult and developing vertebrate central nervous system. <i>Journal of Comparative Neurology</i> , 2017, 525, 478-497.	0.9	15

#	ARTICLE	IF	CITATIONS
1363	Coupling hybridization chain reaction with DNzyme recycling for enzyme-free and dual amplified sensitive fluorescent detection of methyltransferase activity. <i>Analytica Chimica Acta</i> , 2017, 949, 83-88.	2.6	32
1364	MethSMRT: an integrative database for DNA N6-methyladenine and N4-methylcytosine generated by single-molecular real-time sequencing. <i>Nucleic Acids Research</i> , 2017, 45, D85-D89.	6.5	111
1365	Increased methylation of repetitive elements and DNA repair genes is associated with higher DNA oxidation in children in an urbanized, industrial environment. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2017, 813, 27-36.	0.9	41
1366	Regulation of Embryogenesis. , 2017, , 39-48.e2.		0
1367	Methylation modification in gastric cancer and approaches to targeted epigenetic therapy (Review). <i>International Journal of Oncology</i> , 2017, 50, 1921-1933.	1.4	30
1368	DNA methylation alterations in Alzheimer's disease. <i>Environmental Epigenetics</i> , 2017, 3, dx008.	0.9	54
1369	Variation in DNA Methylation Is Not Consistently Reflected by Sociality in Hymenoptera. <i>Genome Biology and Evolution</i> , 2017, 9, 1687-1698.	1.1	46
1370	Accumulation of long-term transcriptionally active integrated retroviral vectors in active promoters and enhancers. <i>Nucleic Acids Research</i> , 2017, 45, 12752-12765.	6.5	5
1371	3-Oxoacid CoA transferase 1 as a therapeutic target gene for cisplatin-resistant ovarian cancer. <i>Oncology Letters</i> , 2018, 15, 2611-2618.	0.8	12
1372	Developmental plasticity research in evolution and human health. <i>Evolution, Medicine and Public Health</i> , 2017, 2017, 201-205.	1.1	7
1373	Epigenetic Programming of Cardiovascular Disease by Perinatal Hypoxia and Fetal Growth Restriction. , 0, , .		2
1374	EpiHRMAssay, in tube and in silico combined approach for the scanning and epityping of heterogeneous DNA methylation. <i>Biology Methods and Protocols</i> , 2017, 2, bpw008.	1.0	4
1375	Potential Roles of Intrinsic Disorder in Maternal-Effect Proteins Involved in the Maintenance of DNA Methylation. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1898.	1.8	9
1376	Tet-mediated DNA hydroxymethylation regulates retinal neurogenesis by modulating cell-extrinsic signaling pathways. <i>PLoS Genetics</i> , 2017, 13, e1006987.	1.5	59
1377	Epigenomics of Major Depressive Disorders and Schizophrenia: Early Life Decides. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1711.	1.8	49
1378	Epigenetic Landscape during Coronavirus Infection. <i>Pathogens</i> , 2017, 6, 8.	1.2	96
1379	Epigenetic and Neural Circuitry Landscape of Psychotherapeutic Interventions. <i>Psychiatry Journal</i> , 2017, 2017, 1-38.	0.7	10
1380	Role of DNA and RNA N6-Adenine Methylation in Regulating Stem Cell Fate. <i>Current Stem Cell Research and Therapy</i> , 2017, 13, 31-38.	0.6	39

#	ARTICLE	IF	CITATIONS
1381	The Genomic Impact of DNA CpG Methylation on Gene Expression; Relationships in Prostate Cancer. <i>Biomolecules</i> , 2017, 7, 15.	1.8	92
1382	Driver or Passenger: Epigenomes in Alzheimer's Disease. <i>Epigenomes</i> , 2017, 1, 5.	0.8	2
1383	Saliva as a Blood Alternative for Genome-Wide DNA Methylation Profiling by Methylated DNA Immunoprecipitation (MeDIP) Sequencing. <i>Epigenomes</i> , 2017, 1, 14.	0.8	8
1384	Genome-Wide Epigenetic Studies in Chicken: A Review. <i>Epigenomes</i> , 2017, 1, 20.	0.8	11
1385	Epigenetic Signature: A New Player as Predictor of Clinically Significant Prostate Cancer (PCa) in Patients on Active Surveillance (AS). <i>International Journal of Molecular Sciences</i> , 2017, 18, 1146.	1.8	13
1386	Interferon-Gamma DNA Methylation Is Affected by Mycophenolic Acid but Not by Tacrolimus after T-Cell Activation. <i>Frontiers in Immunology</i> , 2017, 8, 822.	2.2	9
1387	Methylation on RNA: A Potential Mechanism Related to Immune Priming within But Not across Generations. <i>Frontiers in Microbiology</i> , 2017, 8, 473.	1.5	48
1388	The Importance of ncRNAs as Epigenetic Mechanisms in Phenotypic Variation and Organic Evolution. <i>Frontiers in Microbiology</i> , 2017, 8, 2483.	1.5	72
1389	Epigenetics of Memory Processes. , 2017, , 347-358.		0
1390	Epigenetic Guardian: A Review of the DNA Methyltransferase DNMT3A in Acute Myeloid Leukaemia and Clonal Haematopoiesis. <i>BioMed Research International</i> , 2017, 2017, 1-13.	0.9	29
1391	Differential Analysis of Genetic, Epigenetic, and Cytogenetic Abnormalities in AML. <i>International Journal of Genomics</i> , 2017, 2017, 1-13.	0.8	8
1392	Body-hypomethylated human genes harbor extensive intragenic transcriptional activity and are prone to cancer-associated dysregulation. <i>Nucleic Acids Research</i> , 2017, 45, gkx020.	6.5	34
1393	Vitamin D receptor gene is epigenetically altered and transcriptionally up-regulated in multiple sclerosis. <i>PLoS ONE</i> , 2017, 12, e0174726.	1.1	26
1394	Tissue expression profiles and transcriptional regulation of elongase of very long chain fatty acid 6 in bovine mammary epithelial cells. <i>PLoS ONE</i> , 2017, 12, e0175777.	1.1	12
1395	High-level dietary cadmium exposure is associated with global DNA hypermethylation in the gastropod hepatopancreas. <i>PLoS ONE</i> , 2017, 12, e0184221.	1.1	28
1396	The <i>Biomphalaria glabrata</i> DNA methylation machinery displays spatial tissue expression, is differentially active in distinct snail populations and is modulated by interactions with <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005246.	1.3	39
1397	Hypomethylated domain-enriched DNA motifs prepattern the accessible nucleosome organization in teleosts. <i>Epigenetics and Chromatin</i> , 2017, 10, 44.	1.8	11
1398	A screening system to identify transcription factors that induce binding site-directed DNA demethylation. <i>Epigenetics and Chromatin</i> , 2017, 10, 60.	1.8	48

#	ARTICLE	IF	CITATIONS
1399	Identification of a key role of widespread epigenetic drift in Barrett's esophagus and esophageal adenocarcinoma. <i>Clinical Epigenetics</i> , 2017, 9, 113.	1.8	19
1400	Rainbow trout exposed to benzo[a]pyrene yields conserved microRNA binding sites in DNA methyltransferases across 500 million years of evolution. <i>Scientific Reports</i> , 2017, 7, 16843.	1.6	17
1401	Quantification of tumour evolution and heterogeneity via Bayesian epiallele detection. <i>BMC Bioinformatics</i> , 2017, 18, 354.	1.2	15
1402	Transcriptomics and methylomics in chronic periodontitis with tobacco use: a pilot study. <i>Clinical Epigenetics</i> , 2017, 9, 81.	1.8	22
1403	Epigenetic Effects of Environmental Chemicals on Reproductive Biology. <i>Current Drug Targets</i> , 2017, 18, 1116-1124.	1.0	10
1404	Beyond mCG. , 2017, , 81-94.		0
1405	The synthetic antihyperlipidemic drug potassium piperate selectively kills breast cancer cells through inhibiting G1-S-phase transition and inducing apoptosis. <i>Oncotarget</i> , 2017, 8, 47250-47268.	0.8	7
1406	The Molecular Biology of Head and Neck Cancer. , 2017, , 243-256.		1
1407	MeTDiff: A Novel Differential RNA Methylation Analysis for MeRIP-Seq Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 526-534.	1.9	79
1408	Interfacial nano-mixing in a miniaturised platform enables signal enhancement and <i>in situ</i> detection of cancer biomarkers. <i>Nanoscale</i> , 2018, 10, 10884-10890.	2.8	18
1409	DNA methylation level of spermatozoa from subfertile and proven fertile and its relation to standard sperm parameters. <i>Andrologia</i> , 2018, 50, e13011.	1.0	9
1410	Epigenetic modifications in the embryonic and induced pluripotent stem cells. <i>Gene Expression Patterns</i> , 2018, 29, 1-9.	0.3	38
1411	Investigating the genetic and epigenetic basis of big biological questions with the parthenogenetic marbled crayfish: A review and perspectives. <i>Journal of Biosciences</i> , 2018, 43, 189-223.	0.5	38
1412	Role of tissue-specific promoter DNA methylation in regulating the human EKLf gene. <i>Blood Cells, Molecules, and Diseases</i> , 2018, 71, 16-22.	0.6	4
1413	A small set of differentially expressed genes was associated with two color morphs in natural populations of the pea aphid <i>Acyrtosiphon pisum</i> . <i>Gene</i> , 2018, 651, 23-32.	1.0	15
1414	Joint Detection of Associations Between DNA Methylation and Gene Expression From Multiple Cancers. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2018, 22, 1960-1969.	3.9	5
1415	Protecting and Diversifying the Germline. <i>Genetics</i> , 2018, 208, 435-471.	1.2	33
1416	Sulfinate Based Selective Labeling of 5-Hydroxymethylcytosine: Application to Biotin Pull Down Assay. <i>Bioconjugate Chemistry</i> , 2018, 29, 245-249.	1.8	8

#	ARTICLE	IF	CITATIONS
1417	Crosstalk between TGF- β ; signaling and epigenome. <i>Acta Biochimica Et Biophysica Sinica</i> , 2018, 50, 60-67.	0.9	32
1418	Environmental, genetic and epigenetic contributions to cocaine addiction. <i>Neuropsychopharmacology</i> , 2018, 43, 1471-1480.	2.8	76
1419	Transcription-Associated Mutation Promotes RNA Complexity in Highly Expressed Genes—A Major New Source of Selectable Variation. <i>Molecular Biology and Evolution</i> , 2018, 35, 1104-1119.	3.5	5
1420	Elevated Global DNA Methylation Is Not Exclusive to Amyotrophic Lateral Sclerosis and Is Also Observed in Spinocerebellar Ataxia Types 1 and 2. <i>Neurodegenerative Diseases</i> , 2018, 18, 38-48.	0.8	27
1421	The zebrafish: A fantastic model for hematopoietic development and disease. <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , 2018, 7, e312.	5.9	134
1422	DNA methylation changes and evolution of RNA-based duplication in <i>Sus scrofa</i> : based on a two-step strategy. <i>Epigenomics</i> , 2018, 10, 199-218.	1.0	6
1423	Epigenetics, microbiota, and intraocular inflammation: New paradigms of immune regulation in the eye. <i>Progress in Retinal and Eye Research</i> , 2018, 64, 84-95.	7.3	46
1424	FAM20C could be targeted by TET1 to promote odontoblastic differentiation potential of human dental pulp cells. <i>Cell Proliferation</i> , 2018, 51, e12426.	2.4	24
1425	Interactions Between Oxytocin Receptor Gene Methylation and Callous-Unemotional Traits Impact Socioaffective Brain Systems in Conduct-Disordered Offenders. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2018, 3, 379-391.	1.1	9
1426	Monoamine Oxidase A Gene Methylation and Its Role in Posttraumatic Stress Disorder: First Evidence from the South Eastern Europe (SEE)-PTSD Study. <i>International Journal of Neuropsychopharmacology</i> , 2018, 21, 423-432.	1.0	33
1427	Bicycle: a bioinformatics pipeline to analyze bisulfite sequencing data. <i>Bioinformatics</i> , 2018, 34, 1414-1415.	1.8	21
1429	Notos - a galaxy tool to analyze CpN observed expected ratios for inferring DNA methylation types. <i>BMC Bioinformatics</i> , 2018, 19, 105.	1.2	8
1430	Epigenetics: DNA Methylation Analysis in Esophageal Adenocarcinoma. <i>Methods in Molecular Biology</i> , 2018, 1756, 247-256.	0.4	5
1431	Hypomethylation of the Interferon γ Gene as a Potential Risk Factor for Essential Hypertension: A Case-Control Study. <i>Tohoku Journal of Experimental Medicine</i> , 2018, 244, 283-290.	0.5	7
1432	Evolving paradigms for the biological response to low dose ionizing radiation; the role of epigenetics. <i>International Journal of Radiation Biology</i> , 2018, 94, 769-781.	1.0	28
1435	Prediction of CpG Islands as an Intrinsic Clustering Property Found in Many Eukaryotic DNA Sequences and Its Relation to DNA Methylation. <i>Methods in Molecular Biology</i> , 2018, 1766, 31-47.	0.4	5
1436	CpG Islands in Cancer: Heads, Tails, and Sides. <i>Methods in Molecular Biology</i> , 2018, 1766, 49-80.	0.4	19
1437	Genome-Wide Profiling of DNA Methyltransferases in Mammalian Cells. <i>Methods in Molecular Biology</i> , 2018, 1766, 157-174.	0.4	1

#	ARTICLE	IF	CITATIONS
1438	Signatures of DNA Methylation across Insects Suggest Reduced DNA Methylation Levels in Holometabola. <i>Genome Biology and Evolution</i> , 2018, 10, 1185-1197.	1.1	100
1439	Unravelling the epigenomic interactions between parental inbreds resulting in an altered hybrid methylome in pigeonpea. <i>DNA Research</i> , 2018, 25, 361-373.	1.5	20
1440	Generation of Whole Genome Bisulfite Sequencing Libraries for Comprehensive DNA Methylome Analysis. <i>Methods in Molecular Biology</i> , 2018, 1767, 291-298.	0.4	4
1441	Developmental DNA methyltransferase expression in the fire ant <i>Solenopsis invicta</i> . <i>Insect Science</i> , 2018, 25, 57-65.	1.5	38
1442	Folic acid is necessary for proliferation and differentiation of C2C12 myoblasts. <i>Journal of Cellular Physiology</i> , 2018, 233, 736-747.	2.0	36
1443	Epigenetics in Alzheimer's Disease: Perspective of DNA Methylation. <i>Molecular Neurobiology</i> , 2018, 55, 1026-1044.	1.9	96
1444	Multiple correlation analyses revealed complex relationship between DNA methylation and mRNA expression in human peripheral blood mononuclear cells. <i>Functional and Integrative Genomics</i> , 2018, 18, 1-10.	1.4	12
1445	IgG glycosylation and DNA methylation are interconnected with smoking. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 637-648.	1.1	33
1446	Adipose Tissue LPL Methylation is Associated with Triglyceride Concentrations in the Metabolic Syndrome. <i>Clinical Chemistry</i> , 2018, 64, 210-218.	1.5	30
1447	Profiling Developmentally and Environmentally Controlled Chromatin Reprogramming. <i>Methods in Molecular Biology</i> , 2018, 1675, 3-30.	0.4	1
1448	A lncRNA-H19 transcript from secondary hair follicle of Liaoning cashmere goat: Identification, regulatory network and expression regulated potentially by its promoter methylation. <i>Gene</i> , 2018, 641, 78-85.	1.0	54
1449	Recent insights into cotton functional genomics: progress and future perspectives. <i>Plant Biotechnology Journal</i> , 2018, 16, 699-713.	4.1	70
1450	Ethnic and population differences in the genetic predisposition to human obesity. <i>Obesity Reviews</i> , 2018, 19, 62-80.	3.1	104
1451	Alzheimer's disease pathogenesis: Is there a role for folate?. <i>Mechanisms of Ageing and Development</i> , 2018, 174, 86-94.	2.2	52
1452	Epigenetics at the crossroads between genes, environment and resilience in anxiety disorders. <i>Genes, Brain and Behavior</i> , 2018, 17, e12423.	1.1	142
1453	A Versatile Assay for Detection of Aberrant DNA Methylation in Bladder Cancer. <i>Methods in Molecular Biology</i> , 2018, 1655, 29-41.	0.4	5
1454	MN1 overexpression is driven by loss of DNMT3B methylation activity in inv(16) pediatric AML. <i>Oncogene</i> , 2018, 37, 107-115.	2.6	15
1455	Genome-wide DNA methylation analysis of senescence in repetitively infected memory cytotoxic T lymphocytes. <i>Immunology</i> , 2018, 153, 253-267.	2.0	3

#	ARTICLE	IF	CITATIONS
1456	Comparative epigenomics reveals evolution of duplicated genes in potato and tomato. <i>Plant Journal</i> , 2018, 93, 460-471.	2.8	33
1457	Comprehensive Whole DNA Methylome Analysis by Integrating MeDIP-seq and MRE-seq. <i>Methods in Molecular Biology</i> , 2018, 1708, 209-246.	0.4	20
1458	Alterations in DNA methylation patterns and gene expression in spermatozoa of subfertile males. <i>Andrologia</i> , 2018, 50, e12934.	1.0	12
1459	The effects of DNA methylation on human psychology. <i>Behavioural Brain Research</i> , 2018, 346, 47-65.	1.2	55
1460	Piecing together cis-regulatory networks: insights from epigenomics studies in plants. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2018, 10, e1411.	6.6	13
1461	Epigenetic Response to Mindfulness in Peripheral Blood Leukocytes Involves Genes Linked to Common Human Diseases. <i>Mindfulness</i> , 2018, 9, 1146-1159.	1.6	30
1462	On the origin of obesity: identifying the biological, environmental and cultural drivers of genetic risk among human populations. <i>Obesity Reviews</i> , 2018, 19, 121-149.	3.1	158
1463	Epigenetic mechanisms of major depression: Targeting neuronal plasticity. <i>Psychiatry and Clinical Neurosciences</i> , 2018, 72, 212-227.	1.0	118
1464	Cancer induction and suppression with transcriptional control and epigenome editing technologies. <i>Journal of Human Genetics</i> , 2018, 63, 187-194.	1.1	10
1465	Readers of DNA methylation, the MBD family as potential therapeutic targets. , 2018, 184, 98-111.		54
1466	Reduced ten-eleven translocation and isocitrate dehydrogenase expression in inflammatory hidradenitis suppurativa lesions. <i>European Journal of Dermatology</i> , 2018, 28, 449-456.	0.3	9
1467	Genome-wide differences in DNA methylation changes in caprine ovaries between oestrous and dioestrous phases. <i>Journal of Animal Science and Biotechnology</i> , 2018, 9, 85.	2.1	28
1469	The polyphenol quercetin induces cell death in leukemia by targeting epigenetic regulators of pro-apoptotic genes. <i>Clinical Epigenetics</i> , 2018, 10, 139.	1.8	65
1470	Complex interplay of lesion-specific DNA repair enzyme on bistranded clustered DNA damage harboring Tg:G mismatch in nucleosome core particles. <i>Journal of Biosciences</i> , 2018, 43, 575-583.	0.5	4
1471	Population Epigenomics: Advancing Understanding of Phenotypic Plasticity, Acclimation, Adaptation and Diseases. <i>Population Genomics</i> , 2018, , 179-260.	0.2	18
1472	Towards the Understanding of Important Coconut Endosperm Phenotypes: Is there an Epigenetic Control?. <i>Agronomy</i> , 2018, 8, 225.	1.3	14
1473	Highly Selective 5-Formyluracil Labeling and Genome-wide Mapping Using (2-Benzimidazolyl)Acetonitrile Probe. <i>IScience</i> , 2018, 9, 423-432.	1.9	18
1474	Epigenetic mechanisms and implications in tendon inflammation (Review). <i>International Journal of Molecular Medicine</i> , 2019, 43, 3-14.	1.8	10

#	ARTICLE	IF	CITATIONS
1475	Functions and mechanisms of epigenetic inheritance in animals. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 774-790.	16.1	335
1476	Cancer RNome: Evolution and Sustenance. , 2018, , 113-242.		1
1477	Epigenetic Modification Mechanisms Involved in Inflammation and Fibrosis in Renal Pathology. <i>Mediators of Inflammation</i> , 2018, 2018, 1-14.	1.4	49
1478	Lifestyle modifications: coordinating the tRNA epitranscriptome with codon bias to adapt translation during stress responses. <i>Genome Biology</i> , 2018, 19, 228.	3.8	61
1479	Aspects of Epigenetic Regulation in Cereals. <i>Advances in Botanical Research</i> , 2018, , 361-386.	0.5	0
1480	The miRNA 361-3p, a Regulator of GZMB and TNF Is Associated With Therapeutic Failure and Longer Time Healing of Cutaneous Leishmaniasis Caused by <i>L. (viannia) braziliensis</i> . <i>Frontiers in Immunology</i> , 2018, 9, 2621.	2.2	25
1481	Epigenetically reprogrammed methylation landscape drives the DNA self-assembly and serves as a universal cancer biomarker. <i>Nature Communications</i> , 2018, 9, 4915.	5.8	135
1482	Immunohistochemical Detection of 5-Methylcytosine and 5-Hydroxymethylcytosine in Developing and Postmitotic Mouse Retina. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	12
1483	In Utero Heat Stress Alters the Offspring Epigenome. <i>Scientific Reports</i> , 2018, 8, 14609.	1.6	78
1484	Methylation divergence of invasive <i>Ciona</i> ascidians: Significant population structure and local environmental influence. <i>Ecology and Evolution</i> , 2018, 8, 10272-10287.	0.8	18
1485	The methylome of the marbled crayfish links gene body methylation to stable expression of poorly accessible genes. <i>Epigenetics and Chromatin</i> , 2018, 11, 57.	1.8	56
1486	Smoking is Associated to DNA Methylation in Atherosclerotic Carotid Lesions. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002030.	1.6	23
1487	Genotype effects contribute to variation in longitudinal methylome patterns in older people. <i>Genome Medicine</i> , 2018, 10, 75.	3.6	37
1488	DNA methylation subpatterns at distinct regulatory regions in human early embryos. <i>Open Biology</i> , 2018, 8, .	1.5	20
1489	A Bayesian hierarchical model for analyzing methylated RNA immunoprecipitation sequencing data. <i>Quantitative Biology</i> , 2018, 6, 275-286.	0.3	5
1490	Major trauma and acceleration of the ageing process. <i>Ageing Research Reviews</i> , 2018, 48, 32-39.	5.0	12
1491	Genomic Landscape of Methylation Islands in Hymenopteran Insects. <i>Genome Biology and Evolution</i> , 2018, 10, 2766-2776.	1.1	19
1492	Progress of Genomics in Hypertension—Cardiac Hypertrophy. <i>Translational Bioinformatics</i> , 2018, , 179-217.	0.0	0

#	ARTICLE	IF	CITATIONS
1494	Mechanics of the Cell Nucleus. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1092, 41-55.	0.8	16
1495	Methylome and Epialleles in Rice Epilines Selected for Energy Use Efficiency. <i>Agronomy</i> , 2018, 8, 163.	1.3	6
1496	Efficient Purification and LC-MS/MS-based Assay Development for Ten-Eleven Translocation-2 5-Methylcytosine Dioxygenase. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	3
1497	Sex-specific dmrt1 and cyp19a1 methylation and alternative splicing in gonads of the protandrous hermaphrodite barramundi. <i>PLoS ONE</i> , 2018, 13, e0204182.	1.1	48
1498	Preterm Birth and the Risk of Neurodevelopmental Disorders - Is There a Role for Epigenetic Dysregulation?. <i>Current Genomics</i> , 2018, 19, 507-521.	0.7	29
1499	Ex Situ Wildlife Conservation in the Age of Population Genomics. <i>Population Genomics</i> , 2018, , 473-492.	0.2	7
1500	DNA methylation footprints during soybean domestication and improvement. <i>Genome Biology</i> , 2018, 19, 128.	3.8	61
1501	CDH23 Methylation Status and Presbycusis Risk in Elderly Women. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 241.	1.7	21
1502	Nucleic Acid Aptamers Targeting Epigenetic Regulators: An Innovative Therapeutic Option. <i>Pharmaceuticals</i> , 2018, 11, 79.	1.7	10
1503	Epitranscriptomics: RNA Modifications in Bacteria and Archaea. , 2018, , 399-420.		3
1504	An epigenetic mechanism for cavefish eye degeneration. <i>Nature Ecology and Evolution</i> , 2018, 2, 1155-1160.	3.4	78
1505	Combined bioinformatics analysis reveals gene expression and DNA methylation patterns in osteoarthritis. <i>Molecular Medicine Reports</i> , 2018, 17, 8069-8078.	1.1	10
1506	Genome-wide mapping reveals that deoxyuridine is enriched in the human centromeric DNA. <i>Nature Chemical Biology</i> , 2018, 14, 680-687.	3.9	45
1507	Molecular Evolution of Metaplasia to Adenocarcinoma in the Esophagus. <i>Digestive Diseases and Sciences</i> , 2018, 63, 2059-2069.	1.1	19
1508	Synthesizing the role of epigenetics in the response and adaptation of species to climate change in freshwater ecosystems. <i>Molecular Ecology</i> , 2018, 27, 2790-2806.	2.0	70
1509	A survey of transcriptome complexity in <i>Sus scrofa</i> using single-molecule long-read sequencing. <i>DNA Research</i> , 2018, 25, 421-437.	1.5	83
1510	Genome-wide DNA methylation profile of prepubertal porcine testis. <i>Reproduction, Fertility and Development</i> , 2018, 30, 349.	0.1	16
1511	An integrative framework for protein interaction network and methylation data to discover epigenetic modules. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 16, 1-1.	1.9	24

#	ARTICLE	IF	CITATIONS
1512	Honey Bees, Royal Jelly, Epigenetics. , 2018, , 722-727.		0
1513	Excited State Decay Pathways of 2-Deoxy-5-methylcytidine and Deoxycytidine Revisited in Solution: A Comprehensive Kinetic Study by Femtosecond Transient Absorption. Journal of Physical Chemistry B, 2018, 122, 7027-7037.	1.2	35
1514	Age- and quality-dependent DNA methylation correlate with melanin-based coloration in a wild bird. Ecology and Evolution, 2018, 8, 6547-6557.	0.8	6
1515	Epitranscriptomics: RNA Modifications in Bacteria and Archaea. Microbiology Spectrum, 2018, 6, .	1.2	33
1516	Epigenetic analysis of human postmortem brain tissue. Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn, 2018, 150, 237-261.	1.0	3
1517	The Dynamic DNA Demethylation during Postnatal Neuronal Development and Neural Stem Cell Differentiation. Stem Cells International, 2018, 2018, 1-10.	1.2	14
1518	Future Challenges and Prospects for the Epigenetics of Autoimmunity. , 2018, , 387-402.		0
1519	siRNAs regulate DNA methylation and interfere with gene and lncRNA expression in the heterozygous polyploid switchgrass. Biotechnology for Biofuels, 2018, 11, 208.	6.2	22
1520	BoostMe accurately predicts DNA methylation values in whole-genome bisulfite sequencing of multiple human tissues. BMC Genomics, 2018, 19, 390.	1.2	34
1521	Changes in DNA Methylation Related to Male Infertility. , 2018, , 189-207.		0
1522	DNA methylation on N6-adenine in lepidopteran Bombyx mori. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2018, 1861, 815-825.	0.9	27
1523	Chemistry-Driven Epigenetic Investigation of Histone and DNA Modifications. Chemical Record, 2018, 18, 1727-1744.	2.9	13
1524	Massive Loss of DNA Methylation in Nitrogen-, but Not in Phosphorus-Deficient Zea mays Roots Is Poorly Correlated With Gene Expression Differences. Frontiers in Plant Science, 2018, 9, 497.	1.7	33
1525	Altered DNA Methylation of Long Noncoding RNA uc.167 Inhibits Cell Differentiation in Heart Development. BioMed Research International, 2018, 2018, 1-9.	0.9	7
1526	Integrative analysis of methylomic and transcriptomic data in fetal sheep muscle tissues in response to maternal diet during pregnancy. BMC Genomics, 2018, 19, 123.	1.2	32
1527	An Introduction to Epigenetics in Cardiovascular Development, Disease, and Sexualization. Advances in Experimental Medicine and Biology, 2018, 1065, 31-47.	0.8	5
1529	Guidelines for whole genome bisulphite sequencing of intact and FFPE DNA on the Illumina HiSeq X Ten. Epigenetics and Chromatin, 2018, 11, 24.	1.8	38
1530	An electrochemical strategy with tetrahedron rolling circle amplification for ultrasensitive detection of DNA methylation. Biosensors and Bioelectronics, 2018, 121, 47-53.	5.3	48

#	ARTICLE	IF	CITATIONS
1531	Psychotherapy and Genetic Neuroscience: An Emerging Dialog. <i>Frontiers in Genetics</i> , 2018, 9, 257.	1.1	35
1532	DNA methylation mediates BmDeaf1-regulated tissue- and stage-specific expression of BmCHSA-2b in the silkworm, <i>Bombyx mori</i> . <i>Epigenetics and Chromatin</i> , 2018, 11, 32.	1.8	19
1533	Comparative Methylome Analysis Reveals Perturbation of Host Epigenome in Chestnut Blight Fungus by a Hypovirus. <i>Frontiers in Microbiology</i> , 2018, 9, 1026.	1.5	13
1534	CB1R-Mediated Activation of Caspase-3 Causes Epigenetic and Neurobehavioral Abnormalities in Postnatal Ethanol-Exposed Mice. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 45.	1.4	25
1535	The Methylome of Vertebrate Sex Chromosomes. <i>Genes</i> , 2018, 9, 230.	1.0	10
1536	Comparative Analysis of DNA Methylation Reveals Specific Regulations on Ethylene Pathway in Tomato Fruit. <i>Genes</i> , 2018, 9, 266.	1.0	18
1537	Selective modulation of local linkages between active transcription and oxidative demethylation activity shapes cardiomyocyte-specific gene-body epigenetic status in mice. <i>BMC Genomics</i> , 2018, 19, 349.	1.2	4
1538	Current Insights into Oral Cancer Epigenetics. <i>International Journal of Molecular Sciences</i> , 2018, 19, 670.	1.8	61
1539	DNA Methyltransferases, DNA Methylation, and Age-Associated Cognitive Function. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1315.	1.8	105
1540	The DNA Methylome and Association of Differentially Methylated Regions with Differential Gene Expression during Heat Stress in <i>Brassica rapa</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 1414.	1.8	80
1541	Topological Characterization of Human and Mouse m ⁵ C Epitranscriptome Revealed by Bisulfite Sequencing. <i>International Journal of Genomics</i> , 2018, 2018, 1-19.	0.8	17
1542	Recent advancement toward significant association between disordered transcripts and virus-infected diseases: a survey. <i>Briefings in Functional Genomics</i> , 2018, 17, 458-470.	1.3	2
1543	Genome-wide expert annotation of the epigenetic machinery of the plant-parasitic nematodes <i>Meloidogyne</i> spp., with a focus on the asexually reproducing species. <i>BMC Genomics</i> , 2018, 19, 321.	1.2	18
1544	The Molecular Biology of HIV Latency. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1075, 187-212.	0.8	43
1545	Developmental Functions of the Dynamic DNA Methylome and Hydroxymethylome in the Mouse and Zebrafish: Similarities and Differences. <i>Frontiers in Cell and Developmental Biology</i> , 2018, 6, 27.	1.8	16
1546	Embryonic exposure to benzo(a)pyrene inhibits reproductive capability in adult female zebrafish and correlation with DNA methylation. <i>Environmental Pollution</i> , 2018, 240, 403-411.	3.7	59
1547	Detecting TF-miRNA-gene network based modules for 5hmC and 5mC brain samples: a intra- and inter-species case-study between human and rhesus. <i>BMC Genetics</i> , 2018, 19, 9.	2.7	19
1549	Adipose tissue inflammation and VDR expression and methylation in colorectal cancer. <i>Clinical Epigenetics</i> , 2018, 10, 60.	1.8	40

#	ARTICLE	IF	CITATIONS
1550	Folate promotes S-adenosyl methionine reactions and the microbial methylation cycle and boosts ruminants production and reproduction. <i>AMB Express</i> , 2018, 8, 65.	1.4	36
1551	MiR-455-3p inhibits the degenerate process of chondrogenic differentiation through modification of DNA methylation. <i>Cell Death and Disease</i> , 2018, 9, 537.	2.7	34
1552	Transposon-associated epigenetic silencing during <i>Pleurotus ostreatus</i> life cycle. <i>DNA Research</i> , 2018, 25, 451-464.	1.5	17
1553	Interfacial Biosensing: Direct Biosensing of Biomolecules at the Bare Metal Interface. , 2018, , 269-277.		3
1554	Epigenetic Effects Induced by Methamphetamine and Methamphetamine-Dependent Oxidative Stress. <i>Oxidative Medicine and Cellular Longevity</i> , 2018, 2018, 1-28.	1.9	63
1555	Differentially methylated regions in T cells identify kidney transplant patients at risk for de novo skin cancer. <i>Clinical Epigenetics</i> , 2018, 10, 81.	1.8	14
1556	Telomere elongation upon transfer to callus culture reflects the reprogramming of telomere stability control in <i>Arabidopsis</i> . <i>Plant Molecular Biology</i> , 2018, 98, 81-99.	2.0	8
1557	Regulation of Plant Growth and Development: A Review From a Chromatin Remodeling Perspective. <i>Frontiers in Plant Science</i> , 2018, 9, 1232.	1.7	77
1558	Can physiological engineering/programming increase multi-generational thermal tolerance to extreme temperature events?. <i>Journal of Experimental Biology</i> , 2018, 221, .	0.8	5
1559	Tracking age-correlated DNA methylation markers in the young. <i>Forensic Science International: Genetics</i> , 2018, 36, 50-59.	1.6	41
1560	Structural basis for eukaryotic mRNA modification. <i>Current Opinion in Structural Biology</i> , 2018, 53, 59-68.	2.6	18
1561	Chromatin immunoprecipitation improvements for the processing of small frozen pieces of adipose tissue. <i>PLoS ONE</i> , 2018, 13, e0192314.	1.1	6
1562	Neuroepigenetics and addiction. <i>Handbook of Clinical Neurology</i> / Edited By P J Vinken and G W Bruyn, 2018, 148, 747-765.	1.0	76
1563	Differential DNA methylation and transcription profiles in date palm roots exposed to salinity. <i>PLoS ONE</i> , 2018, 13, e0191492.	1.1	45
1564	Environmental Epigenomics and Its Applications in Marine Organisms. <i>Population Genomics</i> , 2018, , 325-359.	0.2	17
1565	Genome-wide DNA methylation signatures of infection status in Trinidadian guppies (<i>Poecilia</i>) Tj ETQq1 1 0.784314 rgBT / Overlock	2.0	34
1566	An Introduction to Epigenetic Mechanisms. <i>Progress in Molecular Biology and Translational Science</i> , 2018, 158, 29-48.	0.9	13
1567	Epigenetic alterations mediate iPSC normalization of DNA-repair expression and TNR stability in Huntington's disease. <i>Journal of Cell Science</i> , 2018, 131, .	1.2	9

#	ARTICLE	IF	CITATIONS
1568	A microchip electrophoretic assay for DNA methyltransferase activity based on methylation-sensitive endonuclease Dpnâ...j. Electrophoresis, 2019, 40, 425-430.	1.3	8
1569	Marine Environmental Epigenetics. Annual Review of Marine Science, 2019, 11, 335-368.	5.1	223
1570	Induced Expression of Endogenous CXCR4 in iPSCs by Targeted CpG Demethylation Enhances Cell Migration Toward the Ligand CXCL12. Inflammation, 2019, 42, 20-34.	1.7	5
1571	DNA co-methylation analysis of lincRNAs across nine cancer types reveals novel potential epigenetic biomarkers in cancer. Epigenomics, 2019, 11, 1177-1190.	1.0	3
1572	DNA Methylation and Hydroxymethylation and Behavior. Current Topics in Behavioral Neurosciences, 2019, 42, 51-82.	0.8	12
1573	SET8 prevents excessive DNA methylation by methylation-mediated degradation of UHRF1 and DNMT1. Nucleic Acids Research, 2019, 47, 9053-9068.	6.5	40
1574	Dietary Patterns are Associated with Leukocyte LINE-1 Methylation in Women: A Cross-Sectional Study in Southern Italy. Nutrients, 2019, 11, 1843.	1.7	34
1575	Unique DNA Methylation Profiles Are Associated with cis-Variation in Honey Bees. Genome Biology and Evolution, 2019, 11, 2517-2530.	1.1	31
1576	Vpr Enhances HIV-1 Env Processing and Virion Infectivity in Macrophages by Modulating TET2-Dependent IFITM3 Expression. MBio, 2019, 10, .	1.8	24
1577	Phytochemicals in cancer prevention: modulating epigenetic alterations of DNA methylation. Phytochemistry Reviews, 2019, 18, 1005-1024.	3.1	38
1578	Nutrition influence on sow reproductive performance and conceptuses development and survival: A review about l-arginine supplementation. Livestock Science, 2019, 228, 97-103.	0.6	7
1579	Endometrial genome-wide DNA methylation patterns of Guanzhong dairy goats at days 5 and 15 of the gestation period. Animal Reproduction Science, 2019, 208, 106124.	0.5	3
1580	Metabolic control of gene transcription in non-alcoholic fatty liver disease: the role of the epigenome. Clinical Epigenetics, 2019, 11, 104.	1.8	34
1581	A Homeostasis Hypothesis of Avian Influenza Resistance in Chickens. Genes, 2019, 10, 543.	1.0	6
1582	Indole-3-acetic acid has long-term effects on long non-coding RNA gene methylation and growth in Populus tomentosa. Molecular Genetics and Genomics, 2019, 294, 1511-1525.	1.0	9
1583	Rational design of transient gene expression process with lipoplexes for high-level therapeutic protein production in HEK293 cells. Process Biochemistry, 2019, 85, 185-194.	1.8	3
1584	Avian ecological epigenetics: pitfalls and promises. Journal of Ornithology, 2019, 160, 1183-1203.	0.5	37
1585	Genome-wide DNA methylomic differences between dorsolateral prefrontal and temporal pole cortices of bipolar disorder. Journal of Psychiatric Research, 2019, 117, 45-54.	1.5	24

#	ARTICLE	IF	CITATIONS
1586	Implication for DNA methylation involved in the host transfer of diamondback moth, <i>Plutella xylostella</i> (L.). <i>Archives of Insect Biochemistry and Physiology</i> , 2019, 102, e21600.	0.6	3
1587	Altered expression of long noncoding RNAs in patients with major depressive disorder. <i>Journal of Psychiatric Research</i> , 2019, 117, 92-99.	1.5	27
1588	Microfluidic epigenomic mapping technologies for precision medicine. <i>Lab on A Chip</i> , 2019, 19, 2630-2650.	3.1	11
1589	m1A Regulated Genes Modulate PI3K/AKT/mTOR and ErbB Pathways in Gastrointestinal Cancer. <i>Translational Oncology</i> , 2019, 12, 1323-1333.	1.7	102
1590	Early life stress and the propensity to develop addictive behaviors. <i>International Journal of Developmental Neuroscience</i> , 2019, 78, 156-169.	0.7	23
1591	NSUN2 introduces 5-methylcytosines in mammalian mitochondrial tRNAs. <i>Nucleic Acids Research</i> , 2019, 47, 8720-8733.	6.5	84
1592	Immunology Driven by Large-Scale Single-Cell Sequencing. <i>Trends in Immunology</i> , 2019, 40, 1011-1021.	2.9	62
1593	DNA Methylation Markers for Pan-Cancer Prediction by Deep Learning. <i>Genes</i> , 2019, 10, 778.	1.0	55
1594	DNA methylation is maintained with high fidelity in the honey bee germline and exhibits global non-functional fluctuations during somatic development. <i>Epigenetics and Chromatin</i> , 2019, 12, 62.	1.8	50
1595	2,7-Dibromocarbazole interferes with tube formation in HUVECs by altering Ang2 promoter DNA methylation status. <i>Science of the Total Environment</i> , 2019, 697, 134156.	3.9	18
1596	Food Safety and Nutraceutical Potential of Caramel Colour Class IV Using In Vivo and In Vitro Assays. <i>Foods</i> , 2019, 8, 392.	1.9	7
1597	Genetic and epigenetic modifications induced by chemotherapeutic drugs: human amniotic fluid stem cells as an in-vitro model. <i>BMC Medical Genomics</i> , 2019, 12, 146.	0.7	1
1598	Data Integration in Poplar: Omics Layers and Integration Strategies. <i>Frontiers in Genetics</i> , 2019, 10, 874.	1.1	15
1599	Cell-Free DNA Methylation Profiling Analysis Technologies and Bioinformatics. <i>Cancers</i> , 2019, 11, 1741.	1.7	37
1600	4mCpred-EL: An Ensemble Learning Framework for Identification of DNA N4-methylcytosine Sites in the Mouse Genome. <i>Cells</i> , 2019, 8, 1332.	1.8	77
1601	Regional epigenetic differentiation of the Z Chromosome between sexes in a female heterogametic system. <i>Genome Research</i> , 2019, 29, 1673-1684.	2.4	19
1602	Reprogramming of DNA methylation at NEUROD2-bound sequences during cortical neuron differentiation. <i>Science Advances</i> , 2019, 5, eaax0080.	4.7	32
1603	Sex-specific changes in the aphid DNA methylation landscape. <i>Molecular Ecology</i> , 2019, 28, 4228-4241.	2.0	45

#	ARTICLE	IF	CITATIONS
1604	Epigenetic, transcriptional and phenotypic responses in two generations of <i>Daphnia magna</i> exposed to the DNA methylation inhibitor 5-azacytidine. <i>Environmental Epigenetics</i> , 2019, 5, dvz016.	0.9	28
1605	5- ^h Hydroxymethylcytosine as a potential epigenetic biomarker in papillary thyroid carcinoma. <i>Oncology Letters</i> , 2019, 18, 2304-2309.	0.8	14
1606	An adenosine derivative (IFC-305) reduced the risk of radiation-induced intestinal toxicity in the treatment of colon cancer by suppressing the methylation of PPAR- α promoter. <i>Biomedicine and Pharmacotherapy</i> , 2019, 118, 109202.	2.5	4
1607	CpG methylation signature predicts prognosis in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2019, 178, 565-572.	1.1	10
1608	Analysis of ¹³ C-Tocopherol methyl transferase3 promoter activity and study of methylation patterns of the promoter and its gene body. <i>Plant Physiology and Biochemistry</i> , 2019, 144, 375-385.	2.8	2
1609	Universality of the DNA methylation codes in Eucaryotes. <i>Scientific Reports</i> , 2019, 9, 173.	1.6	37
1610	Microfluidic MeDIP-seq for low-input methylomic analysis of mammary tumorigenesis in mice. <i>Analyst</i> , 2019, 144, 1904-1915.	1.7	8
1611	Association mapping in plants in the post-GWAS genomics era. <i>Advances in Genetics</i> , 2019, 104, 75-154.	0.8	100
1612	Dynamics of DNA Methylation and DNMT Expression During Gametogenesis and Early Development of Scallop <i>Patinopecten yessoensis</i> . <i>Marine Biotechnology</i> , 2019, 21, 196-205.	1.1	26
1613	Epigenetic Mechanisms of Quercetin and Other Flavonoids in Cancer Therapy and Prevention. , 2019, , 187-202.		6
1614	Persistent changes in liver methylation and microbiome composition following reversal of diet-induced non-alcoholic-fatty liver disease. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 4341-4354.	2.4	32
1615	<i>Arabidopsis</i> S2Lb links AtCOMPASS-like and SDG2 activity in H3K4me3 independently from histone H2B monoubiquitination. <i>Genome Biology</i> , 2019, 20, 100.	3.8	56
1616	Genome-Wide DNA Methylation Profiling in the Lotus (<i>Nelumbo nucifera</i>) Flower Showing its Contribution to the Stamen Petaloid. <i>Plants</i> , 2019, 8, 135.	1.6	18
1617	Acute and chronic response to a change in salinity of the euryhaline polychaete <i>Pygospio elegans</i> (Claparède). <i>Journal of Experimental Marine Biology and Ecology</i> , 2019, 516, 79-88.	0.7	4
1618	Evolutionary transition between invertebrates and vertebrates via methylation reprogramming in embryogenesis. <i>National Science Review</i> , 2019, 6, 993-1003.	4.6	58
1619	LightCpG: a multi-view CpG sites detection on single-cell whole genome sequence data. <i>BMC Genomics</i> , 2019, 20, 306.	1.2	20
1620	LMP2A induces DNA methylation and expression repression of AQP3 in EBV-associated gastric carcinoma. <i>Virology</i> , 2019, 534, 87-95.	1.1	31
1621	A novel photoelectrochemical strategy based on quenching effect of CdS quantum dots on PTB7 as photoelectroactive material for methylated DNA detection. <i>Journal of Electroanalytical Chemistry</i> , 2019, 847, 113220.	1.9	3

#	ARTICLE	IF	CITATIONS
1622	Capture of a functionally active methyl-CpG binding domain by an arthropod retrotransposon family. <i>Genome Research</i> , 2019, 29, 1277-1286.	2.4	19
1623	DNA Methylation-Based Point-of-Care Cancer Detection: Challenges and Possibilities. <i>Trends in Molecular Medicine</i> , 2019, 25, 955-966.	3.5	30
1624	Alzheimer's Disease Associated Genes Ankyrin and Tau Cause Shortened Lifespan and Memory Loss in <i>Drosophila</i> . <i>Frontiers in Cellular Neuroscience</i> , 2019, 13, 260.	1.8	32
1625	Clinicopathological Significance and Diagnostic Value of DLEC1 Hypermethylation in Lung Cancer: A Meta-analysis. <i>Journal of Nippon Medical School</i> , 2019, 86, 62-69.	0.3	5
1626	Toward a transdiagnostic model of common and unique processes leading to the major disorders of childhood: The REAL model of attention, responsiveness and learning. <i>Behaviour Research and Therapy</i> , 2019, 119, 103410.	1.6	28
1627	Differential effects of the methylenetetrahydrofolate reductase polymorphisms (C677T and A1298C) on hematological malignancies among Latinos: a meta-analysis. <i>Genetics and Molecular Biology</i> , 2019, 42, 549-559.	0.6	1
1628	Perinatal Lead (Pb) Exposure and Cortical Neuron-Specific DNA Methylation in Male Mice. <i>Genes</i> , 2019, 10, 274.	1.0	33
1629	Hidden Markov Modelling Reveals Neighborhood Dependence of Dnmt3a and 3b Activity. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1598-1609.	1.9	5
1630	Epigenetic Function of TET Family, 5-Methylcytosine, and 5-Hydroxymethylcytosine in Hematologic Malignancies. <i>Oncology Research and Treatment</i> , 2019, 42, 309-318.	0.8	19
1631	Epigenetic aberrations in human pluripotent stem cells. <i>EMBO Journal</i> , 2019, 38, .	3.5	86
1632	SALL3 expression balance underlies lineage biases in human induced pluripotent stem cell differentiation. <i>Nature Communications</i> , 2019, 10, 2175.	5.8	21
1633	Identification and sequencing of the gene encoding DNA methyltransferase 3 (DNMT3) from sea cucumber, <i>Apostichopus japonicus</i> . <i>Molecular Biology Reports</i> , 2019, 46, 3791-3800.	1.0	2
1634	Epigenetic control of the angiotensin-converting enzyme in endothelial cells during inflammation. <i>PLoS ONE</i> , 2019, 14, e0216218.	1.1	13
1635	TAGOOS: genome-wide supervised learning of non-coding loci associated to complex phenotypes. <i>Nucleic Acids Research</i> , 2019, 47, e79-e79.	6.5	3
1636	Transcriptomic profiling identifies novel mechanisms of transcriptional regulation of the cytochrome P450 (Cyp)3a11 gene. <i>Scientific Reports</i> , 2019, 9, 6663.	1.6	14
1637	Epigenetic Response of Plants to Abiotic Stress: Nature, Consequences and Applications in Breeding. <i>Sustainable Development and Biodiversity</i> , 2019, , 53-72.	1.4	1
1638	Absence of mitochondrial DNA methylation in mouse oocyte maturation, aging and early embryo development. <i>Biochemical and Biophysical Research Communications</i> , 2019, 513, 912-918.	1.0	18
1639	Epigenetic Regulations in Neuropsychiatric Disorders. <i>Frontiers in Genetics</i> , 2019, 10, 268.	1.1	116

#	ARTICLE	IF	CITATIONS
1640	Epigenomics in an extraterrestrial environment: organ-specific alteration of DNA methylation and gene expression elicited by spaceflight in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2019, 20, 205.	1.2	47
1642	Glucocorticoid Receptor Stimulation Resulting from Early Life Stress Affects Expression of DNA Methyltransferases in Rat Prefrontal Cortex. <i>Journal of Molecular Neuroscience</i> , 2019, 68, 99-110.	1.1	16
1643	An integrated whole genome analysis of <i>Mycobacterium tuberculosis</i> reveals insights into relationship between its genome, transcriptome and methylome. <i>Scientific Reports</i> , 2019, 9, 5204.	1.6	26
1644	Seasonal Variation in Genome-Wide DNA Methylation Patterns and the Onset of Seasonal Timing of Reproduction in Great Tits. <i>Genome Biology and Evolution</i> , 2019, 11, 970-983.	1.1	54
1645	Genome-wide DNA methylation profiles in Tibetan and Yorkshire pigs under high-altitude hypoxia. <i>Journal of Animal Science and Biotechnology</i> , 2019, 10, 25.	2.1	29
1646	MRCNN: a deep learning model for regression of genome-wide DNA methylation. <i>BMC Genomics</i> , 2019, 20, 192.	1.2	36
1647	Structural analyses reveal that MBD3 is a methylated CG binder. <i>FEBS Journal</i> , 2019, 286, 3240-3254.	2.2	15
1648	A (fire)cloud-based DNA methylation data preprocessing and quality control platform. <i>BMC Bioinformatics</i> , 2019, 20, 160.	1.2	7
1649	Genetic and epigenetic alterations induced by the small-molecule panobinostat: A mechanistic study at the chromosome and gene levels. <i>DNA Repair</i> , 2019, 78, 70-80.	1.3	18
1650	DNA methylation estimation using methylation-sensitive restriction enzyme bisulfite sequencing (MREBS). <i>PLoS ONE</i> , 2019, 14, e0214368.	1.1	14
1651	Genome-wide DNA methylation profiles in human bone marrow mesenchymal stem cells on titanium surfaces. <i>European Journal of Oral Sciences</i> , 2019, 127, 196-209.	0.7	3
1652	Epigenetic Effects of Curcumin in Cancer Prevention. , 2019, , 107-128.		12
1653	Recent Progress in Electrochemical Biosensors for Detection of DNA Methylation and Methyltransferase Activity. <i>International Journal of Electrochemical Science</i> , 2019, 14, 1843-1854.	0.5	6
1654	Reduced aquaporin-1 transcript expression in colorectal carcinoma is associated with promoter hypermethylation. <i>Epigenetics</i> , 2019, 14, 158-170.	1.3	7
1655	Changes in gene DNA methylation and expression networks accompany caste specialization and age-related physiological changes in a social insect. <i>Molecular Ecology</i> , 2019, 28, 1975-1993.	2.0	30
1656	New guidelines for DNA methylome studies regarding 5-hydroxymethylcytosine for understanding transcriptional regulation. <i>Genome Research</i> , 2019, 29, 543-553.	2.4	21
1657	Progress Toward Development of Climate-Smart Flax: A Perspective on Omics-Assisted Breeding. , 2019, , 239-274.		10
1658	Epigenomic Reprogramming in Cardiovascular Disease. , 2019, , 149-163.		1

#	ARTICLE	IF	CITATIONS
1659	Epigenome-wide analysis of sperm cells identifies IL22 as a possible germ line risk locus for psoriatic arthritis. <i>PLoS ONE</i> , 2019, 14, e0212043.	1.1	23
1660	DNA Methylation Patterns in the Social Spider, <i>Stegodyphus dumicola</i> . <i>Genes</i> , 2019, 10, 137.	1.0	46
1661	IBD-associated Colon Cancers Differ in DNA Methylation and Gene Expression Profiles Compared With Sporadic Colon Cancers. <i>Journal of Crohn's and Colitis</i> , 2019, 13, 884-893.	0.6	15
1662	Emergent Properties and Stability in Hierarchical Biosystems: There Is no Privileged Level of Causation. , 2019, , 217-234.		3
1663	Emergence and Modularity in Life Sciences. , 2019, , .		7
1664	Induction, identification and genetics analysis of tetraploid <i>Actinidia chinensis</i> . <i>Royal Society Open Science</i> , 2019, 6, 191052.	1.1	10
1665	SIMON: Simple methods for analyzing DNA methylation by targeted bisulfite next-generation sequencing. <i>Plant Biotechnology</i> , 2019, 36, 213-222.	0.5	2
1666	A Hybrid Ensemble Approach for Identifying Robust Differentially Methylated Loci in Pan-Cancers. <i>Frontiers in Genetics</i> , 2019, 10, 774.	1.1	4
1667	Changes in DNA methylation from pre- to post-adolescence are associated with pubertal exposures. <i>Clinical Epigenetics</i> , 2019, 11, 176.	1.8	35
1668	The DNA methylome in panic disorder: a case-control and longitudinal psychotherapy-epigenetic study. <i>Translational Psychiatry</i> , 2019, 9, 314.	2.4	29
1669	DNA Methylation Profile of β -1,3-Glucanase and Chitinase Genes in Flax Shows Specificity Towards <i>Fusarium Oxysporum</i> Strains Differing in Pathogenicity. <i>Microorganisms</i> , 2019, 7, 589.	1.6	10
1670	Small Particles, Big Effects: The Interplay Between Exosomes and Dendritic Cells in Antitumor Immunity and Immunotherapy. <i>Cells</i> , 2019, 8, 1648.	1.8	16
1671	Convergent evolution of a vertebrate-like methylome in a marine sponge. <i>Nature Ecology and Evolution</i> , 2019, 3, 1464-1473.	3.4	47
1672	Prenatal Glucocorticoid Exposure Results in Changes in Gene Transcription and DNA Methylation in the Female Juvenile Guinea Pig Hippocampus Across Three Generations. <i>Scientific Reports</i> , 2019, 9, 18211.	1.6	21
1673	Histone acetyltransferase and Polo-like kinase 3 inhibitors prevent rat galactose-induced cataract. <i>Scientific Reports</i> , 2019, 9, 20085.	1.6	18
1674	Long intergenic noncoding RNA 299 methylation in peripheral blood is a biomarker for triple-negative breast cancer. <i>Epigenomics</i> , 2019, 11, 81-93.	1.0	32
1675	Mechanisms Regulating Compulsive Drug Behaviors. , 2019, , 137-155.		4
1676	DNA methylation variability in Alzheimer's disease. <i>Neurobiology of Aging</i> , 2019, 76, 35-44.	1.5	25

#	ARTICLE	IF	CITATIONS
1677	The effect of glutamate-induced excitotoxicity on DNA methylation in astrocytes in a new in vitro neuron-astrocyte-endothelium co-culture system. <i>Biochemical and Biophysical Research Communications</i> , 2019, 508, 1209-1214.	1.0	12
1678	DNA methyltransferase <i>BmDnmt1</i> and <i>BmDnmt2</i> in silkworm (<i>Bombyx mori</i>) and the regulation of silkworm embryonic development. <i>Archives of Insect Biochemistry and Physiology</i> , 2019, 100, e21529.	0.6	13
1679	Bioinformatic Analysis of Methylation Patterns Using Bisulfite Sequencing Data. <i>Methods in Molecular Biology</i> , 2019, 1858, 157-175.	0.4	3
1680	Insect Genomics. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	0
1681	Whole-Genome Bisulfite Sequencing for the Methylation Analysis of Insect Genomes. <i>Methods in Molecular Biology</i> , 2019, 1858, 141-156.	0.4	1
1682	Long noncoding RNA uc.4 inhibits cell differentiation in heart development by altering DNA methylation. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 8061-8068.	1.2	6
1683	Functional Annotation of Animal Genomes (FAANG): Current Achievements and Roadmap. <i>Annual Review of Animal Biosciences</i> , 2019, 7, 65-88.	3.6	172
1684	Epigenetic modification, co-culture and genomic methods for natural product discovery. <i>Physical Sciences Reviews</i> , 2019, 4, .	0.8	10
1685	The Role of DNA Methylation in Gene Regulation. , 2019, , 127-151.		11
1686	DNA Methylation as a Biomarker in Environmental Epidemiology. , 2019, , 173-189.		1
1687	Epigenetic control in skin development, homeostasis and injury repair. <i>Experimental Dermatology</i> , 2019, 28, 453-463.	1.4	32
1688	Altered Adipose Tissue DNA Methylation Status in Metabolic Syndrome: Relationships Between Global DNA Methylation and Specific Methylation at Adipogenic, Lipid Metabolism and Inflammatory Candidate Genes and Metabolic Variables. <i>Journal of Clinical Medicine</i> , 2019, 8, 87.	1.0	67
1689	Epigenetic control of hypersensitivity in chronic inflammatory pain by the de novo DNA methyltransferase <i>Dnmt3a2</i> . <i>Molecular Pain</i> , 2019, 15, 174480691982746.	1.0	14
1690	The influence of CpG (5'-d(CpG)-3' dinucleotides) methylation on ultrasonic DNA fragmentation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 3877-3886.	2.0	4
1691	Cellular Epigenetics and Behavioral Evolution. , 2019, , 13-19.		0
1692	<i>Thy1</i> (CD90) expression is regulated by DNA methylation during adipogenesis. <i>FASEB Journal</i> , 2019, 33, 3353-3363.	0.2	8
1693	Identification and molecular analysis of a lncRNA-HOTAIR transcript from secondary hair follicle of cashmere goat reveal integrated regulatory network with the expression regulated potentially by its promoter methylation. <i>Gene</i> , 2019, 688, 182-192.	1.0	42
1694	Cognitive deficits in mice lacking <i>Nsun5</i> , a cytosine RNA methyltransferase, with impairment of oligodendrocyte precursor cells. <i>Glia</i> , 2019, 67, 688-702.	2.5	20

#	ARTICLE	IF	CITATIONS
1695	Improved yield of rhEPO in CHO cells with synthetic 5' UTR. <i>Biotechnology Letters</i> , 2019, 41, 231-239.	1.1	7
1696	Noninvasive Prenatal Testing for Genetic Diseases. , 2019, , 597-625.		1
1697	Epigenetics in Insects: Genome Regulation and the Generation of Phenotypic Diversity. <i>Annual Review of Entomology</i> , 2019, 64, 185-203.	5.7	137
1698	Longitudinal Analyses of Blood Transcriptome During Conversion to Psychosis. <i>Schizophrenia Bulletin</i> , 2019, 45, 247-255.	2.3	24
1699	LncRNA-000133 from secondary hair follicle of Cashmere goat: identification, regulatory network and its effects on inductive property of dermal papilla cells. <i>Animal Biotechnology</i> , 2020, 31, 122-134.	0.7	38
1700	Childhood emotional neglect and oxytocin receptor variants: Association with limbic brain volumes. <i>World Journal of Biological Psychiatry</i> , 2020, 21, 513-528.	1.3	22
1701	Epigenetic downregulation of TET3 reduces genome-wide 5hmC levels and promotes glioblastoma tumorigenesis. <i>International Journal of Cancer</i> , 2020, 146, 373-387.	2.3	45
1702	DNA Methylation Analysis Identifies Differentially Methylated Sites Associated with Early-Onset Intracranial Atherosclerotic Stenosis. <i>Journal of Atherosclerosis and Thrombosis</i> , 2020, 27, 71-99.	0.9	3
1703	Epigenetic mechanisms related to cognitive decline during aging. <i>Journal of Neuroscience Research</i> , 2020, 98, 234-246.	1.3	50
1704	Linking endotypes to omics profiles in difficult-to-control asthma using the diagnostic Chinese medicine syndrome differentiation algorithm. <i>Journal of Asthma</i> , 2020, 57, 532-542.	0.9	5
1705	Linking epigenetics and biological conservation: Towards a conservation epigenetics perspective. <i>Functional Ecology</i> , 2020, 34, 414-427.	1.7	67
1706	Phylogenetic Shifts in Gene Body Methylation Correlate with Gene Expression and Reflect Trait Conservation. <i>Molecular Biology and Evolution</i> , 2020, 37, 31-43.	3.5	29
1707	Lower folate levels in methamphetamine-induced psychosis: A cross-sectional study. <i>Drug and Alcohol Dependence</i> , 2020, 207, 107682.	1.6	2
1708	Toward a Mechanistic Understanding of DNA Methylation Readout by Transcription Factors. <i>Journal of Molecular Biology</i> , 2020, 432, 1801-1815.	2.0	54
1709	Methylation of adenosine at the N6 position post-transcriptionally regulates hepatic P450s expression. <i>Biochemical Pharmacology</i> , 2020, 171, 113697.	2.0	26
1710	Evolution of DNA Methylome Diversity in Eukaryotes. <i>Journal of Molecular Biology</i> , 2020, 432, 1687-1705.	2.0	82
1711	DNA Methylation and Histone H1 Jointly Repress Transposable Elements and Aberrant Intragenic Transcripts. <i>Molecular Cell</i> , 2020, 77, 310-323.e7.	4.5	99
1712	DNA methylation and expression analyses reveal epialleles for the foliar disease resistance genes in peanut (<i>Arachis hypogaea</i> L.). <i>BMC Research Notes</i> , 2020, 13, 20.	0.6	9

#	ARTICLE	IF	CITATIONS
1713	Insights into Drought Stress Signaling in Plants and the Molecular Genetic Basis of Cotton Drought Tolerance. <i>Cells</i> , 2020, 9, 105.	1.8	189
1714	DNA methylation changes in Down syndrome derived neural iPSCs uncover co-dysregulation of ZNF and HOX3 families of transcription factors. <i>Clinical Epigenetics</i> , 2020, 12, 9.	1.8	20
1715	Structural Insights into the Specific Recognition of 5-methylcytosine and 5-hydroxymethylcytosine by TAL Effectors. <i>Journal of Molecular Biology</i> , 2020, 432, 1035-1047.	2.0	6
1716	DNA Modification Readers and Writers and Their Interplay. <i>Journal of Molecular Biology</i> , 2020, 432, 1731-1746.	2.0	48
1717	Identification and functional characterization of methyl-CpG binding domain protein from <i>Tribolium castaneum</i> . <i>Genomics</i> , 2020, 112, 2223-2232.	1.3	12
1718	Genetic, epigenetic, and lineage-directed mechanisms in benzene-induced malignancies and hematotoxicity targeting hematopoietic stem cells niche. <i>Human and Experimental Toxicology</i> , 2020, 39, 577-595.	1.1	11
1719	Directional X Chromosome Skewing of White Blood Cells from Subjects with Heterozygous Mosaicism for the Variant IRAK1 Haplotype. <i>Inflammation</i> , 2020, 43, 370-381.	1.7	3
1720	Direct Reprogramming of Mouse Fibroblasts into Functional Osteoblasts. <i>Journal of Bone and Mineral Research</i> , 2020, 35, 698-713.	3.1	11
1721	Epigenetic and miRNA Expression Changes in People with Pain: A Systematic Review. <i>Journal of Pain</i> , 2020, 21, 763-780.	0.7	35
1723	Advances and applications of environmental stress adaptation research. <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2020, 240, 110623.	0.8	12
1724	ATP-Dependent Chromatin Remodeling Complex in the Lineage Specification of Mesenchymal Stem Cells. <i>Stem Cells International</i> , 2020, 2020, 1-10.	1.2	3
1725	Combined Methylome, Transcriptome and Proteome Analyses Document Rapid Acclimatization of a Bacterium to Environmental Changes. <i>Frontiers in Microbiology</i> , 2020, 11, 544785.	1.5	9
1726	Human papillomavirus-positivity is associated with EREG down-regulation and promoter hypermethylation in head and neck squamous cell carcinoma. <i>Experimental and Molecular Pathology</i> , 2020, 117, 104549.	0.9	5
1727	Chromatin-modifying drugs and metabolites in cell fate control. <i>Cell Proliferation</i> , 2020, 53, e12898.	2.4	11
1728	Inside the supergene of the bird with four sexes. <i>Hormones and Behavior</i> , 2020, 126, 104850.	1.0	11
1729	Differential Transgeneration Methylation of Exogenous Promoters in T1 Transgenic Wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Over	0.2	1
1730	Epigenetic Control of IFN- β Host Responses During Infection With <i>Toxoplasma gondii</i> . <i>Frontiers in Immunology</i> , 2020, 11, 581241.	2.2	15
1731	Positive/negative ion-switching-based LC-MS/MS method for quantification of cytosine derivatives produced by the TET-family 5-methylcytosine dioxygenases. <i>Biology Methods and Protocols</i> , 2020, 5, bpaa019.	1.0	4

#	ARTICLE	IF	CITATIONS
1732	On the Use of Blood Samples for Measuring DNA Methylation in Ecological Epigenetic Studies. Integrative and Comparative Biology, 2020, 60, 1558-1566.	0.9	44
1733	Differentially Methylated Regions in Desmoid-Type Fibromatosis: A Comparison Between CTNNB1 S45F and T41A Tumors. Frontiers in Oncology, 2020, 10, 565031.	1.3	7
1734	<p>The Association Between RAPSN Methylation in Peripheral Blood and Early Stage Lung Cancer Detected in Case"Control Cohort<p>. Cancer Management and Research, 2020, Volume 12, 11063-11075.	0.9	9
1735	Changes in DNA Methylation Induced by Dioxins and Dioxin-Like Compounds as Potential Predictor of Disease Risk. Russian Journal of Genetics, 2020, 56, 1180-1192.	0.2	3
1736	Epigenetic regulation by polyphenols in diabetes and related complications. Mediterranean Journal of Nutrition and Metabolism, 2020, 13, 289-310.	0.2	26
1737	A DNA methylation state transition model reveals the programmed epigenetic heterogeneity in human pre-implantation embryos. Genome Biology, 2020, 21, 277.	3.8	3
1738	Genome-Wide Differential DNA Methylation in Reproductive, Morphological, and Visual System Differences Between Queen Bee and Worker Bee (Apis mellifera). Frontiers in Genetics, 2020, 11, 770.	1.1	14
1739	Polymer models for the mechanisms of chromatin 3D folding: review and perspective. Physical Chemistry Chemical Physics, 2020, 22, 20189-20201.	1.3	12
1740	Identification of Differentially Methylated miRNA Genes During Compatible and Incompatible Interactions Between Soybean and Soybean Cyst Nematode. Molecular Plant-Microbe Interactions, 2020, 33, 1340-1352.	1.4	27
1741	The functional epigenetic landscape of aberrant gene expression in molecular subgroups of newly diagnosed multiple myeloma. Journal of Hematology and Oncology, 2020, 13, 108.	6.9	20
1742	Targeting kinases with thymoquinone: a molecular approach to cancer therapeutics. Drug Discovery Today, 2020, 25, 2294-2306.	3.2	22
1743	Epigenetic mechanisms activated by childhood adversity. Epigenomics, 2020, 12, 1239-1255.	1.0	16
1744	DNC4mC-Deep: Identification and Analysis of DNA N4-Methylcytosine Sites Based on Different Encoding Schemes By Using Deep Learning. Cells, 2020, 9, 1756.	1.8	30
1745	In vivo locus-specific editing of the neuroepigenome. Nature Reviews Neuroscience, 2020, 21, 471-484.	4.9	44
1746	Recent Advances in Genetic and Epigenetic Modulation of Animal Exposure to High Temperature. Frontiers in Genetics, 2020, 11, 653.	1.1	10
1747	Global DNA Methylation as a Potential Underlying Mechanism of Congenital Disease Development. , 0, , .		1
1748	HLA-G Expression in Human Mesenchymal Stem Cells (MSCs) Is Related to Unique Methylation Pattern in the Proximal Promoter as well as Gene Body DNA. International Journal of Molecular Sciences, 2020, 21, 5075.	1.8	14
1749	Genome-Wide DNA Methylation and Gene Expression Profiles in Cows Subjected to Different Stress Level as Assessed by Cortisol in Milk. Genes, 2020, 11, 850.	1.0	11

#	ARTICLE	IF	CITATIONS
1750	Phenotypes from cell-free DNA. <i>Open Biology</i> , 2020, 10, 200119.	1.5	9
1751	Thyroid Hormone Induces DNA Demethylation in <i>Xenopus</i> Tadpole Brain. <i>Endocrinology</i> , 2020, 161, .	1.4	14
1752	Investigating the Role of Methylation in Silencing of VDR Gene Expression in Normal Cells during Hematopoiesis and in Their Leukemic Counterparts. <i>Cells</i> , 2020, 9, 1991.	1.8	6
1753	Snapshot of epigenetic regulation in legumes. , 2021, 3, e60.		4
1754	DNA methylation suppresses chitin degradation and promotes the wing development by inhibiting Bmara-mediated chitinase expression in the silkworm, <i>Bombyx mori</i> . <i>Epigenetics and Chromatin</i> , 2020, 13, 34.	1.8	13
1755	Exacerbated obesogenic response in female mice exposed to early life stress is linked to fat depot-specific upregulation of leptin protein expression. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2020, 319, E852-E862.	1.8	8
1756	Sperm DNA Hypomethylation Proximal to Reproduction Pathway Genes in Maturing Elite Norwegian Red Bulls. <i>Frontiers in Genetics</i> , 2020, 11, 922.	1.1	9
1757	Spotlight on the Granules (Grainyhead-Like Proteins) – From an Evolutionary Conserved Controller of Epithelial Trait to Pioneering the Chromatin Landscape. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 213.	1.6	14
1758	DNA Methylation in Adipose Tissue and Metabolic Syndrome. <i>Journal of Clinical Medicine</i> , 2020, 9, 2699.	1.0	5
1759	Nutrition, Bioenergetics, and Metabolic Syndrome. <i>Nutrients</i> , 2020, 12, 2785.	1.7	26
1760	Maternal obesity is associated with a sex-specific epigenetic programming in human neonatal monocytes. <i>Epigenomics</i> , 2020, 12, 1999-2018.	1.0	4
1761	Epidrug Repurposing: Discovering New Faces of Old Acquaintances in Cancer Therapy. <i>Frontiers in Oncology</i> , 2020, 10, 605386.	1.3	44
1762	Circulating Cell-Free Tumour DNA for Early Detection of Pancreatic Cancer. <i>Cancers</i> , 2020, 12, 3704.	1.7	18
1763	Application of the MSAP Technique to Evaluate Epigenetic Changes in Plant Conservation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7459.	1.8	14
1764	Rapid miniaturization of <i>Salvelinus</i> fish as an adaptation to the volcanic impact. <i>Hydrobiologia</i> , 2020, 847, 2947-2962.	1.0	6
1765	Methylation of CpG sites in C1QTNF1 (C1q and tumor necrosis factor related protein 1) differs by gender in acute coronary syndrome in Han population: a case-control study. <i>Genes and Genomics</i> , 2020, 42, 681-689.	0.5	5
1766	DNA methylation dynamics underlie metamorphic gene regulation programs in <i>Xenopus</i> tadpole brain. <i>Developmental Biology</i> , 2020, 462, 180-196.	0.9	9
1767	The Effect of Chronic Mild Stress and Venlafaxine on the Expression and Methylation Levels of Genes Involved in the Tryptophan Catabolites Pathway in the Blood and Brain Structures of Rats. <i>Journal of Molecular Neuroscience</i> , 2020, 70, 1425-1436.	1.1	6

#	ARTICLE	IF	CITATIONS
1768	Biocatalytic Alkylation Cascades: Recent Advances and Future Opportunities for Late-Stage Functionalization. <i>ChemBioChem</i> , 2020, 21, 2890-2897.	1.3	29
1769	The Role of Stochasticity in the Origin of Epigenetic Variation in Animal Populations. <i>Integrative and Comparative Biology</i> , 2020, 60, 1544-1557.	0.9	10
1770	DNA hypomethylation of the Krüppel-like factor 11 (KLF11) gene promoter: a putative biomarker of depression comorbidity in panic disorder and of non-anxious depression?. <i>Journal of Neural Transmission</i> , 2020, 127, 1539-1546.	1.4	6
1771	The genome of the Cauliflower mosaic virus, a plant pararetrovirus, is highly methylated in the nucleus. <i>FEBS Letters</i> , 2020, 594, 1974-1988.	1.3	6
1772	DAMEfinder: a method to detect differential allele-specific methylation. <i>Epigenetics and Chromatin</i> , 2020, 13, 25.	1.8	13
1773	Establishment of diagnostic criteria for upper urinary tract urothelial carcinoma based on genome-wide DNA methylation analysis. <i>Epigenetics</i> , 2020, 15, 1289-1301.	1.3	9
1774	Epigenetic regulation of white adipose tissue in the onset of obesity and metabolic diseases. <i>Obesity Reviews</i> , 2020, 21, e13054.	3.1	8
1775	Epigenome-wide association study in healthy individuals identifies significant associations with DNA methylation and PBMC extract VEGF-A concentration. <i>Clinical Epigenetics</i> , 2020, 12, 79.	1.8	4
1776	Epigenetic Molecular Mechanisms in Insects. <i>Neotropical Entomology</i> , 2020, 49, 615-642.	0.5	27
1777	Hepatic DNA Methylation in Response to Early Stimulation of Microbiota with Lactobacillus Synbiotics in Broiler Chickens. <i>Genes</i> , 2020, 11, 579.	1.0	15
1778	Genome-Wide Identification and Characterization of DNA Methylation and Long Non-Coding RNA Expression in Gastric Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 91.	1.1	13
1779	Identification of a transcriptional regulatory module that reduces leaf temperature in poplar under heat stress. <i>Tree Physiology</i> , 2020, 40, 1108-1125.	1.4	5
1780	Intraspecific and interspecific investigations of skeletal DNA methylation and femur morphology in primates. <i>American Journal of Physical Anthropology</i> , 2020, 173, 34-49.	2.1	14
1781	Intramolecular Charge Transfer in 5-Halogen Cytidines Revealed by Femtosecond Time-Resolved Spectroscopy. <i>Journal of Physical Chemistry B</i> , 2020, 124, 2560-2567.	1.2	6
1782	Clinical significance of promoter methylation status of tumor suppressor genes in circulating DNA of pancreatic cancer patients. <i>Journal of Cancer Research and Clinical Oncology</i> , 2020, 146, 897-907.	1.2	39
1783	Genome-wide DNA Methylation Analysis of Mantle Edge and Mantle Central from Pearl Oyster <i>Pinctada fucata martensii</i> . <i>Marine Biotechnology</i> , 2020, 22, 380-390.	1.1	19
1784	Epigenetic engineering of yeast reveals dynamic molecular adaptation to methylation stress and genetic modulators of specific DNMT3 family members. <i>Nucleic Acids Research</i> , 2020, 48, 4081-4099.	6.5	16
1785	Comparative analysis of genome-wide DNA methylation in <i>Neurospora</i> . <i>Epigenetics</i> , 2020, 15, 972-987.	1.3	10

#	ARTICLE	IF	CITATIONS
1786	Characterization of Allele-Specific Regulation of Telomerase Reverse Transcriptase in Promoter Mutant Thyroid Cancer Cell Lines. <i>Thyroid</i> , 2020, 30, 1470-1481.	2.4	14
1787	Divergent DNA Methylation Signatures of Juvenile Seedlings, Grafts and Adult Apple Trees. <i>Epigenomes</i> , 2020, 4, 4.	0.8	12
1788	Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods. <i>PLoS Genetics</i> , 2020, 16, e1008864.	1.5	56
1789	Epigenetics for Clinicians from the Perspective of Pediatric Rheumatic Diseases. <i>Current Rheumatology Reports</i> , 2020, 22, 46.	2.1	5
1790	DeepH&M: Estimating single-CpG hydroxymethylation and methylation levels from enrichment and restriction enzyme sequencing methods. <i>Science Advances</i> , 2020, 6, .	4.7	8
1791	Methylation of Exogenous Promoters Regulates Soybean Isoflavone Synthase (GmIFS) Transgene in TO Transgenic Wheat (<i>Triticum aestivum</i>). <i>Cytology and Genetics</i> , 2020, 54, 271-282.	0.2	4
1792	The applied implications of epigenetics in anxiety, affective and stress-related disorders - A review and synthesis on psychosocial stress, psychotherapy and prevention. <i>Clinical Psychology Review</i> , 2020, 77, 101830.	6.0	76
1793	Effect of titanium dioxide nanoparticles on DNA methylation in multiple human cell lines. <i>Nanotoxicology</i> , 2020, 14, 534-553.	1.6	34
1794	Integrative analyses identify a DNA damage repair gene signature for prognosis prediction in lower grade gliomas. <i>Future Oncology</i> , 2020, 16, 367-382.	1.1	11
1795	A Deep Neural Network for Identifying DNA N4-Methylcytosine Sites. <i>Frontiers in Genetics</i> , 2020, 11, 209.	1.1	22
1796	Frequent methylation of the tumour suppressor miRâ€1258 targeting PDL1: implication in multiple myelomaâ€specific cytotoxicity and prognostification. <i>British Journal of Haematology</i> , 2020, 190, 249-261.	1.2	12
1797	Cytosine Methylation Affects the Mutability of Neighboring Nucleotides in Germline and Soma. <i>Genetics</i> , 2020, 214, 809-823.	1.2	16
1798	METTL14 suppresses proliferation and metastasis of colorectal cancer by down-regulating oncogenic long non-coding RNA XIST. <i>Molecular Cancer</i> , 2020, 19, 46.	7.9	336
1799	DNA methylation of the TERT promoter and its impact on human cancer. <i>Current Opinion in Genetics and Development</i> , 2020, 60, 17-24.	1.5	40
1800	Molecular markers of neuroendocrine function and mitochondrial biogenesis associated with early life stress. <i>Psychoneuroendocrinology</i> , 2020, 116, 104632.	1.3	15
1801	DFT Study on the Deglycosylation of Methylated, Oxidized, and Canonical Pyrimidine Nucleosides in Water: Implications for Epigenetic Regulation and DNA Repair. <i>Journal of Physical Chemistry B</i> , 2020, 124, 2392-2400.	1.2	3
1802	The Pattern and Function of DNA Methylation in Fungal Plant Pathogens. <i>Microorganisms</i> , 2020, 8, 227.	1.6	26
1803	LncRNA <i>Dnmt3a</i> regulates <i>Dnmt3a</i> expression leading to aberrant DNA methylation in macrophage polarization. <i>FASEB Journal</i> , 2020, 34, 5077-5091.	0.2	29

#	ARTICLE	IF	CITATIONS
1805	LINC00662 promotes hepatocellular carcinoma progression via altering genomic methylation profiles. <i>Cell Death and Differentiation</i> , 2020, 27, 2191-2205.	5.0	44
1806	DNA Methylation Is Correlated with Gene Expression during Diapause Termination of Early Embryonic Development in the Silkworm (<i>Bombyx mori</i>). <i>International Journal of Molecular Sciences</i> , 2020, 21, 671.	1.8	14
1807	DNA methylation in Schwann cells and in oligodendrocytes. <i>Glia</i> , 2020, 68, 1568-1583.	2.5	10
1808	The regulatory function of dlno80 correlates with its DNA binding activity. <i>Gene</i> , 2020, 732, 144368.	1.0	1
1809	Genetic and epigenetic stability of stem cells: Epigenetic modifiers modulate the fate of mesenchymal stem cells. <i>Genomics</i> , 2020, 112, 3615-3623.	1.3	19
1810	General DNA Methylation Patterns and Environmentally-Induced Differential Methylation in the Eastern Oyster (<i>Crassostrea virginica</i>). <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	28
1811	Air Exposure Affects Physiological Responses, Innate Immunity, Apoptosis and DNA Methylation of Kuruma Shrimp, <i>Marsupenaeus japonicus</i> . <i>Frontiers in Physiology</i> , 2020, 11, 223.	1.3	16
1812	i4mC-Mouse: Improved identification of DNA N4-methylcytosine sites in the mouse genome using multiple encoding schemes. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 906-912.	1.9	57
1813	DNA methylation patterns in the tobacco budworm, <i>Chloridea virescens</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2020, 121, 103370.	1.2	1
1814	The myonuclear DNA methylome in response to an acute hypertrophic stimulus. <i>Epigenetics</i> , 2020, 15, 1151-1162.	1.3	27
1815	Gene Duplication in the Honeybee: Patterns of DNA Methylation, Gene Expression, and Genomic Environment. <i>Molecular Biology and Evolution</i> , 2020, 37, 2322-2331.	3.5	16
1816	Sources of epigenetic variation and their applications in natural populations. <i>Evolutionary Applications</i> , 2020, 13, 1262-1278.	1.5	40
1817	Codon usage bias affects α -amylase mRNA level by altering RNA stability and cytosine methylation patterns in <i>Escherichia coli</i> . <i>Canadian Journal of Microbiology</i> , 2020, 66, 521-528.	0.8	4
1818	Integrative Analysis of Methylome and Transcriptome Reveals the Regulatory Mechanisms of Hair Follicle Morphogenesis in Cashmere Goat. <i>Cells</i> , 2020, 9, 969.	1.8	25
1819	Integration of whole-genome DNA methylation data with RNA sequencing data to identify markers for bull fertility. <i>Animal Genetics</i> , 2020, 51, 502-510.	0.6	17
1820	Pilot study of combined aerobic and resistance exercise on fatigue for patients with head and neck cancer: Inflammatory and epigenetic changes. <i>Brain, Behavior, and Immunity</i> , 2020, 88, 184-192.	2.0	11
1821	DNA Methylation Inhibits the Expression of CFSH in Mud Crab. <i>Frontiers in Endocrinology</i> , 2020, 11, 163.	1.5	10
1822	Perfluorooctanoic acid (PFOA) exposure inhibits DNA methyltransferase activities and alters constitutive heterochromatin organization. <i>Food and Chemical Toxicology</i> , 2020, 141, 111358.	1.8	17

#	ARTICLE	IF	CITATIONS
1823	The DNA hypermethylation phenotype of colorectal cancer liver metastases resembles that of the primary colorectal cancers. <i>BMC Cancer</i> , 2020, 20, 290.	1.1	13
1824	Epigenetics Underlying Susceptibility and Resilience Relating to Daily Life Stress, Work Stress, and Socioeconomic Status. <i>Frontiers in Psychiatry</i> , 2020, 11, 163.	1.3	37
1825	Interaction of <i>DRD4</i> Methylation and Phthalate Metabolites Affects Continuous Performance Test Performance in ADHD. <i>Journal of Attention Disorders</i> , 2021, 25, 161-170.	1.5	4
1826	Serotonin Transporter Gene Promoter Hypomethylation as a Predictor of Antidepressant Treatment Response in Major Depression: A Replication Study. <i>International Journal of Neuropsychopharmacology</i> , 2021, 24, 191-199.	1.0	19
1827	Differential DNA methylomes of clinical MDR, XDR and XXDR <i>Mycobacterium tuberculosis</i> isolates revealed by using single-molecule real-time sequencing. <i>Journal of Drug Targeting</i> , 2021, 29, 69-77.	2.1	6
1828	Epigenetic Neuropharmacology: Drugs Affecting the Epigenome in the Brain. <i>Annual Review of Pharmacology and Toxicology</i> , 2021, 61, 181-201.	4.2	12
1829	Maternal exposure to phenanthrene during gestation disturbs glucose homeostasis in adult mouse offspring. <i>Chemosphere</i> , 2021, 270, 128635.	4.2	8
1830	Effect of mobile phone signal radiation on epigenetic modulation in the hippocampus of Wistar rat. <i>Environmental Research</i> , 2021, 192, 110297.	3.7	15
1831	DNA methylation changes in response to ocean acidification at the time of larval metamorphosis in the edible oyster, <i>Crassostrea hongkongensis</i> . <i>Marine Environmental Research</i> , 2021, 163, 105217.	1.1	11
1832	Cause and effect in epigenetics “where lies the truth, and how can experiments reveal it?”. <i>BioEssays</i> , 2021, 43, e2000262.	1.2	3
1833	Increased isoform-specific phosphodiesterase 4D expression is associated with pathology and cognitive impairment in Alzheimer’s disease. <i>Neurobiology of Aging</i> , 2021, 97, 56-64.	1.5	15
1834	DNA methylation changes in response to ocean acidification at the time of larval metamorphosis in the edible oyster, <i>Crassostrea hongkongensis</i> . <i>Marine Environmental Research</i> , 2021, 163, 105214.	1.1	14
1835	DNA methylation signatures of autoimmune diseases in human B lymphocytes. <i>Clinical Immunology</i> , 2021, 222, 108622.	1.4	21
1836	Role of GABRD Gene Methylation in the Nucleus Accumbens in Heroin-Seeking Behavior in Rats. <i>Frontiers in Pharmacology</i> , 2021, 11, 612200.	1.6	10
1837	One Carbon Metabolism and Mammalian Pregnancy Outcomes. <i>Molecular Nutrition and Food Research</i> , 2021, 65, e2000734.	1.5	20
1838	The use of DNA methylation clock in aging research. <i>Experimental Biology and Medicine</i> , 2021, 246, 436-446.	1.1	12
1839	Expression of MAP9 in Epstein-Barr virus-associated gastric carcinoma. <i>Virus Research</i> , 2021, 293, 198253.	1.1	2
1840	Comparative genome-wide methylation analysis of longissimus dorsi muscles in Yorkshire and Wannanhu pigs. <i>Animal Genetics</i> , 2021, 52, 78-89.	0.6	9

#	ARTICLE	IF	CITATIONS
1841	Tracking the time-dependent and tissue-specific processes of arsenic accumulation and stress responses in rice (<i>Oryza sativa</i> L.). <i>Journal of Hazardous Materials</i> , 2021, 406, 124307.	6.5	22
1843	Environmental and socio-cultural impacts on global DNA methylation in the indigenous Huichol population of Nayarit, Mexico. <i>Environmental Science and Pollution Research</i> , 2021, 28, 4472-4487.	2.7	5
1844	Genome-wide DNA methylation alteration in prenatally stressed Brahman heifer calves with the advancement of age. <i>Epigenetics</i> , 2021, 16, 519-536.	1.3	4
1845	The potential association between <i>Wolbachia</i> infection and DNA methylation in <i>Hylyphantes graminicola</i> (Araneae: Linyphiidae). <i>Symbiosis</i> , 2021, 83, 183-191.	1.2	0
1846	Childhood DNA methylation as a marker of early life rapid weight gain and subsequent overweight. <i>Clinical Epigenetics</i> , 2021, 13, 8.	1.8	11
1847	DNA Methylation may be a testicular plateau adaptation in Tibetan pig. <i>Journal of Applied Animal Research</i> , 2021, 49, 62-67.	0.4	0
1848	The Great Pond Snail (<i>Lymnaea stagnalis</i>) as a Model of Aging and Age-Related Memory Impairment: An Overview. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021, 76, 975-982.	1.7	8
1849	Opinion: Genetic Conflict With Mobile Elements Drives Eukaryotic Genome Evolution, and Perhaps Also Eukaryogenesis. <i>Journal of Heredity</i> , 2021, 112, 140-144.	1.0	8
1850	Stem cell epigenetics in medical therapy. , 2021, , 873-884.		0
1851	Regulation of RNA Stability Through RNA Modification. <i>RNA Technologies</i> , 2021, , 217-246.	0.2	1
1852	The chromosomal protein SMCHD1 regulates DNA methylation and the 2c-like state of embryonic stem cells by antagonizing TET proteins. <i>Science Advances</i> , 2021, 7, .	4.7	28
1853	DIM5/KMT1 controls fungal insect pathogenicity and genome stability by methylation of histone H3K4, H3K9 and H3K36. <i>Virulence</i> , 2021, 12, 1306-1322.	1.8	11
1854	Gene regulation by H2S in plants. , 2021, , 171-199.		9
1855	A comprehensive epigenome atlas reveals DNA methylation regulating skeletal muscle development. <i>Nucleic Acids Research</i> , 2021, 49, 1313-1329.	6.5	68
1856	Epigenetic regulations in gastrointestinal: Implications on sensitivity to ionizing radiation, inflammatory diseases, and cancer development. , 2021, , 199-235.		0
1857	The emergence of the brain non-CpG methylation system in vertebrates. <i>Nature Ecology and Evolution</i> , 2021, 5, 369-378.	3.4	63
1858	Epigenetics, estrogenic endocrine-disrupting chemicals (EDCs), and the brain. <i>Advances in Pharmacology</i> , 2021, 92, 73-99.	1.2	14
1859	epihet for intra-tumoral epigenetic heterogeneity analysis and visualization. <i>Scientific Reports</i> , 2021, 11, 376.	1.6	6

#	ARTICLE	IF	CITATIONS
1860	A far-red emissive two-photon fluorescent probe for quantification of uracil in genomic DNA. <i>Chemical Communications</i> , 2021, 57, 2784-2787.	2.2	0
1861	Heritability of DNA methylation in threespine stickleback (<i>Gasterosteus aculeatus</i>). <i>Genetics</i> , 2021, 217, 1-15.	1.2	31
1862	Distinct Responses of Arabidopsis Telomeres and Transposable Elements to Zebularine Exposure. <i>International Journal of Molecular Sciences</i> , 2021, 22, 468.	1.8	7
1864	Population Genomics of Peanut. <i>Population Genomics</i> , 2021, , 1.	0.2	3
1865	Calling differentially methylated regions from whole genome bisulphite sequencing with DMRcate. <i>Nucleic Acids Research</i> , 2021, 49, e109-e109.	6.5	31
1866	Intragenic DNA methylation regulates insect gene expression and reproduction through the MBD/Tip60 complex. <i>IScience</i> , 2021, 24, 102040.	1.9	27
1867	Genetic Background Effects on the Expression of an Odorant Receptor Gene. <i>Frontiers in Cellular Neuroscience</i> , 2021, 15, 646413.	1.8	0
1868	Integrative analysis of genome-wide DNA methylation and gene expression profiles reveals important epigenetic genes related to milk production traits in dairy cattle. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 562-573.	0.8	8
1869	Rapid changes in DNA methylation associated with the initiation of reproduction in a small songbird. <i>Molecular Ecology</i> , 2021, 30, 3645-3659.	2.0	24
1870	Causal roles of stress kinase JNK2 in DNA methylation and binge alcohol withdrawal-evoked behavioral deficits. <i>Pharmacological Research</i> , 2021, 164, 105375.	3.1	3
1871	Study of Sexual-Linked Genes (OGI and MeGI) on the Performance of Androecious Persimmons (<i>Diospyros kaki</i> Thunb.). <i>Plants</i> , 2021, 10, 390.	1.6	2
1872	JKAMP inhibits the osteogenic capacity of adipose-derived stem cells in diabetic osteoporosis by modulating the Wnt signaling pathway through intragenic DNA methylation. <i>Stem Cell Research and Therapy</i> , 2021, 12, 120.	2.4	16
1873	Epigenetic responses of hare barley (<i>Hordeum murinum</i> subsp. <i>leporinum</i>) to climate change: an experimental, trait-based approach. <i>Heredity</i> , 2021, 126, 748-762.	1.2	11
1877	DNA methylation impact on Fabry disease. <i>Clinical Epigenetics</i> , 2021, 13, 24.	1.8	16
1878	Molecular mechanism for vitamin C-derived C5-glyceryl-methylcytosine DNA modification catalyzed by algal TET homologue CMD1. <i>Nature Communications</i> , 2021, 12, 744.	5.8	12
1879	Increased transcript expression levels of DNA methyltransferases type 1 and 3A during cardiac muscle long-term cell culture. <i>Medical Journal of Cell Biology (discontinued)</i> , 2021, 9, 27-32.	0.2	1
1880	Toward incorporating epigenetics into regulation of gene expression in the parasite <i>Trichomonas vaginalis</i> . <i>Molecular Microbiology</i> , 2021, 115, 959-967.	1.2	2
1881	Cloning, expression and functional analysis of the desert hedgehog (<i>dhh</i>) gene in Chinese tongue sole (<i>Cynoglossus semilaevis</i>). <i>Gene Expression Patterns</i> , 2021, 39, 119163.	0.3	3

#	ARTICLE	IF	CITATIONS
1883	Current Advances in DNA Methylation Analysis Methods. <i>BioMed Research International</i> , 2021, 2021, 1-9.	0.9	16
1884	The Tumor Suppressor MTUS1/ATIP1 Modulates Tumor Promotion in Glioma: Association with Epigenetics and DNA Repair. <i>Cancers</i> , 2021, 13, 1245.	1.7	8
1885	How do established developmental risk-factors for schizophrenia change the way the brain develops?. <i>Translational Psychiatry</i> , 2021, 11, 158.	2.4	24
1886	Cell-free DNA methylome profiling by MBD-seq with ultra-low input. <i>Epigenetics</i> , 2022, 17, 239-252.	1.3	14
1887	Sex-specific expression and DNA methylation in a species with extreme sexual dimorphism and paternal genome elimination. <i>Molecular Ecology</i> , 2021, 30, 5687-5703.	2.0	29
1888	On the Role of Transposable Elements in the Regulation of Gene Expression and Subgenomic Interactions in Crop Genomes. <i>Critical Reviews in Plant Sciences</i> , 2021, 40, 157-189.	2.7	28
1889	Evaluation of genome-wide DNA methylation profile of human embryos with different developmental competences. <i>Human Reproduction</i> , 2021, 36, 1682-1690.	0.4	8
1890	The role of epigenetics, particularly DNA methylation, in the evolution of caste in insect societies. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200115.	1.8	40
1891	Intelligent analysis of methylation data in Head and Neck Squamous Cell Carcinoma (HNSCC) interactomes. , 2021, , .		0
1893	Identification, methylation profiling, and expression analysis of stress-responsive cytochrome P450 genes in rice under abiotic and phytohormones stresses. <i>GM Crops and Food</i> , 2021, 12, 551-563.	2.0	6
1894	Epigenetics in Necrotizing Enterocolitis. <i>Current Pediatric Reviews</i> , 2021, 17, 172-184.	0.4	5
1895	A New Approach to Identify the Methylation Sites in the Control Region of Mitochondrial DNA. <i>Current Molecular Medicine</i> , 2021, 21, 151-164.	0.6	1
1896	Dynamics of m6A RNA Methylome on the Hallmarks of Hepatocellular Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 642443.	1.8	13
1897	DNMT3.1 controls trade-offs between growth, reproduction, and life span under starved conditions in <i>Daphnia magna</i> . <i>Scientific Reports</i> , 2021, 11, 7326.	1.6	7
1898	The interplay between DNA and histone methylation: molecular mechanisms and disease implications. <i>EMBO Reports</i> , 2021, 22, e51803.	2.0	83
1901	RNF217 regulates iron homeostasis through its E3 ubiquitin ligase activity by modulating ferroportin degradation. <i>Blood</i> , 2021, 138, 689-705.	0.6	56
1902	Could Changing the DNA Methylation Landscape Promote the Destruction of Epstein-Barr Virus-Associated Cancers?. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 695093.	1.8	3
1903	Epigenetic regulation of drosophila germline stem cell maintenance and differentiation. <i>Developmental Biology</i> , 2021, 473, 105-118.	0.9	18

#	ARTICLE	IF	CITATIONS
1904	Halophytes and other molecular strategies for the generation of salt-tolerant crops. <i>Plant Physiology and Biochemistry</i> , 2021, 162, 581-591.	2.8	14
1905	Intestinal mucosa-derived DNA methylation signatures in the penetrating intestinal mucosal lesions of Crohn's disease. <i>Scientific Reports</i> , 2021, 11, 9771.	1.6	8
1906	Identification of Putative Virulence Genes by DNA Methylation Studies in the Cereal Pathogen <i>Fusarium graminearum</i> . <i>Cells</i> , 2021, 10, 1192.	1.8	4
1907	PUM1 is upregulated by DNA methylation to suppress antitumor immunity and results in poor prognosis in pancreatic cancer. <i>Translational Cancer Research</i> , 2021, 10, 2153-2168.	0.4	8
1908	Conserved noncoding sequences provide insights into regulatory sequence and loss of gene expression in maize. <i>Genome Research</i> , 2021, 31, 1245-1257.	2.4	29
1909	Heat stress and immune response phenotype affect DNA methylation in blood mononuclear cells from Holstein dairy cows. <i>Scientific Reports</i> , 2021, 11, 11371.	1.6	18
1910	Increased PARylation impacts the DNA methylation process in type 2 diabetes mellitus. <i>Clinical Epigenetics</i> , 2021, 13, 114.	1.8	11
1912	Epigenetic Effects of Benzene in Hematologic Neoplasms: The Altered Gene Expression. <i>Cancers</i> , 2021, 13, 2392.	1.7	14
1913	Circulating Biomarkers of CDK4/6 Inhibitors Response in Hormone Receptor Positive and HER2 Negative Breast Cancer. <i>Cancers</i> , 2021, 13, 2640.	1.7	8
1914	Impact of DNA methylation on 3D genome structure. <i>Nature Communications</i> , 2021, 12, 3243.	5.8	61
1915	iRG-4mC: Neural Network Based Tool for Identification of DNA 4mC Sites in Rosaceae Genome. <i>Symmetry</i> , 2021, 13, 899.	1.1	10
1916	Molecular Complexes at Euchromatin, Heterochromatin and Centromeric Chromatin. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6922.	1.8	35
1917	A Luciferase-EGFP Reporter System for the Evaluation of DNA Methylation in Mammalian Cells. <i>Molecular Biology</i> , 2021, 55, 742-751.	0.4	3
1918	Toward personalized medicine in schizophrenia: Genetics and epigenetics of antipsychotic treatment. <i>Schizophrenia Research</i> , 2021, 232, 112-124.	1.1	28
1919	A comprehensive database for integrated analysis of omics data in autoimmune diseases. <i>BMC Bioinformatics</i> , 2021, 22, 343.	1.2	12
1920	Islet Epigenetic Impacts on β -Cell Identity and Function. , 2021, 11, 1961-1978.		0
1921	Early-life phenanthrene exposure inhibits reproductive ability in adult zebrafish and the mechanism of action. <i>Chemosphere</i> , 2021, 272, 129635.	4.2	18
1922	Cytosine base modifications regulate DNA duplex stability and metabolism. <i>Nucleic Acids Research</i> , 2021, 49, 12870-12894.	6.5	21

#	ARTICLE	IF	CITATIONS
1923	Cognizance of posttranslational modifications in vaccines: A way to enhanced immunogenicity. <i>Journal of Cellular Physiology</i> , 2021, , .	2.0	10
1924	Long Non-Coding RNA Epigenetics. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6166.	1.8	23
1925	Computational Insights into Molecular Adsorption Characteristics of Methylated DNA on Graphene Oxide for Multicancer Early Detection. <i>Journal of Physical Chemistry B</i> , 2021, 125, 6697-6708.	1.2	8
1928	DNA Hypermethylation Involves in the Down-Regulation of Chloride Intracellular Channel 4 (CLIC4) Induced by Photodynamic Therapy. <i>Biomedicines</i> , 2021, 9, 927.	1.4	1
1929	Identification potential epigenetic biomarkers of a human immunodeficiency virus/tuberculosis co-infection based on weighted gene co-expression network analysis. <i>Microbiology and Immunology</i> , 2021, 65, 422-431.	0.7	3
1930	Diagnostic value of neuronal pentraxin II methylation in patients with pancreatic cancer: Meta-analysis. <i>International Journal of Clinical Practice</i> , 2021, 75, e14443.	0.8	0
1931	Genome-Wide Correlation of DNA Methylation and Gene Expression in Postmortem Brain Tissues of Opioid Use Disorder Patients. <i>International Journal of Neuropsychopharmacology</i> , 2021, 24, 879-891.	1.0	29
1932	NF- κ B-mediated TET2-dependent TNF promoter demethylation drives Mtb upregulation TNF expression in macrophages. <i>Tuberculosis</i> , 2021, 129, 102108.	0.8	1
1933	The Molecular Basis of Depression: Implications of Sex-Related Differences in Epigenetic Regulation. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 708004.	1.4	11
1934	Multi-omics analyses on <i>Kandelia obovata</i> reveal its response to transplanting and genetic differentiation among populations. <i>BMC Plant Biology</i> , 2021, 21, 341.	1.6	4
1935	Chromatin Dynamics and Gene Expression Response to Heat Exposure in Field-Conditioned versus Laboratory-Cultured <i>Nematostella vectensis</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 7454.	1.8	4
1936	Integrative methylome-transcriptome analysis unravels cancer cell vulnerabilities in infant MLL-rearranged B cell acute lymphoblastic leukemia. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	14
1937	Gly, GlyGly, and GlyAsp Modulate Expression of Genes of the SNF2 Family and DNA Methyltransferases in Regenerants from Calluses of Tobacco <i>Nicotiana tabacum</i> . <i>Biology Bulletin</i> , 2021, 48, 450-458.	0.1	1
1938	Nuclear Organization during Hepatogenesis in Zebrafish Requires Uhrf1. <i>Genes</i> , 2021, 12, 1081.	1.0	4
1939	Dnmt3b Deficiency in Myf5+ Brown Fat Precursor Cells Promotes Obesity in Female Mice. <i>Biomolecules</i> , 2021, 11, 1087.	1.8	8
1940	Computational Probing the Methylation Sites Related to EGFR Inhibitor-Responsive Genes. <i>Biomolecules</i> , 2021, 11, 1042.	1.8	2
1941	Quantum squirrel inspired algorithm for gene selection in methylation and expression data of prostate cancer. <i>Applied Soft Computing Journal</i> , 2021, 105, 107221.	4.1	16
1944	Introduction to Single-Cell DNA Methylation Profiling Methods. <i>Biomolecules</i> , 2021, 11, 1013.	1.8	35

#	ARTICLE	IF	CITATIONS
1945	Epigenetic regulation of gene expression in response to environmental exposures: From bench to model. <i>Science of the Total Environment</i> , 2021, 776, 145998.	3.9	15
1946	Doxorubicin-induced cardiotoxicity: An update on the molecular mechanism and novel therapeutic strategies for effective management. <i>Biomedicine and Pharmacotherapy</i> , 2021, 139, 111708.	2.5	296
1947	Inferring Functional Epigenetic Modules by Integrative Analysis of Multiple Heterogeneous Networks. <i>Frontiers in Genetics</i> , 2021, 12, 706952.	1.1	0
1948	Heat and Hypoxia Exposure Mediates Circadian Rhythms Response via Methylation Modification in <i>Apostichopus japonicas</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	2
1949	Epigenetics Is Implicated in the Basis of Gender Incongruence: An Epigenome-Wide Association Analysis. <i>Frontiers in Neuroscience</i> , 2021, 15, 701017.	1.4	22
1950	Assessment of quality attributes for adeno-associated viral vectors. <i>Biotechnology and Bioengineering</i> , 2021, 118, 4186-4203.	1.7	22
1952	A systematic analysis of <i>Trypanosoma brucei</i> chromatin factors identifies novel protein interaction networks associated with sites of transcription initiation and termination. <i>Genome Research</i> , 2021, 31, 2138-2154.	2.4	33
1953	Gene Body Methylation of the Lymphocyte-Specific Gene <i>CARD11</i> Results in Its Overexpression and Regulates Cancer mTOR Signaling. <i>Molecular Cancer Research</i> , 2022, 19, 1917-1928.	1.5	3
1954	Progression in Alzheimer's Disease Correlates With Epigenetics and Cerebral Formaldehyde: From Potential Hereditary Mechanism and Environmental Factors to Therapeutic Measures. <i>Current Pharmacology Reports</i> , 2021, 7, 187.	1.5	0
1955	Spatial Learning Is Associated with Antagonist Outcomes for DNA Methylation and DNA Hydroxymethylation in the Transcriptional Regulation of the Ryanodine Receptor 3. <i>Neural Plasticity</i> , 2021, 2021, 1-8.	1.0	1
1957	Dual-modality loop-mediated isothermal amplification for pretreatment-free detection of Septin9 methylated DNA in colorectal cancer. <i>Mikrochimica Acta</i> , 2021, 188, 307.	2.5	6
1958	Epigenetic Basis of Psychiatric Disorders: A Narrative Review. <i>CNS and Neurological Disorders - Drug Targets</i> , 2022, 21, 302-315.	0.8	4
1959	DNA methylation atlas and machinery in the developing and regenerating annelid <i>Platynereis dumerilii</i> . <i>BMC Biology</i> , 2021, 19, 148.	1.7	18
1960	DNA Methylation of Fibroblast Phenotypes and Contributions to Lung Fibrosis. <i>Cells</i> , 2021, 10, 1977.	1.8	3
1961	Ten Years of EWAS. <i>Advanced Science</i> , 2021, 8, e2100727.	5.6	18
1962	DNA Methyltransferases Regulate Pathogenicity of <i>Botrytis cinerea</i> to Horticultural Crops. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 659.	1.5	7
1963	Epigenetic Mediation of AKT1 rs1130233's Effect on Delta-9-Tetrahydrocannabinol-Induced Medial Temporal Function during Fear Processing. <i>Brain Sciences</i> , 2021, 11, 1240.	1.1	6
1964	Gene body methylation safeguards ribosomal DNA transcription by preventing PHF6-mediated enrichment of repressive histone mark H4K20me3. <i>Journal of Biological Chemistry</i> , 2021, 297, 101195.	1.6	12

#	ARTICLE	IF	CITATIONS
1966	Changes in Methylation Patterns of Tumor Suppressor Genes during Extended Human Embryonic Stem Cell Cultures. <i>Stem Cells International</i> , 2021, 2021, 1-8.	1.2	0
1967	Environmental enrichment during early rearing provokes epigenetic changes in the brain of a salmonid fish. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 39, 100838.	0.4	7
1968	The first mitochondrial 5-methylcytosine map in a non-model teleost (<i>Oreochromis niloticus</i>) reveals extensive strand-specific and non-CpG methylation. <i>Genomics</i> , 2021, 113, 3050-3057.	1.3	6
1969	Epigenome plasticity in plants. <i>Nature Reviews Genetics</i> , 2022, 23, 55-68.	7.7	73
1970	Performance of methods to detect genetic variants from bisulphite sequencing data in a non-model species. <i>Molecular Ecology Resources</i> , 2022, 22, 834-846.	2.2	10
1971	Methylation Modelling and Epigenetic Analysis of Sunflower (<i>Helianthus annuus</i> L.) Seedlings Exposed to Cadmium Heavy Metal Stress. <i>Kahramanmaraş Sâdîk Âlî Şâhî 4 Âmam Âeniversitesi Tarâm Ve DoĀa Dergisi</i> , 2022, 25, 467-475.		4
1972	Epigenetic regulation in Huntington's disease. <i>Neurochemistry International</i> , 2021, 148, 105074.	1.9	14
1973	Genetic Variations and Differential DNA Methylation to Face Contrasted Climates in Small Ruminants: An Analysis on Traditionally-Managed Sheep and Goats. <i>Frontiers in Genetics</i> , 2021, 12, 745284.	1.1	4
1974	Evolution of CG Methylation Maintenance Machinery in Plants. <i>Epigenomes</i> , 2021, 5, 19.	0.8	11
1975	Associations between childhood maltreatment and DNA methylation of the oxytocin receptor gene in immune cells of mother-newborn dyads. <i>Translational Psychiatry</i> , 2021, 11, 449.	2.4	17
1976	DNA methylation changes following narrative exposure therapy in a randomized controlled trial with female former child soldiers. <i>Scientific Reports</i> , 2021, 11, 18493.	1.6	8
1977	DNA Demethylation in the Processes of Repair and Epigenetic Regulation Performed by 2-Ketoglutarate-Dependent DNA Dioxygenases. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10540.	1.8	6
1978	Evaluating of the Oxytocin Gene and the Region. <i>Methods in Molecular Biology</i> , 2022, 2384, 81-103.	0.4	0
1979	A semiparametric isotonic regression model for skewed distributions with application to DNA-RNA-protein analysis. <i>Biometrics</i> , 2022, 78, 1464-1474.	0.8	0
1980	Ecotoxicological epigenetics in invertebrates: Emerging tool for the evaluation of present and past pollution burden. <i>Chemosphere</i> , 2021, 282, 131026.	4.2	23
1981	Gene regulation by NO in plants. , 2022, , 615-651.		5
1982	Characterization of the effects of age and childhood maltreatment on ELOVL2 DNA methylation. <i>Development and Psychopathology</i> , 2021, , 1-11.	1.4	1
1983	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	95

#	ARTICLE	IF	CITATIONS
1984	Identifying DNA N4-methylcytosine sites in the rosaceae genome with a deep learning model relying on distributed feature representation. Computational and Structural Biotechnology Journal, 2021, 19, 1612-1619.	1.9	21
1985	<i>e</i> -MagnetoMethyl IP: a magnetic nanoparticle-mediated immunoprecipitation and electrochemical detection method for global DNA methylation. Analyst, The, 2021, 146, 3654-3665.	1.7	3
1986	Epigenetic regulation in stem cells. , 2021, , 69-79.		1
1987	Computational identification of N4-methylcytosine sites in the mouse genome with machine-learning method. Mathematical Biosciences and Engineering, 2021, 18, 3348-3363.	1.0	13
1988	DNA sequences performs as natural language processing by exploiting deep learning algorithm for the identification of N4-methylcytosine. Scientific Reports, 2021, 11, 212.	1.6	25
1989	Epigenetics in systemic lupus erythematosus and the integration of molecular pathways. , 2021, , 35-61.		0
1990	Structural dynamics of DNA depending on methylation pattern. Physical Review E, 2021, 103, 012404.	0.8	4
1991	TET3 dioxygenase modulates gene conversion at the avian immunoglobulin variable region via demethylation of nonâ€CpG sites in pseudogene templates. Genes To Cells, 2021, 26, 121-135.	0.5	3
1992	MECHANISMS IN ENDOCRINOLOGY: Pioneer transcription factors in pituitary development and tumorigenesis. European Journal of Endocrinology, 2021, 184, R1-R15.	1.9	4
1993	Prospective advances in medical epigenetics. , 2021, , 919-935.		0
1995	Detection of DNA Methylation by MeDIP and MBDCap Assays: An Overview of Techniques. Methods in Molecular Biology, 2020, 2102, 225-234.	0.4	9
1996	Genetics and Epigenetics of Head and Neck Cancer. , 2011, , 93-106.		1
1997	Advances in Host and Vector Development for the Production of Plasmid DNA Vaccines. Methods in Molecular Biology, 2014, 1139, 505-541.	0.4	20
1998	Epigenetics in Childhood Health and Disease. , 2014, , 1-62.		2
1999	Whole-Genome DNA Methylation Profiling with Nucleotide Resolution. Methods in Molecular Biology, 2015, 1284, 27-40.	0.4	4
2000	Methylated DNA Immunoprecipitation and Microarray-Based Analysis: Detection of DNA Methylation in Breast Cancer Cell Lines. Methods in Molecular Biology, 2009, 590, 165-176.	0.4	50
2001	Methylated DNA Immunoprecipitation Genome-Wide Analysis. Methods in Molecular Biology, 2011, 791, 113-123.	0.4	2
2002	Automated Computational Analysis of Genome-Wide DNA Methylation Profiling Data from HELP-Tagging Assays. Methods in Molecular Biology, 2012, 815, 79-87.	0.4	13

#	ARTICLE	IF	CITATIONS
2003	Analysis of Genome-Wide DNA Methylation Profiles by BeadChip Technology. <i>Methods in Molecular Biology</i> , 2013, 1049, 21-33.	0.4	2
2004	Breast Cancer Epigenetics: Biomarkers and Therapeutic Potential. , 2013, , 211-259.		1
2005	Methyl-Combing: Single-Molecule Analysis of DNA Methylation on Stretched DNA Fibers. <i>Methods in Molecular Biology</i> , 2014, 1094, 233-241.	0.4	3
2006	Detection of DNA Methylation by MeDIP and MBDCap Assays: An Overview of Techniques. <i>Methods in Molecular Biology</i> , 2014, 1105, 61-70.	0.4	18
2007	Origin and Mechanisms of DNA Methylation Dynamics in Cancers. <i>RNA Technologies</i> , 2019, , 27-52.	0.2	2
2008	Targeting DNA Hypomethylation in Malignancy by Epigenetic Therapies. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1164, 179-196.	0.8	27
2009	A Stochastic Model for the Formation of Spatial Methylation Patterns. <i>Lecture Notes in Computer Science</i> , 2017, , 160-178.	1.0	6
2010	Future Directions: Gene Polymorphism Diagnostics Relevant to Hair. , 2010, , 221-232.		2
2011	Root Apical Meristem Pattern: Hormone Circuitry and Transcriptional Networks. <i>Progress in Botany Fortschritte Der Botanik</i> , 2010, , 37-71.	0.1	4
2012	Toward an Understanding of the Dynamic Interdependence of Genes and Environment in the Regulation of Phenotype. , 2011, , 209-243.		5
2013	Chromatin Organization and the Mammalian Nucleolus. , 2013, , 119-148.		5
2014	Characterization of DNA methylation variations during fruit development and ripening of <i>Vitis vinifera</i> (cv. "Fujiminori"). <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 617-637.	1.4	13
2015	Aluminum-Induced Changes on DNA Damage, DNA Methylation and LTR Retrotransposon Polymorphism in Maize. <i>Arabian Journal for Science and Engineering</i> , 2018, 43, 123-131.	1.7	34
2016	ATP Hydrolysis by the SNF2 Domain of Dnmt5 Is Coupled to Both Specific Recognition and Modification of Hemimethylated DNA. <i>Molecular Cell</i> , 2020, 79, 127-139.e4.	4.5	15
2017	DNA N6-methyladenine in metazoans: functional epigenetic mark or bystander?. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 503-506.	3.6	73
2018	Detecting methylation signatures in neurodegenerative disease by density-based clustering of applications with reducing noise. <i>Scientific Reports</i> , 2020, 10, 22164.	1.6	7
2019	Environmental epigenomics: understanding the effects of parental care on the epigenome. <i>Essays in Biochemistry</i> , 2010, 48, 275-287.	2.1	32
2020	Epigenetics in bipolar disorder: a critical review of the literature. <i>Psychiatric Genetics</i> , 2021, 31, 1-12.	0.6	22

#	ARTICLE	IF	CITATIONS
2037	Structure and function of dioxygenases in histone demethylation and DNA/RNA demethylation. <i>IUCr</i> , 2014, 1, 540-549.	1.0	26
2038	Prospects for incorporation of epigenetic biomarkers in human health and environmental risk assessment of chemicals. <i>Biological Reviews</i> , 2020, 95, 822-846.	4.7	19
2039	DNA Methylation Epigenetically Regulates Gene Expression in <i>Burkholderia cenocepacia</i> and Controls Biofilm Formation, Cell Aggregation, and Motility. <i>MSphere</i> , 2020, 5, .	1.3	13
2040	Experimental Treatment with a Hypomethylating Agent Alters Life History Traits and Fitness in <i>Brassica rapa</i> . <i>Journal of Botany</i> , 2018, 2018, 1-10.	1.2	5
2041	Epigenetic regulation of macrophage polarization and inflammation by DNA methylation in obesity. <i>JCI Insight</i> , 2016, 1, e87748.	2.3	138
2042	Methylation of immune synapse genes modulates tumor immunogenicity. <i>Journal of Clinical Investigation</i> , 2020, 130, 974-980.	3.9	34
2044	intePareto: an R package for integrative analyses of RNA-Seq and CHIP-Seq data. <i>BMC Genomics</i> , 2020, 21, 802.	1.2	11
2045	Genome-wide methylation and transcriptome of blood neutrophils reveal the roles of DNA methylation in affecting transcription of protein-coding genes and miRNAs in <i>E. coli</i> -infected mastitis cows. <i>BMC Genomics</i> , 2020, 21, 102.	1.2	31
2046	Detection and analysis of RNA methylation. <i>F1000Research</i> , 2019, 8, 559.	0.8	36
2047	Correlation between miRNA-targeted-gene promoter methylation and miRNA regulation of target genes. <i>F1000Research</i> , 0, 2, 21.	0.8	1
2048	Correlation between miRNA-targeted-gene promoter methylation and miRNA regulation of target genes. <i>F1000Research</i> , 0, 2, 21.	0.8	2
2049	Dnmt3a Regulates Proliferation of Muscle Satellite Cells via p57Kip2. <i>PLoS Genetics</i> , 2016, 12, e1006167.	1.5	44
2050	HOXB13, a Target of DNMT3B, Is Methylated at an Upstream CpG Island, and Functions as a Tumor Suppressor in Primary Colorectal Tumors. <i>PLoS ONE</i> , 2010, 5, e10338.	1.1	60
2051	Investigating the Epigenetic Effects of a Prototype Smoke-Derived Carcinogen in Human Cells. <i>PLoS ONE</i> , 2010, 5, e10594.	1.1	16
2052	The Human Proteins MBD5 and MBD6 Associate with Heterochromatin but They Do Not Bind Methylated DNA. <i>PLoS ONE</i> , 2010, 5, e11982.	1.1	97
2053	DNA Methylation of the First Exon Is Tightly Linked to Transcriptional Silencing. <i>PLoS ONE</i> , 2011, 6, e14524.	1.1	503
2054	Different Binding Properties and Function of CXXC Zinc Finger Domains in Dnmt1 and Tet1. <i>PLoS ONE</i> , 2011, 6, e16627.	1.1	87
2055	Statistical Quantification of Methylation Levels by Next-Generation Sequencing. <i>PLoS ONE</i> , 2011, 6, e21034.	1.1	14

#	ARTICLE	IF	CITATIONS
2056	A SILAC-Based Screen for Methyl-CpG Binding Proteins Identifies RBP-J as a DNA Methylation and Sequence-Specific Binding Protein. PLoS ONE, 2011, 6, e25884.	1.1	49
2057	Bisulfite Sequencing Reveals That <i>Aspergillus flavus</i> Holds a Hollow in DNA Methylation. PLoS ONE, 2012, 7, e30349.	1.1	74
2058	Global Methylation Patterns in Idiopathic Pulmonary Fibrosis. PLoS ONE, 2012, 7, e33770.	1.1	169
2059	Promoter Variation and Transcript Divergence in Brassicaceae Lineages of FLOWERING LOCUS T. PLoS ONE, 2012, 7, e47127.	1.1	37
2060	Identification of New Differentially Methylated Genes That Have Potential Functional Consequences in Prostate Cancer. PLoS ONE, 2012, 7, e48455.	1.1	65
2061	A Comparison of the Whole Genome Approach of MeDIP-Seq to the Targeted Approach of the Infinium HumanMethylation450 BeadChip® for Methylome Profiling. PLoS ONE, 2012, 7, e50233.	1.1	83
2062	Identification of Transcriptome SNPs for Assessing Allele-Specific Gene Expression in a Super-Hybrid Rice Xieyou9308. PLoS ONE, 2013, 8, e60668.	1.1	12
2063	Construction and Characterization of Normalized cDNA Libraries by 454 Pyrosequencing and Estimation of DNA Methylation Levels in Three Distantly Related Termite Species. PLoS ONE, 2013, 8, e76678.	1.1	12
2064	A Reference Methylome Database and Analysis Pipeline to Facilitate Integrative and Comparative Epigenomics. PLoS ONE, 2013, 8, e81148.	1.1	351
2065	Targeted Methylation of the Epithelial Cell Adhesion Molecule (EPCAM) Promoter to Silence Its Expression in Ovarian Cancer Cells. PLoS ONE, 2014, 9, e87703.	1.1	60
2066	Differential Methylation of TCF7L2 Promoter in Peripheral Blood DNA in Newly Diagnosed, Drug-Naïve Patients with Type 2 Diabetes. PLoS ONE, 2014, 9, e99310.	1.1	31
2067	Divergence of Gene Body DNA Methylation and Evolution of Plant Duplicate Genes. PLoS ONE, 2014, 9, e110357.	1.1	48
2068	Systematic CpT (ApG) Depletion and CpG Excess Are Unique Genomic Signatures of Large DNA Viruses Infecting Invertebrates. PLoS ONE, 2014, 9, e111793.	1.1	9
2069	Simultaneous Statistical Inference for Epigenetic Data. PLoS ONE, 2015, 10, e0125587.	1.1	7
2070	Effects of Antiepileptic Drug Monotherapy on One-Carbon Metabolism and DNA Methylation in Patients with Epilepsy. PLoS ONE, 2015, 10, e0125656.	1.1	23
2071	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.	1.1	35
2072	Genome-Wide Profiling of PARP1 Reveals an Interplay with Gene Regulatory Regions and DNA Methylation. PLoS ONE, 2015, 10, e0135410.	1.1	55
2073	Locus- and Site-Specific DNA Methylation of 19 kDa Zein Genes in Maize. PLoS ONE, 2016, 11, e0146416.	1.1	5

#	ARTICLE	IF	CITATIONS
2074	Epigenetic Activation of Antibacterial Property of an Endophytic <i>Streptomyces coelicolor</i> Strain AZRA 37 and Identification of the Induced Protein Using MALDI TOF MS/MS. <i>PLoS ONE</i> , 2016, 11, e0147876.	1.1	26
2075	DNA Methylation and Potential for Epigenetic Regulation in <i>Pygospio elegans</i> . <i>PLoS ONE</i> , 2016, 11, e0151863.	1.1	9
2076	Genetic background and embryonic temperature affect DNA methylation and expression of myogenin and muscle development in Atlantic salmon (<i>Salmo salar</i>). <i>PLoS ONE</i> , 2017, 12, e0179918.	1.1	63
2077	DNA methylation patterns and gene expression associated with litter size in Berkshire pig placenta. <i>PLoS ONE</i> , 2017, 12, e0184539.	1.1	24
2078	The association between DNA methylation and exon expression in the Pacific oyster <i>Crassostrea gigas</i> . <i>PLoS ONE</i> , 2017, 12, e0185224.	1.1	48
2079	Integration of neural and epigenetic contributions to posttraumatic stress symptoms: The role of hippocampal volume and glucocorticoid receptor gene methylation. <i>PLoS ONE</i> , 2018, 13, e0192222.	1.1	24
2080	DNA methylation in blood—Potential to provide new insights into cell biology. <i>PLoS ONE</i> , 2020, 15, e0241367.	1.1	3
2081	Causal explanation beyond the gene: manipulation and causality in epigenetics. <i>Theoria (Spain)</i> , 2012, 27, 153-174.	0.2	9
2082	Molecular mechanism of hepatitis B virus (HBV) on suppression of raf kinase inhibitor protein (RKIP) expression. <i>Oncotarget</i> , 2017, 8, 1132-1140.	0.8	6
2083	Differential DNA Methylation under Drought Stress in Maize. <i>International Journal of Current Microbiology and Applied Sciences</i> , 2019, 8, 2527-2543.	0.0	2
2084	It's Time for An Epigenomics Roadmap of Heart Failure. <i>Current Genomics</i> , 2015, 16, 237-244.	0.7	10
2085	Epigenetic Mechanisms of Maternal Dietary Protein and Amino Acids Affecting Growth and Development of Offspring. <i>Current Protein and Peptide Science</i> , 2019, 20, 727-735.	0.7	3
2086	Epigenetic Targets and their Inhibitors in Cancer Therapy. <i>Current Topics in Medicinal Chemistry</i> , 2019, 18, 2395-2419.	1.0	33
2087	Nerve Growth Factor in Alcohol Use Disorders. <i>Current Neuropharmacology</i> , 2020, 19, 45-60.	1.4	17
2088	DNA Methylation as a Target of Epigenetic Therapeutics in Cancer. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2013, 13, 242-247.	0.9	35
2089	Determination of DNA Methylation Levels with CRED-RA Technique in the Genome of Sunflower Seedlings (<i>Helianthus annuus</i> L.) Subjected to Zinc Stress. <i>International Journal of Environment Agriculture and Biotechnology</i> , 2016, 1, 438-444.	0.0	7
2090	Roles of inflammatory and anabolic cytokines in cartilage metabolism: signals and multiple effectors converge upon MMP-13 regulation in osteoarthritis. , 2011, 21, 202-220.		386
2091	Promoter Methylation of Four Tumor Suppressor Genes in Human Papillary Thyroid Carcinoma. , 2019, 14, 290-298.		7

#	ARTICLE	IF	CITATIONS
2092	Chromatin regulation in drug addiction and depression. <i>Dialogues in Clinical Neuroscience</i> , 2009, 11, 257-268.	1.8	72
2093	Head and Neck Squamous Cell Carcinoma: Epigenetic Landscape. <i>Diagnostics</i> , 2021, 11, 34.	1.3	22
2097	Epigenetic regulation of DNA repair machinery in <i>Helicobacter pylori</i> -induced gastric carcinogenesis. <i>World Journal of Gastroenterology</i> , 2015, 21, 9021.	1.4	16
2098	Epigenetic regulation of insulin-like growth factor axis in hepatocellular carcinoma. <i>World Journal of Gastroenterology</i> , 2016, 22, 2668.	1.4	11
2099	Epigenetic silencing during early lineage commitment. <i>Stembook</i> , 2009, , .	0.3	8
2100	The epigenetic landscape of innate immunity. <i>AIMS Molecular Science</i> , 2017, 4, 110-139.	0.3	2
2101	Effect of lenalidomide on the human gastric cancer cell line SGC7901/vincristine Notch signaling. <i>Journal of Cancer Research and Therapeutics</i> , 2018, 14, S237-S242.	0.3	6
2102	Integrative Analysis of Genome-wide Expression and Methylation Data. <i>Journal of Biometrics & Biostatistics</i> , 2013, 04, .	4.0	3
2103	Epigenetics: Integrating Genetic Programs, Brain Development and Emergent Phenotypes. <i>Cell & Developmental Biology</i> , 2014, 03, .	0.3	1
2104	FLT3-ITD compared with DNMT3A R882 mutation is a more powerful independent inferior prognostic factor in adult AML patients after Allogeneic Hematopoietic Stem Cell Transplantation: A retrospective cohort study. <i>Turkish Journal of Haematology</i> , 2018, 35, 158-167.	0.2	15
2105	Next-Generation DNA Sequencing Technologies. <i>Erciyes Tip Dergisi</i> , 2014, 36, 99-103.	0.1	2
2106	Epigenetic therapy in allogeneic hematopoietic stem cell transplantation. <i>Revista Brasileira De Hematologia E Hemoterapia</i> , 2013, 35, 126-33.	0.7	17
2107	DNA methylation: a cause and consequence of type 2 diabetes. <i>Genomics and Informatics</i> , 2019, 17, e38.	0.4	13
2108	Aberrant Methylation of Genes in Sputum Samples as Diagnostic Biomarkers for Non-small Cell Lung Cancer: a Meta-analysis. <i>Asian Pacific Journal of Cancer Prevention</i> , 2014, 15, 4467-4474.	0.5	5
2109	Epigenetic regulation of hematopoiesis by DNA methylation. <i>ELife</i> , 2016, 5, e11813.	2.8	36
2110	Loss of Fam60a, a Sin3a subunit, results in embryonic lethality and is associated with aberrant methylation at a subset of gene promoters. <i>ELife</i> , 2018, 7, .	2.8	9
2111	Pericentromeric hypomethylation elicits an interferon response in an animal model of ICF syndrome. <i>ELife</i> , 2018, 7, .	2.8	38
2112	Hypermethylation of Prkcz Regulated by E6/Dnmt1 Inhibits Invasion and Emt Via Cdc42 in Hpv-Related Head and Neck Squamous Cell Carcinoma. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
2113	DNA sequence and methylation prescribe the inside-out conformational dynamics and bending energetics of DNA minicircles. <i>Nucleic Acids Research</i> , 2021, 49, 11459-11475.	6.5	11
2114	CpG Transformer for imputation of single-cell methylomes. <i>Bioinformatics</i> , 2022, 38, 597-603.	1.8	17
2115	The methylome of <i>Biomphalaria glabrata</i> and other mollusks: enduring modification of epigenetic landscape and phenotypic traits by a new DNA methylation inhibitor. <i>Epigenetics and Chromatin</i> , 2021, 14, 48.	1.8	8
2116	DNA Methylation Profiling of MYC, SMAD2/3 and DNMT3A in Colorectal Cancer. <i>Oman Medical Journal</i> , 2021, 36, e315-e315.	0.3	4
2117	DNA methylation and sexual dimorphism: new insights from mealybugs. <i>Molecular Ecology</i> , 2021, 30, 5621-5623.	2.0	1
2118	Multi-distance based spectral embedding fusion for clustering single-cell methylation data. , 2021, , .		1
2119	Mapping epigenetic divergence in the massive radiation of Lake Malawi cichlid fishes. <i>Nature Communications</i> , 2021, 12, 5870.	5.8	17
2124	Genetics in relation to psychiatry. , 2010, , 141-156.		0
2125	Toxicogenomics, Proteomics, and Metabolomics. , 2010, , 389-410.		0
2127	A Novel Method for Quantifying the Demethylation Potential of Environmental Chemical Pollutants. <i>Communications in Computer and Information Science</i> , 2011, , 62-71.	0.4	0
2130	Epigenetic Reprogramming Induced Pluripotency. <i>Indonesian Biomedical Journal</i> , 2011, 3, 93.	0.2	0
2131	Principles of Molecular Biology. , 2012, , 1209-1223.		1
2132	Epigenetic Reprogramming in Lung Carcinomas. , 2012, , 159-177.		1
2133	Epigenetics and Tumor Suppressor Genes. , 0, , .		0
2134	The effects of reciprocal cross on inheritance of DNA methylation in cotton (<i>Gossypium hirsutum</i>). <i>African Journal of Biotechnology</i> , 2012, 11, .	0.3	0
2135	Epigenetic Modifications in Testicular Germ Cell Tumors. , 0, , .		0
2137	Possible miRNA Coregulation of Target Genes in Brain Regions by Both Differential miRNA Expression and miRNA-Targeting-Specific Promoter Methylation. <i>Communications in Computer and Information Science</i> , 2013, , 225-230.	0.4	0
2138	Establishment of Tissue-Specific Epigenetic States During Development. , 2013, , 35-62.		0

#	ARTICLE	IF	CITATIONS
2139	Mechanisms of Somatic Cell Reprogramming. <i>Pancreatic Islet Biology</i> , 2013, , 301-316.	0.1	0
2141	Role of epigenetic modifications in stem cell regulatory regions (Oct4, Sox2 and Nanog) and cancer. <i>IOSR Journal of Pharmacy and Biological Sciences</i> , 2013, 5, 76-81.	0.1	0
2142	<i>Epigenome.</i> , 2013, , 43-71.		1
2143	Thiophene-derivatized Fluorescent Benzamides as Possible Probes for Histone Deacetylases. <i>Bulletin of the Korean Chemical Society</i> , 2013, 34, 2249-2250.	1.0	0
2144	The Fundamental Role of Epigenetic Regulation in Normal and Disturbed Cell Growth, Differentiation, and Stemness. , 2014, , 1-41.		0
2145	<i>Systems Toxicology Approaches.</i> , 2013, , 121-139.		0
2147	<i>Epigenetics of Host-Pathogen Interactions.</i> , 2013, , 1-22.		0
2148	<i>Dynamics of DNA Methylation Patterns in Human Cells.</i> , 2014, , .		0
2149	<i>Epigenetics of Psychiatric Diseases.</i> , 2014, , .		0
2150	<i>Cell Proliferation from Regulated to Deregulated States Via Epigenomic Responses.</i> , 2014, , 229-251.		0
2151	<i>Covert Operations: the Adaptable Plan of Attack Deployed by Pathogenic Bacteria.</i> , 0, , 185-200.		0
2152	<i>Bayesian Networks in the Study of Genome-wide DNA Methylation.</i> , 2014, , 363-386.		0
2154	<i>Prostate and Bladder Carcinomas: Histology, Immunohistochemistry, Genetic Biomarkers.</i> , 2015, , 79-91.		0
2155	<i>Genetic and Epigenetic Alterations in Urothelial Carcinoma.</i> , 2015, , 253-259.		0
2157	Maternal Diet, Developmental Origins, and the Intergenerational Transmission of Cardiometabolic Traits: A Window of Opportunity for the Prevention of Metabolic Syndrome?. , 2015, , 181-201.		1
2158	Dosing “When Less is More. <i>RSC Drug Discovery Series</i> , 2015, , 249-266.	0.2	0
2159	Transgenerational Transmission of Stress Pathology. <i>Zeitschrift Fur Psychologie / Journal of Psychology</i> , 2015, 223, 181-191.	0.7	2
2160	The Role of DNA Methylation in Type 1 and 2 Diabetes as Related to Endothelial Cell Dysfunction. <i>MOJ Anatomy & Physiology</i> , 2015, 1, .	0.2	0

#	ARTICLE	IF	CITATIONS
2161	DNA Methylation Status of the Methylenetetrahydrofolate Reductase Gene is associated with Depressive Symptoms in Japanese Workers: A Cross-Sectional Study. <i>Journal of Neurology and Neurological Disorders</i> , 2015, 2, .	0.0	1
2163	Differential Regulation of Androgen Receptor and DNA Methylation in Songbirds. <i>Epigenetics and Human Health</i> , 2016, , 233-241.	0.2	0
2164	A Protocol for the Simultaneous Analysis of Gene DNA Methylation and mRNA Expression Levels in the Rodent Brain. <i>Neuromethods</i> , 2016, , 65-85.	0.2	1
2165	Genetics and Epigenetics of Head and Neck Cancer. , 2016, , 115-132.		0
2166	Interplay of Epigenetics with Gynecological Cancer. , 0, , .		0
2167	Effect of Environmental Chemical Exposures on Epigenetics of Diseases: A Systematic Review. , 2016, 2, .		1
2169	Tasks of some dietary essential nutrients on epigenetics and one carbon metabolism in livestock during production. <i>IOSR Journal of Agriculture and Veterinary Science</i> , 2016, 09, 86-90.	0.1	0
2170	Identification and Characterization of Reverse Transcriptase Fragments of Long Interspersed Nuclear Elements (LINEs) in the <i>Morus notabilis</i> Genome. <i>American Journal of Molecular Biology</i> , 2017, 07, 138-152.	0.1	1
2171	Dynamic Detection and Visualization of RNA Methylation by Photochemical Organic Transformations. , 2017, , .		0
2174	Maternal Undernutrition and Type 2 Diabetes in Australian Aboriginal and Torres Strait Islander People: History and Future Direction. <i>Exploratory Research and Hypothesis in Medicine</i> , 2017, 2, 1-5.	0.1	1
2175	Physiologic and Epigenetic Changes with Pulmonary Vascular Injury After Lung Transplantation. , 2018, , 161-182.		0
2176	Evolution and Genetic Model of Cooperative Breeding. <i>Open Journal of Natural Science</i> , 2018, 06, 151-156.	0.1	0
2177	Maximum DNA Methylation Fidelity in the Germline Tolerates Global Non-Functional Gene Body Methylation Dynamics During Development. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
2185	Inflammatory Bowel Disease and Epigenetics. , 2019, , 183-201.		1
2186	Epigenetics to Solve Crimes. <i>RSC Detection Science</i> , 2019, , 253-274.	0.0	0
2197	6. Asexuality and Epigenetic Variation. , 2019, , 87-102.		0
2200	Application of the Luminometric Methylatoion Assay for plant ecological researches: the study of global DNA methylation in leaves of <i>Elodea canadensis</i> under laboratory conditions and in leaves of fen orchid from wild populations. <i>Plant OMICS</i> , 2020, , 30-36.	0.4	1
2204	Immunohistochemical Detection of 5-Hydroxymethylcytosine and 5-Carboxylcytosine in Sections of Zebrafish Embryos. <i>Methods in Molecular Biology</i> , 2021, 2198, 193-208.	0.4	1

#	ARTICLE	IF	CITATIONS
2206	DNA Methylation and Schizophrenia: Current Literature and Future Perspective. <i>Cells</i> , 2021, 10, 2890.	1.8	26
2207	Impact of transposable elements on the evolution of complex living systems and their epigenetic control. <i>BioSystems</i> , 2021, 210, 104566.	0.9	6
2208	Single cell heterogeneity in human pluripotent stem cells. <i>BMB Reports</i> , 2021, 54, 505-515.	1.1	15
2209	DCNN-4mC: Densely connected neural network based N4-methylcytosine site prediction in multiple species. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6009-6019.	1.9	33
2210	Electrochemical Biosensor for Multiple Methylation-Locus Analysis Based on DNA-AuNPs and Bienzymatic Dual Signal Amplifications. <i>American Journal of Analytical Chemistry</i> , 2020, 11, 61-74.	0.3	0
2212	Molecular Evolution: A Brief Introduction. , 2020, , 25-34.		0
2213	Discrete Multiple Testing in Detecting Differential Methylation Using Sequencing Data. <i>Emerging Topics in Statistics and Biostatistics</i> , 2020, , 65-91.	0.1	0
2214	The Pliable Genome: Epigenomics of Norway Spruce. <i>Compendium of Plant Genomes</i> , 2020, , 65-95.	0.3	2
2219	The role of toll like receptor 9 in maintaining gut homeostasis. , 2020, 3, 010-014.		2
2221	Mindfulness intervention improves cognitive function in older adults by enhancing the level of miRNA-29c in neuron-derived extracellular vesicles. <i>Scientific Reports</i> , 2021, 11, 21848.	1.6	7
2222	The Impact of the HydroxyMethylCytosine epigenetic signature on DNA structure and function. <i>PLoS Computational Biology</i> , 2021, 17, e1009547.	1.5	6
2223	Epigenetics: key to improve delayed wound healing in type 2 diabetes. <i>Molecular and Cellular Biochemistry</i> , 2022, 477, 371-383.	1.4	12
2224	Common mechanisms cannot explain time- and dose-dependent DNA methylation changes in earthworms exposed to cadmium. <i>Science of the Total Environment</i> , 2021, , 151468.	3.9	4
2225	Skeletal muscle methylome and transcriptome integration reveals profound sex differences related to muscle function and substrate metabolism. <i>Clinical Epigenetics</i> , 2021, 13, 202.	1.8	20
2226	Describing Epigenomic Information in Arabidopsis. , 2009, , 163-175.		0
2227	The Expanding View of Cytosine Methylation. , 2009, , 69-83.		0
2228	Heat Shock Proteins Expression Is Regulated by Promoter CpG Methylation/demethylation under Heat Stress in Wheat Varieties. <i>Pakistan Journal of Biological Sciences</i> , 2020, 23, 1310-1320.	0.2	4
2229	Bioinformatics Analysis of DNA Methylation Through Bisulfite Sequencing Data. <i>Methods in Molecular Biology</i> , 2021, 2198, 441-450.	0.4	2

#	ARTICLE	IF	CITATIONS
2233	Analysis of DNA methylation-driven genes for predicting the prognosis of patients with colorectal cancer. <i>Aging</i> , 2020, 12, 22814-22839.	1.4	3
2236	DNA methylation changes in inflammatory bowel disease. <i>Annals of Gastroenterology</i> , 2014, 27, 125-132.	0.4	44
2237	Hydroxymethylation of DNA: an epigenetic marker. <i>EXCLI Journal</i> , 2014, 13, 592-610.	0.5	40
2239	Decreased 5-Hydroxymethylcytosine (5-hmC) predicts poor prognosis in early-stage laryngeal squamous cell carcinoma. <i>American Journal of Cancer Research</i> , 2016, 6, 1089-98.	1.4	9
2241	Intrinsic abnormalities of adipose tissue and adipose tissue dysfunction in PCOS. , 2022, , 73-96.		0
2242	Cancer Detection and Classification by CpG Island Hypermethylation Signatures in Plasma Cell-Free DNA. <i>Cancers</i> , 2021, 13, 5611.	1.7	7
2243	Latency-associated DNA methylation patterns among HIV-1 infected individuals with distinct disease progression courses or antiretroviral virologic response. <i>Scientific Reports</i> , 2021, 11, 22993.	1.6	3
2244	Brown Fat Dnmt3b Deficiency Ameliorates Obesity in Female Mice. <i>Life</i> , 2021, 11, 1325.	1.1	2
2245	Non-Cell Autonomous and Epigenetic Mechanisms of Huntingtonâ€™s Disease. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12499.	1.8	6
2246	Gene expression and epigenetic responses of the marine Cladoceran, <i>Evadne nordmanni</i> , and the copepod, <i>Acartia clausi</i> , to elevated CO ₂ . <i>Ecology and Evolution</i> , 2021, 11, 16776-16785.	0.8	6
2248	A review on the role of epidermal growth factor signaling in the development, progression and treatment of cervical cancer. <i>International Journal of Biological Macromolecules</i> , 2022, 194, 179-187.	3.6	13
2249	scRNA modifications as emerging therapeutic targets. <i>Wiley Interdisciplinary Reviews RNA</i> , 2022, 13, e1702.	3.2	10
2250	Characterization of DNA methylation and promoter activity of long terminal repeat elements of feline endogenous retrovirus RDRS C2a. <i>Virus Genes</i> , 2021, , 1.	0.7	0
2251	Dynamic epigenetic modifications in plant sugar signal transduction. <i>Trends in Plant Science</i> , 2022, 27, 379-390.	4.3	24
2252	Histone H1 prevents non-CG methylation-mediated small RNA biogenesis in Arabidopsis heterochromatin. <i>ELife</i> , 2021, 10, .	2.8	23
2253	Novel technologies in cfDNA analysis and potential utility in clinic. <i>Chinese Journal of Cancer Research: Official Journal of China Anti-Cancer Association, Beijing Institute for Cancer Research</i> , 2021, 33, 708-718.	0.7	5
2254	LONG-TERM GENETIC AND EPIGENETIC DISORDERS IN PERSONS EXPOSED TO IONIZING RADIATION AND THEIR DESCENDANTS (review). <i>Problemy Radiatsiinoi Medytsyny Ta Radiobiologii</i> , 2021, 26, 36-56.	0.5	1
2256	Hypermethylation Effects of Yiqihuoxue Decoction in Diabetic Atherosclerosis Using Genome-Wide DNA Methylation Analyses. <i>Journal of Inflammation Research</i> , 2022, Volume 15, 163-176.	1.6	5

#	ARTICLE	IF	CITATIONS
2257	The Impact of Exercise on Telomere Length, DNA Methylation and Metabolic Footprints. <i>Cells</i> , 2022, 11, 153.	1.8	5
2259	A Review of Gene Sequencing in Infertility. <i>Folia Biologica</i> , 2020, 68, 97-105.	0.1	0
2260	Modulating gene expression in breast cancer via DNA secondary structure and the CRISPR toolbox. <i>NAR Cancer</i> , 2021, 3, zcab048.	1.6	8
2261	Cluster mean-field theory accurately predicts statistical properties of large-scale DNA methylation patterns. <i>Journal of the Royal Society Interface</i> , 2022, 19, 20210707.	1.5	0
2262	Deciphering the etiology and role in oncogenic transformation of the CpG island methylator phenotype: a pan-cancer analysis. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	9
2263	Genome-wide DNA methylation profiling and identification of potential pan-cancer and tumor-specific biomarkers. <i>Molecular Oncology</i> , 2022, 16, 2432-2447.	2.1	9
2264	Associations of Maternal Polyunsaturated Fatty Acids With Telomere Length in the Cord Blood and Placenta in Chinese Population. <i>Frontiers in Nutrition</i> , 2021, 8, 779306.	1.6	5
2266	Analysis of 5-Methylcytosine Regulators and DNA Methylation-Driven Genes in Colon Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 657092.	1.8	5
2267	A pilot study of multilevel analysis of BDNF in paternal and maternal perinatal depression. <i>Archives of Women's Mental Health</i> , 2022, 25, 237-249.	1.2	8
2268	Dissecting cricket genomes for the advancement of entomology and entomophagy. <i>Biophysical Reviews</i> , 2022, 14, 75-97.	1.5	9
2269	Structure analysis of genes involved in flower color formation of the orchid <i>Spathoglottis plicata</i> Blume. <i>Acta Horticulturae</i> , 2022, , 143-152.	0.1	0
2270	CYP81A68 confers metabolic resistance to ALS and ACCase-inhibiting herbicides and its epigenetic regulation in <i>Echinochloa crus-galli</i> . <i>Journal of Hazardous Materials</i> , 2022, 428, 128225.	6.5	50
2271	Epigenetic Links between Microbiota and Gestational Diabetes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1831.	1.8	6
2272	Prediction of transcription factors associated with DNA demethylation during human cellular development. <i>Chromosome Research</i> , 2022, 30, 109-121.	1.0	4
2273	The use of new CRISPR tools in cardiovascular research and medicine. <i>Nature Reviews Cardiology</i> , 2022, 19, 505-521.	6.1	21
2274	Micronutrient supplementation affects DNA methylation in male gonads with potential intergenerational epigenetic inheritance involving the embryonic development through glutamate receptor-associated genes. <i>BMC Genomics</i> , 2022, 23, 115.	1.2	5
2275	Tools and applications for integrative analysis of DNA methylation in social insects. <i>Molecular Ecology Resources</i> , 2022, 22, 1656-1674.	2.2	4
2276	Genome-wide methylation and expression analyses reveal the epigenetic landscape of immune-related diseases for tobacco smoking. <i>Clinical Epigenetics</i> , 2021, 13, 215.	1.8	13

#	ARTICLE	IF	CITATIONS
2277	Epigenetic regulation of vascular smooth muscle cell function in atherosclerosis. <i>Current Atherosclerosis Reports</i> , 2013, 15, 319.	2.0	7
2278	Investigating the genetic and epigenetic basis of big biological questions with the parthenogenetic marbled crayfish: A review and perspectives. <i>Journal of Biosciences</i> , 2018, 43, 189-223.	0.5	8
2279	Complex interplay of lesion-specific DNA repair enzyme on bistranded clustered DNA damage harboring Tg:G mismatch in nucleosome core particles. <i>Journal of Biosciences</i> , 2018, 43, 575-583.	0.5	0
2280	Single cell heterogeneity in human pluripotent stem cells. <i>BMB Reports</i> , 2021, 54, 505-515.	1.1	2
2281	DNA methylation markers in esophageal cancer: an emerging tool for cancer surveillance and treatment. <i>American Journal of Cancer Research</i> , 2021, 11, 5644-5658.	1.4	1
2282	How stress affects gene expression through epigenetic modifications. , 2022, , 99-118.		0
2283	Implications of Heterogeneity of Epithelial-Mesenchymal States in Acromegaly Therapeutic Pharmacologic Response. <i>Biomedicines</i> , 2022, 10, 460.	1.4	7
2284	Hypermethylation of PDX1, EN2, and MSX1 predicts the prognosis of colorectal cancer. <i>Experimental and Molecular Medicine</i> , 2022, 54, 156-168.	3.2	13
2285	Exploring the Ecological Implications of Microbiota Diversity in Birds: Natural Barriers Against Avian Malaria. <i>Frontiers in Immunology</i> , 2022, 13, 807682.	2.2	6
2286	miR-486-5p expression is regulated by DNA methylation in osteosarcoma. <i>BMC Genomics</i> , 2022, 23, 142.	1.2	8
2287	The Role of Epigenetic Mechanisms in Autoimmune, Neurodegenerative, Cardiovascular, and Imprinting Disorders. <i>Mini-Reviews in Medicinal Chemistry</i> , 2022, 22, 1977-2011.	1.1	1
2288	In silico identification of single nucleotide variations at CpG sites regulating CpG island existence and size. <i>Scientific Reports</i> , 2022, 12, 3574.	1.6	7
2289	Excited State Dynamics of Methylated Guanosine Derivatives Revealed by Femtosecond Time-resolved Spectroscopy. <i>Photochemistry and Photobiology</i> , 2022, 98, 1008-1016.	1.3	2
2290	Epigenome-Wide Analysis of DNA Methylation in Parkinson's Disease Cortex. <i>Life</i> , 2022, 12, 502.	1.1	14
2291	Variability in Global DNA Methylation Rate Across Tissues and Over Time in Sheep. <i>Frontiers in Genetics</i> , 2022, 13, 791283.	1.1	1
2292	TET2 is required for Type I IFN-mediated inhibition of bat-origin swine acute diarrhea syndrome coronavirus. <i>Journal of Medical Virology</i> , 2022, 94, 3251-3256.	2.5	2
2294	Systematic Analysis and Accurate Identification of DNA N4-Methylcytosine Sites by Deep Learning. <i>Frontiers in Microbiology</i> , 2022, 13, 843425.	1.5	4
2295	Neurobiology of early life adversity: A systematic review of meta-analyses towards an integrative account of its neurobiological trajectories to mental disorders. <i>Frontiers in Neuroendocrinology</i> , 2022, 65, 100994.	2.5	38

#	ARTICLE	IF	CITATIONS
2296	Genome-Wide DNA Methylation and Its Effect on Gene Expression During Subclinical Mastitis in Water Buffalo. <i>Frontiers in Genetics</i> , 2022, 13, 828292.	1.1	5
2297	Chemical modulation of the metabolism of an endophytic fungal strain of <i>Cophinorma mamane</i> using epigenetic modifiers and amino-acids. <i>Fungal Biology</i> , 2022, 126, 385-394.	1.1	5
2298	Methylation at CpG sites related to growth differentiation factor-15 was not prospectively associated with cardiovascular death in discordant monozygotic twins. <i>Scientific Reports</i> , 2022, 12, 4410.	1.6	0
2299	LncRNA-mediated DNA methylation: an emerging mechanism in cancer and beyond. <i>Journal of Experimental and Clinical Cancer Research</i> , 2022, 41, 100.	3.5	77
2300	Molecular and epigenetic regulation of seasonal reproduction in Terai tree frog (<i>Polypedates</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582	1.6	4
2301	DNA Methylation Malleability and Dysregulation in Cancer Progression: Understanding the Role of PARP1. <i>Biomolecules</i> , 2022, 12, 417.	1.8	6
2302	A comparative methylome analysis reveals conservation and divergence of DNA methylation patterns and functions in vertebrates. <i>BMC Biology</i> , 2022, 20, 70.	1.7	12
2303	Heterozygous loss of <i>Zbtb38</i> leads to early embryonic lethality via the suppression of <i>Nanog</i> and <i>Sox2</i> expression. <i>Cell Proliferation</i> , 2022, 55, e13215.	2.4	4
2305	Interplay Between Stress and Reproduction: Novel Epigenetic Markers in Response to Shearing Patterns in Australian Merino Sheep (<i>Ovis aries</i>). <i>Frontiers in Veterinary Science</i> , 2022, 9, 830450.	0.9	1
2306	New advances of DNA/RNA methylation modification in liver fibrosis. <i>Cellular Signalling</i> , 2022, 92, 110224.	1.7	3
2307	TET1 overexpression attenuates paclitaxel-induced neuropathic pain through rescuing K2p1.1 expression in primary sensory neurons of male rats. <i>Life Sciences</i> , 2022, 297, 120486.	2.0	7
2308	A cascade amplification strategy for the detection of DNA methyltransferase activity by elemental labeling inductively coupled plasma mass spectrometry. <i>Sensors and Actuators B: Chemical</i> , 2022, 362, 131758.	4.0	4
2310	Radiation-Induced DNA Methylation Disorders: In Vitro and In Vivo Studies. <i>Biology Bulletin</i> , 2021, 48, 2015-2037.	0.1	0
2311	Identification of Let-7 miRNA Activity as a Prognostic Biomarker of SHH Medulloblastoma. <i>Cancers</i> , 2022, 14, 139.	1.7	3
2313	Integration of Transcriptome and Methylome Analyses Provides Insight Into the Pathway of Floral Scent Biosynthesis in <i>Prunus mume</i> . <i>Frontiers in Genetics</i> , 2021, 12, 779557.	1.1	9
2314	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021, 12, 7173.	5.8	8
2315	Methylation Markers in Cutaneous Melanoma: Unravelling the Potential Utility of Their Tracking by Liquid Biopsy. <i>Cancers</i> , 2021, 13, 6217.	1.7	9
2316	Genome-Scale DNA Methylation Analysis Identifies Repeat Element Alterations that Modulate the Genomic Stability of Melanocytic Nevi. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1893-1902.e7.	0.3	14

#	ARTICLE	IF	CITATIONS
2317	Transcriptional and Epigenetic Bioinformatic Analysis of Claudin-9 Regulation in Gastric Cancer. <i>Journal of Oncology</i> , 2021, 2021, 1-16.	0.6	21
2318	Chronic stress increases DNA methylation of the GR promoter in the central nucleus of the amygdala of female rats. <i>Neurogastroenterology and Motility</i> , 2022, 34, e14377.	1.6	6
2319	Osteosarcoma: Novel prognostic biomarkers using circulating and cell-free tumour DNA. <i>European Journal of Cancer</i> , 2022, 168, 1-11.	1.3	8
2370	A reappraisal of the form: function problemâ€”theory and phenomenology. <i>Theory in Biosciences</i> , 2022, , 1.	0.6	0
2371	Detection of free DNA septin 9 gene methylation in plasma. <i>Journal of Central South University (Medical Sciences)</i> , 2021, 46, 127-134.	0.1	0
2372	Epigenetic studies in insects and the valproic acid perspective. <i>Brazilian Journal of Biology</i> , 2022, 84, e256045.	0.4	2
2373	Relationship between Exposure to Low Dose of x-ray and DNA Hypomethylation in Solid Tumors and Hematological Malignancies. <i>Biomedical and Environmental Sciences</i> , 2020, 33, 528-537.	0.2	1
2374	DNA methylation: a historical perspective. <i>Trends in Genetics</i> , 2022, 38, 676-707.	2.9	176
2376	Obesity-Associated Differentially Methylated Regions in Colon Cancer. <i>Journal of Personalized Medicine</i> , 2022, 12, 660.	1.1	3
2377	DNA binding by polycomb-group proteins: searching for the link to CpG islands. <i>Nucleic Acids Research</i> , 2022, 50, 4813-4839.	6.5	15
2378	<i>De novo</i> programming: establishment of epigenome in mammalian oocytes. <i>Biology of Reproduction</i> , 2022, , .	1.2	1
2379	The early-life exposome modulates the effect of polymorphic inversions on DNA methylation. <i>Communications Biology</i> , 2022, 5, 455.	2.0	6
2380	Aberrant promoter hypermethylation regulates thrombomodulin in high altitude induced deep vein thrombosis. <i>Thrombosis Research</i> , 2022, 215, 5-13.	0.8	0
2381	Pan-cancer analysis of the DNA methylation patterns of long non-coding RNA. <i>Genomics</i> , 2022, 114, 110377.	1.3	5
2383	Encyclopaedia of eukaryotic DNA methylation: from patterns to mechanisms and functions. <i>Biochemical Society Transactions</i> , 2022, , .	1.6	8
2384	Signatures of polygenic adaptation align with genome-wide methylation patterns in wild strawberry plants. <i>New Phytologist</i> , 2022, 235, 1501-1514.	3.5	6
2385	Promoter hypermethylation of GALR1 acts as an early epigenetic susceptibility event in colorectal carcinogenesis. <i>Journal of Human Genetics</i> , 2022, 67, 519-525.	1.1	2
2386	Genome-Wide DNA Methylation Patterns of Muscle and Tail-Fat in DairyMeade Sheep and Mongolian Sheep. <i>Animals</i> , 2022, 12, 1399.	1.0	6

#	ARTICLE	IF	CITATIONS
2387	Investigating the potential clinical significance of long non-coding RNA 00092 in patients with breast cancer. <i>Annals of Translational Medicine</i> , 2022, 10, 602-602.	0.7	2
2388	Post-translational modifications drive secondary metabolite biosynthesis in <i>Aspergillus</i> : a review. <i>Environmental Microbiology</i> , 2022, 24, 2857-2881.	1.8	17
2389	Immunomodulatory Effects of Endocrine-Disrupting Chemicals. , 2022, , 463-509.		1
2390	The Landscape of Genome-Wide and Gender-Specific Microsatellites in Indo-Pacific Humpback Dolphin and Potential Applications in Cetacean Resource Investigation. <i>Journal of Marine Science and Engineering</i> , 2022, 10, 834.	1.2	2
2392	Recent Advances in DNA Methylation and Their Potential Breeding Applications in Plants. <i>Horticulturae</i> , 2022, 8, 562.	1.2	5
2393	Origin of the genome editing systems: application for crop improvement. , 2022, 77, 3353-3383.		1
2394	New trend in genotoxicity research taking into account genome instability. <i>Folia Pharmacologica Japonica</i> , 2022, 157, 265-270.	0.1	0
2395	Integrated Analyses of DNA Methylation and Gene Expression of Rainbow Trout Muscle under Variable Ploidy and Muscle Atrophy Conditions. <i>Genes</i> , 2022, 13, 1151.	1.0	2
2396	Catching Nucleosome by Its Decorated Tails Determines Its Functional States. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
2397	Total Barley Maiya Alkaloids Prevent Increased Prolactin Levels Caused by Antipsychotic Drugs and Reduce Dopamine Receptor D2 via Epigenetic Mechanisms. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	3
2398	DNA methylation profile in beef cattle is influenced by additive genetics and age. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
2399	Brain Region- and Age-Dependent 5-Hydroxymethylcytosine Activity in the Non-Human Primate. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	1.7	5
2400	Structure and Methylation of 35S rDNA in Allopolyploids <i>Anemone multifida</i> (2n = 4x = 32, BBDD) and <i>Anemone baldensis</i> (2n = 6x = 48, AABBDD) and Their Parental Species Show Evidence of Nucleolar Dominance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
2401	Change of Heart: the Epitranscriptome of Small Non-coding RNAs in Heart Failure. <i>Current Heart Failure Reports</i> , 0, , .	1.3	3
2402	Shifts in the immunoepigenomic landscape of monocytes in response to a diabetes-specific social support intervention: a pilot study among Native Hawaiian adults with diabetes. <i>Clinical Epigenetics</i> , 2022, 14, .	1.8	2
2403	Environmental Epigenetics in Soil Ecosystems: Earthworms as Model Organisms. <i>Toxics</i> , 2022, 10, 406.	1.6	3
2406	Development of DNA methylation-based epigenetic age predictors in loblolly pine (<i>Pinus</i>)	2.2	9
2407	Genome-wide DNA methylation in an animal model and human studies of schizophrenia: a protocol for a meta-analysis. <i>BMJ Open Science</i> , 2022, 6, .	0.8	1

#	ARTICLE	IF	CITATIONS
2408	Role of Epigenetic Mechanisms in Chronic Pain. <i>Cells</i> , 2022, 11, 2613.	1.8	13
2409	Heritable Epigenomic Modifications Influence Stress Resilience and Rapid Adaptations in the Brown Planthopper (<i>Nilaparvata lugens</i>). <i>International Journal of Molecular Sciences</i> , 2022, 23, 8728.	1.8	6
2410	Association of N6-methyladenosine readers' genes variation and expression level with pulmonary tuberculosis. <i>Frontiers in Public Health</i> , 0, 10, .	1.3	1
2411	Single-cell multi-omics of human preimplantation embryos shows susceptibility to glucocorticoids. <i>Genome Research</i> , 2022, 32, 1627-1641.	2.4	9
2412	Aberrant DNA methylation in multiple myeloma: A major obstacle or an opportunity?. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	4
2414	Role of 19 SNPs in 10 genes with type 2 diabetes in the Pakistani population. <i>Gene</i> , 2023, 848, 146899.	1.0	1
2415	Molecular dynamics analysis of biomolecular systems including nucleic acids. <i>Biophysics and Physicobiology</i> , 2022, 19, n/a.	0.5	2
2416	Construction of a massive genetic resource by transcriptome sequencing and genetic characterization of <i>Megasyllis nipponica</i> (Annelida: Syllidae). <i>Genes and Genetic Systems</i> , 2022, 97, 153-166.	0.2	1
2417	Hypermethylation of PRKCZ Regulated by E6 Inhibits Invasion and EMT via Cdc42 in HPV-Related Head and Neck Squamous Cell Carcinoma. <i>Cancers</i> , 2022, 14, 4151.	1.7	2
2418	Analysis of Systemic Epigenetic Alterations in Inflammatory Bowel Disease: Defining Geographical, Genetic and Immune-Inflammatory influences on the Circulating Methylome. <i>Journal of Crohn's and Colitis</i> , 2023, 17, 170-184.	0.6	14
2419	DNA methylation changes and inflammaging in aging-associated diseases. <i>Epigenomics</i> , 2022, 14, 965-986.	1.0	6
2420	The Arabidopsis APOLO and human UPAT sequence-unrelated long noncoding RNAs can modulate DNA and histone methylation machineries in plants. <i>Genome Biology</i> , 2022, 23, .	3.8	19
2421	Epigenetic machinery is functionally conserved in cephalopods. <i>BMC Biology</i> , 2022, 20, .	1.7	6
2423	The Concept of the Modern Molecular Clock and Experience in Estimating Divergence Times of Eulipotyphla and Rodentia. <i>Biology Bulletin Reviews</i> , 2022, 12, 459-482.	0.3	0
2424	Population Epigenetics: The Extent of DNA Methylation Variation in Wild Animal Populations. <i>Epigenomes</i> , 2022, 6, 31.	0.8	11
2425	Melatonin and cancer suppression: insights into its effects on DNA methylation. <i>Cellular and Molecular Biology Letters</i> , 2022, 27, .	2.7	15
2426	Analysis of genome and methylation changes in Chinese indigenous chickens over time provides insight into species conservation. <i>Communications Biology</i> , 2022, 5, .	2.0	5
2427	RNA m6A regulates transcription via DNA demethylation and chromatin accessibility. <i>Nature Genetics</i> , 2022, 54, 1427-1437.	9.4	49

#	ARTICLE	IF	CITATIONS
2428	CpG Methylation of the Proximal Promoter Region Regulates the Expression of NAC6D Gene in Response to High Temperature in Wheat (<i>Triticum aestivum</i>). <i>Cytology and Genetics</i> , 2022, 56, 449-457.	0.2	0
2429	CDH1 (E-cadherin) Gene Methylation in Human Breast Cancer: Critical Appraisal of a Long and Twisted Story. <i>Cancers</i> , 2022, 14, 4377.	1.7	13
2430	Mesenchymal stem cells derived from patients with premature aging syndromes display hallmarks of physiological aging. <i>Life Science Alliance</i> , 2022, 5, e202201501.	1.3	3
2431	Epigenetic Regulation of Methylation in Determining the Fate of Dental Mesenchymal Stem Cells. <i>Stem Cells International</i> , 2022, 2022, 1-19.	1.2	2
2432	An overview of salinity stress, mechanism of salinity tolerance and strategies for its management in cotton. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	15
2433	Transgenerational Epigenetic Programming. , 2022, , 123-148.		0
2434	Epigenetic Regulation Towards Acquired Drug Resistance in Cancer. <i>Sub-Cellular Biochemistry</i> , 2022, , 473-502.	1.0	2
2435	Epigenetic-associated phenotypic plasticity of the ocean acidification-acclimated edible oyster in the mariculture environment. <i>Molecular Ecology</i> , 2023, 32, 412-427.	2.0	10
2436	The Mutagenic Consequences of DNA Methylation within and across Generations. <i>Epigenomes</i> , 2022, 6, 33.	0.8	5
2439	Low Energy Photoionization of Phosphorothioate DNA-Oligomers and Ensuing Hole Transfer. <i>Journal of Physical Chemistry B</i> , 2022, 126, 8699-8707.	1.2	1
2440	Local CpG density affects the trajectory and variance of age-associated DNA methylation changes. <i>Genome Biology</i> , 2022, 23, .	3.8	11
2441	Classification of Subgroups with Immune Characteristics Based on DNA Methylation in Luminal Breast Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12747.	1.8	0
2442	Allele-specific cis-regulatory methylation of the gene for vasoactive intestinal peptide in white-throated sparrows. <i>Genes, Brain and Behavior</i> , 2022, 21, .	1.1	4
2443	Integrated analyses of the methylome and transcriptome to unravel sex differences in the perirenal fat from suckling lambs. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
2444	Emerging Role of RNA m5C Modification in Cardiovascular Diseases. <i>Journal of Cardiovascular Translational Research</i> , 0, , .	1.1	2
2445	Prenatal EGCG consumption causes obesity and perturbs glucose homeostasis in adult mice. <i>Journal of Nutritional Biochemistry</i> , 2023, 111, 109179.	1.9	2
2446	DNA Methyltransferases and DNA Damage. <i>Advances in Experimental Medicine and Biology</i> , 2022, , 349-361.	0.8	1
2447	DNA Methylation in Honey Bees and the Unresolved Questions in Insect Methylomics. <i>Advances in Experimental Medicine and Biology</i> , 2022, , 159-176.	0.8	1

#	ARTICLE	IF	CITATIONS
2449	Photo-Cross-Linking To Delineate Epigenetic Interactome. <i>Journal of the American Chemical Society</i> , 2022, 144, 20979-20997.	6.6	6
2450	Septin 9 controls <i>CCNB1</i> stabilization via <i>APC</i> / <i>C^{sup}CDC20</i> during meiotic metaphase I/anaphase I transition in mouse oocytes. <i>Cell Proliferation</i> , 2023, 56, .	2.4	2
2452	Local diversity of drought resistance and resilience in <i>Populus tomentosa</i> correlates with the variation of DNA methylation. <i>Plant, Cell and Environment</i> , 2023, 46, 479-497.	2.8	5
2453	Multi-View Clustering for Integration of Gene Expression and Methylation Data With Tensor Decomposition and Self-Representation Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 2050-2063.	1.9	4
2454	Epigenome-wide association study of short-term temperature fluctuations based on within-sibship analyses in Australian females. <i>Environment International</i> , 2023, 171, 107655.	4.8	3
2455	Integrative methylome and transcriptome analysis of porcine abdominal fat indicates changes in fat metabolism and immune responses during different development. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	1
2456	Correlating ¹³ C Isotope in Oligomeric Proanthocyanidins with their Anticancer Properties. <i>Journal of Cancer Genetics and Biomarkers</i> , 2019, 1, 33-69.	0.0	0
2457	MicroRNAs as novel peripheral markers for suicidality in patients with major depressive disorder. <i>Frontiers in Psychiatry</i> , 0, 13, .	1.3	1
2458	Transcriptome and DNA Methylation Responses in the Liver of Yellowfin Seabream Under Starvation Stress. <i>Marine Biotechnology</i> , 2023, 25, 150-160.	1.1	3
2459	Inference of epigenetic subnetworks by Bayesian regression with the incorporation of prior information. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
2460	i4mC-CPXG: A Computational Model for Identifying DNA N4-methylcytosine Sites in Rosaceae Genome Using Novel Encoding Strategy. <i>Current Bioinformatics</i> , 2022, 18, .	0.7	0
2461	Changes in the rearing environment cause reorganization of molecular networks associated with <i>DNA</i> methylation. <i>Journal of Animal Ecology</i> , 2023, 92, 648-664.	1.3	2
2463	The role of plastic and evolved <i>DNA</i> methylation in parallel adaptation of threespine stickleback (<i>Gasterosteus aculeatus</i>). <i>Molecular Ecology</i> , 2023, 32, 1581-1591.	2.0	4
2464	Active DNA demethylation in plants: 20 years of discovery and beyond. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 2217-2239.	4.1	6
2466	Active DNA demethylation of developmental <i>cis</i> -regulatory regions predates vertebrate origins. <i>Science Advances</i> , 2022, 8, .	4.7	7
2468	The sound of silence: Transgene silencing in mammalian cell engineering. <i>Cell Systems</i> , 2022, 13, 950-973.	2.9	26
2469	Identification and Mechanism of Action of the Global Secondary Metabolism Regulator SaraC in <i>Stereum hirsutum</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
2470	Epigenetic biomarkers for animal welfare monitoring. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	5

#	ARTICLE	IF	CITATIONS
2471	Sunitinib resistance in renal cell carcinoma: From molecular mechanisms to predictive biomarkers. <i>Drug Resistance Updates</i> , 2023, 67, 100929.	6.5	23
2472	Comparative analysis of genome-scale, base-resolution DNA methylation profiles across 580 animal species. <i>Nature Communications</i> , 2023, 14, .	5.8	23
2473	Epigenetic regulations as drivers of insecticide resistance and resilience to climate change in arthropod pests. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
2474	Navigating the pitfalls of mapping DNA and RNA modifications. <i>Nature Reviews Genetics</i> , 2023, 24, 363-381.	7.7	8
2475	Rapid detection of cancer DNA in human blood using cysteamine-capped AuNPs and a machine learning-enabled smartphone. <i>RSC Advances</i> , 2023, 13, 1301-1311.	1.7	7
2477	Big Data in Gastroenterology Research. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2458.	1.8	6
2478	Maternal diet induces persistent DNA methylation changes in the muscle of beef calves. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
2480	Sex-specific changes in autosomal methylation rate in ageing common terns. <i>Frontiers in Ecology and Evolution</i> , 0, 11, .	1.1	2
2482	Dynamic Regulation of DNA Methylation and Brain Functions. <i>Biology</i> , 2023, 12, 152.	1.3	9
2483	Epigenetic and Genetic Population Structure is Coupled in a Marine Invertebrate. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	4
2484	The Immuno-Oncology and Genomic Aspects of DNA-Hypomethylating Therapeutics in Acute Myeloid Leukemia. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3727.	1.8	0
2485	Epigenetic potential: Promoter CpG content positively covaries with lifespan and is dependent on gene function among vertebrates. <i>Journal of Heredity</i> , 2023, 114, 207-218.	1.0	1
2486	RNA methylation in plants: An overview. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	14
2488	Epigenetics and the role of nutraceuticals in health and disease. <i>Environmental Science and Pollution Research</i> , 2023, 30, 28480-28505.	2.7	2
2489	Epigenetic Dysregulation in Alcohol-Associated Behaviors: Preclinical and Clinical Evidence. <i>Current Topics in Behavioral Neurosciences</i> , 2023, , .	0.8	1
2490	Methylated $\hat{A}ZNF582$: a therapeutic target in oral cancer. <i>Epigenomics</i> , 2022, 14, 1389-1392.	1.0	0
2491	Pilot study suggests DNA methylation of the glucocorticoid receptor gene (NR3C1) is associated with MDMA-assisted therapy treatment response for severe PTSD. <i>Frontiers in Psychiatry</i> , 0, 14, .	1.3	8
2492	Acute Transcriptomic and Epigenetic Alterations at T12 After Rat T10 Spinal Cord Contusive Injury. <i>Molecular Neurobiology</i> , 2023, 60, 2937-2953.	1.9	1

#	ARTICLE	IF	CITATIONS
2493	The Cutting Edge of Epigenetic Clocks: In Search of Mechanisms Linking Aging and Mental Health. <i>Biological Psychiatry</i> , 2023, 94, 694-705.	0.7	8
2494	Comparative and integrative analysis of transcriptomic and epigenomic-wide DNA methylation changes in African American prostate cancer. <i>Epigenetics</i> , 2023, 18, .	1.3	1
2495	Chemoprevention of lotus leaf ethanolic extract through epigenetic activation of the NRF2-mediated pathway in murine skin JB6 P+ cell neoplastic transformation. <i>Journal of Traditional and Complementary Medicine</i> , 2023, 13, 337-344.	1.5	1
2496	Crosstalk between microRNAs and epigenetics during brain development and neurological diseases. , 2023, , 173-207.		0
2497	MicroRNA Profiles in Intestinal Epithelial Cells in a Mouse Model of Sepsis. <i>Cells</i> , 2023, 12, 726.	1.8	1
2498	Coordinated alternation of DNA methylation and alternative splicing of PBRM1 affect bovine sperm structure and motility. <i>Epigenetics</i> , 2023, 18, .	1.3	1
2499	<sc>ALKBH5</sc>â€induced <sc>circular RNA NRIP1</sc> promotes glycolysis in thyroid cancer cells by targeting <sc>PKM2</sc>. <i>Cancer Science</i> , 2023, 114, 2318-2334.	1.7	8
2500	Modeling DNA Methylation Profiles and Epigenetic Analysis of Safflower (<i>Carthamus tinctorius</i> L.) Seedlings Exposed to Copper Heavy Metal. <i>Toxics</i> , 2023, 11, 255.	1.6	2
2501	Tracing 100 million years of grass genome evolutionary plasticity. <i>Plant Journal</i> , 2023, 114, 1243-1266.	2.8	3
2502	Analysis of DNA methylation markers for tissue identification in individuals with different clinical phenotypes. <i>Electrophoresis</i> , 2023, 44, 1037-1046.	1.3	0
2504	Altered DNA methylation and gene expression predict disease severity in patients with Aicardi-GoutiÃres syndrome. <i>Clinical Immunology</i> , 2023, 249, 109299.	1.4	1
2505	Mediation effects of DNA methylation and hydroxymethylation on birth outcomes after prenatal per- and polyfluoroalkyl substances (PFAS) exposure in the Michigan motherâ€infant Pairs cohort. <i>Clinical Epigenetics</i> , 2023, 15, .	1.8	10
2506	H3K4me1 Modification Functions in Caste Differentiation in Honey Bees. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6217.	1.8	2
2507	The EN-TEx resource of multi-tissue personal epigenomes& variant-impact models. <i>Cell</i> , 2023, 186, 1493-1511.e40.	13.5	13
2508	Characterization of the dual role of <i>Plasmodium falciparum</i> DNA methyltransferase in regulating transcription and translation. <i>Nucleic Acids Research</i> , 2023, 51, 3918-3933.	6.5	5
2509	A narrative review of precision medicine in neonatal sepsis: genetic and epigenetic factors associated with disease susceptibility. <i>Translational Pediatrics</i> , 2023, 12, 749-767.	0.5	1
2510	Zebularin'in Antioksidan Enzimleri ve <i>Galleria mellonella</i> (Lepidoptera: Pyralidae) Lipit Peroksidasyonu Åzerindeki Etkisi. <i>Turkish Journal of Agricultural and Natural Sciences</i> , 0, , .	0.1	0
2511	Methylation Genome-Wide Profiling in Lowly and Highly Efficient Somatic Cell Nuclear Transfer in Pigs. <i>Applied Sciences (Switzerland)</i> , 2023, 13, 4798.	1.3	0

#	ARTICLE	IF	CITATIONS
2512	Analysis of global DNA methylation and epigenetic modifiers (DNMTs and HDACs) in human foetal endothelium exposed to gestational and type 2 diabetes. <i>Epigenetics</i> , 2023, 18, .	1.3	2
2513	The <i>Dictyostelium discoideum</i> genome lacks significant DNA methylation and uncovers palindromic sequences as a source of false positives in bisulfite sequencing. <i>NAR Genomics and Bioinformatics</i> , 2023, 5, .	1.5	1
2514	Study of DNA methylation of hsd17 ^{Î²} , er and reproductive endocrine disrupting effects in female <i>Chlamys farreri</i> under benzo[a]pyrene stress. <i>Environmental Pollution</i> , 2023, 328, 121667.	3.7	4
2515	Noninvasive prenatal testing for genetic diseases. , 2023, , 789-821.		0
2516	Umbilical cord DNA methylation is associated with body mass index trajectories from birth to adolescence. <i>EBioMedicine</i> , 2023, 91, 104550.	2.7	2
2517	The epigenetics of animal personality. <i>Neuroscience and Biobehavioral Reviews</i> , 2023, 150, 105194.	2.9	2
2524	Methylation and hydroxymethylation in cancer. , 2023, , 11-37.		0
2531	Targeting epigenetic deregulations for the management of esophageal carcinoma: recent advances and emerging approaches. <i>Cell Biology and Toxicology</i> , 0, , .	2.4	1
2536	Who Will Own Our Global Digital Twin: The Power of Genetic and Biographic Information to Shape Our Lives. , 2023, , 11-35.		1
2559	ctDNA and Lung Cancer. <i>Current Cancer Research</i> , 2023, , 511-537.	0.2	0
2573	The role of epigenetics in anxiety disorders. <i>Molecular Biology Reports</i> , 0, , .	1.0	1
2592	5-Hydroxymethylcytosine: the many faces of the sixth base of mammalian DNA. <i>Chemical Society Reviews</i> , 2024, 53, 2264-2283.	18.7	0
2594	Epigenetics and substance use disorders: translational aspects. , 2024, , 353-378.		0
2596	Best practices for epigenome-wide DNA modification data collection and analysis. , 2024, , 261-284.		0
2599	Multiple approaches to understanding the benthos. , 2024, , 75-130.		0
2616	Honey Bees, Royal Jelly, Epigenetics. , 2024, , .		0