

Functions of DNA methylation: islands, start sites, gene

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Tissue-Restricted Transcription from a Conserved Intragenic CpG Island in the Klf1 Gene in Mice1. <i>Biology of Reproduction</i> , 2012, 87, 108.	1.2	9
3	Dnmt3a Protects Active Chromosome Domains against Cancer-Associated Hypomethylation. <i>PLoS Genetics</i> , 2012, 8, e1003146.	1.5	43
4	Normal DNA Methylation Dynamics in DICER1-Deficient Mouse Embryonic Stem Cells. <i>PLoS Genetics</i> , 2012, 8, e1002919.	1.5	18
5	La formalisation de la GRH dans une PME comme enjeu d'une certification RSE. <i>Revue De Gestion Des Ressources Humaines</i> , 2012, NÂ° 83, 20-30.	0.1	8
6	Epigenetic Editing: targeted rewriting of epigenetic marks to modulate expression of selected target genes. <i>Nucleic Acids Research</i> , 2012, 40, 10596-10613.	6.5	150
7	Measuring the methylome in clinical samples: Improved processing of the Infinium Human Methylation450 BeadChip Array. <i>Epigenetics</i> , 2012, 7, 1173-1187.	1.3	68
8	Demethylation initiated by ROS1 glycosylase involves random sliding along DNA. <i>Nucleic Acids Research</i> , 2012, 40, 11554-11562.	6.5	23
9	Detection of cancer-specific epigenomic changes in biofluids: Powerful tools in biomarker discovery and application. <i>Molecular Oncology</i> , 2012, 6, 704-715.	2.1	20
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11	Mapping recently identified nucleotide variants in the genome and transcriptome. <i>Nature Biotechnology</i> , 2012, 30, 1107-1116.	9.4	197
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1458	Progress towards human primordial germ cell specification <i>in vitro</i> . <i>Molecular Human Reproduction</i> , 2017, 23, 4-15.	1.3	19
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1669	Exposure to the gut microbiota drives distinct methylome and transcriptome changes in intestinal epithelial cells during postnatal development. <i>Genome Medicine</i> , 2018, 10, 27.	3.6	117
1670	Galactic Cosmic Radiation Induces Persistent Epigenome Alterations Relevant to Human Lung Cancer. <i>Scientific Reports</i> , 2018, 8, 6709.	1.6	26
1671	Effect of Methylation on Local Mechanics and Hydration Structure of DNA. <i>Biophysical Journal</i> , 2018, 114, 1791-1803.	0.2	38
1672	DNA methylation, through DNMT1, has an essential role in the development of gastrointestinal smooth muscle cells and disease. <i>Cell Death and Disease</i> , 2018, 9, 474.	2.7	20
1673	Associations of monoamine oxidase A gene first exon methylation with sexual abuse and current depression in women. <i>Journal of Neural Transmission</i> , 2018, 125, 1053-1064.	1.4	32
1674	Effect of TET2 on the pathogenesis of diabetic nephropathy through activation of transforming growth factor β 1 expression via DNA demethylation. <i>Life Sciences</i> , 2018, 207, 127-137.	2.0	24
1675	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
1676	Azacitidine (5-AzaC)-treatment and mutations in DNA methylase genes affect embryogenic response and expression of the genes that are involved in somatic embryogenesis in Arabidopsis. <i>Plant Growth Regulation</i> , 2018, 85, 243-256.	1.8	65
1677	Integration of DNA methylation & health scores identifies subtypes in myalgic encephalomyelitis/chronic fatigue syndrome. <i>Epigenomics</i> , 2018, 10, 539-557.	1.0	21
1678	Lightning Discharges, Cosmic Rays and Climate. <i>Surveys in Geophysics</i> , 2018, 39, 861-899.	2.1	15
1679	The N6-adenine methylation in yeast genome profiled by single-molecule technology. <i>Journal of Genetics and Genomics</i> , 2018, 45, 223-225.	1.7	21
1681	Hypomethylation of <i>GRHL3</i> gene is associated with the occurrence of neural tube defects. <i>Epigenomics</i> , 2018, 10, 891-901.	1.0	20
1682	Biochemical Identification of Nonmethylated DNA by BioCAP-Seq. <i>Methods in Molecular Biology</i> , 2018, 1766, 15-29.	0.4	2
1683	Modified nucleoside triphosphates exist in mammals. <i>Chemical Science</i> , 2018, 9, 4160-4167.	3.7	38
1684	Generation of TALE-Based Designer Epigenome Modifiers. <i>Methods in Molecular Biology</i> , 2018, 1767, 89-109.	0.4	5
1685	Epigenetic control of gene regulation during development and disease: A view from the retina. <i>Progress in Retinal and Eye Research</i> , 2018, 65, 1-27.	7.3	105
1686	Genome-Wide DNA Methylation in Prediagnostic Blood and Bladder Cancer Risk in the Women's Health Initiative. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 689-695.	1.1	11

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1688	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
1689	A comprehensive evaluation of alignment software for reduced representation bisulfite sequencing data. <i>Bioinformatics</i> , 2018, 34, 2715-2723.	1.8	29
1690	Effects of developmental lead exposure on the hippocampal methylome: Influences of sex and timing and level of exposure. <i>Toxicology Letters</i> , 2018, 290, 63-72.	0.4	31
1691	Epigenetic therapy: azacytidine and decitabine in acute myeloid leukemia. <i>Expert Review of Hematology</i> , 2018, 11, 361-371.	1.0	70
1692	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
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1694	Developmental DNA methyltransferase expression in the fire ant <i>Solenopsis invicta</i> . <i>Insect Science</i> , 2018, 25, 57-65.	1.5	38
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1696	Epigenetic processes in sporadic parathyroid neoplasms. <i>Molecular and Cellular Endocrinology</i> , 2018, 469, 54-59.	1.6	13
1697	Genome-Wide DNA Methylation Patterns Analysis of Noncoding RNAs in Temporal Lobe Epilepsy Patients. <i>Molecular Neurobiology</i> , 2018, 55, 793-803.	1.9	36
1698	Divergent methylation pattern in adult stage between two forms of <i>Tetranychus urticae</i> (Acari: Tj ETQq1 1 0.784314 µgBT /Over	1.5	15
1699	Neuroanatomic, epigenetic and genetic differences in monozygotic twins discordant for attention deficit hyperactivity disorder. <i>Molecular Psychiatry</i> , 2018, 23, 683-690.	4.1	44
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1702	Neuronal DNA Methyltransferases: Epigenetic Mediators between Synaptic Activity and Gene Expression?. <i>Neuroscientist</i> , 2018, 24, 171-185.	2.6	67
1703	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
1704	Alcohol exposure promotes DNA methyltransferase DNMT3A upregulation through reactive oxygen species-dependent mechanisms. <i>Cell Stress and Chaperones</i> , 2018, 23, 115-126.	1.2	25

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1706	DNA methylation signatures in peripheral blood mononuclear cells from a lifestyle intervention for women at midlife: a pilot randomized controlled trial. <i>Applied Physiology, Nutrition and Metabolism</i> , 2018, 43, 233-239.	0.9	14
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1708	BKCa channel activity and vascular contractility alterations with hypertension and aging via β 1 subunit promoter methylation in mesenteric arteries. <i>Hypertension Research</i> , 2018, 41, 96-103.	1.5	14
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1713	Polymorphisms in adrenergic receptor genes in Qinchuan cattle show associations with selected carcass traits. <i>Meat Science</i> , 2018, 135, 166-173.	2.7	13
1714	DNA methylation of methylation complex genes in relation to stress and genome-wide methylation in mother-newborn dyads. <i>American Journal of Physical Anthropology</i> , 2018, 165, 173-182.	2.1	18
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1718	Regulating microRNA expression: at the heart of diabetes mellitus and the mitochondrion. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2018, 314, H293-H310.	1.5	48
1719	DNA methylation aberrancies delineate clinically distinct subsets of colorectal cancer and provide novel targets for epigenetic therapies. <i>Oncogene</i> , 2018, 37, 566-577.	2.6	65
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1725	Roadmap for investigating epigenome deregulation and environmental origins of cancer. <i>International Journal of Cancer</i> , 2018, 142, 874-882.	2.3	64
1726	Indirect regulation of CYP2C19 gene expression via DNA methylation. <i>Xenobiotica</i> , 2018, 48, 781-792.	0.5	3
1727	Markers as mediators: A review and synthesis of epigenetics literature. <i>BioSocieties</i> , 2018, 13, 276-303.	0.8	30
1728	Correlation analyses revealed global microRNA-mRNA expression associations in human peripheral blood mononuclear cells. <i>Molecular Genetics and Genomics</i> , 2018, 293, 95-105.	1.0	12
1729	DNA Methylation Analysis from Body Fluids. <i>Methods in Molecular Biology</i> , 2018, 1655, 239-249.	0.4	13
1730	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
1731	Genome-wide DNA methylation analysis of senescence in repetitively infected memory cytotoxic T lymphocytes. <i>Immunology</i> , 2018, 153, 253-267.	2.0	3
1732	Effects of maternal methyl donor on the pork characteristics of offspring pigs with prenatal exposure to bisphenol A. <i>Animal</i> , 2018, 12, 1306-1315.	1.3	8
1733	The effects of high glucose exposure on global gene expression and DNA methylation in human pancreatic islets. <i>Molecular and Cellular Endocrinology</i> , 2018, 472, 57-67.	1.6	72
1734	Selective inhibition of CTCF binding by iAs directs TET-mediated reprogramming of 5-hydroxymethylation patterns in iAs-transformed cells. <i>Toxicology and Applied Pharmacology</i> , 2018, 338, 124-133.	1.3	12
1735	Epigenetic profiles in polyglutamine disorders. <i>Epigenomics</i> , 2018, 10, 9-25.	1.0	10
1736	Linking inter-individual variability to endocrine disruptors: insights for epigenetic inheritance. <i>Mammalian Genome</i> , 2018, 29, 141-152.	1.0	13
1737	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
1738	Methylation-Specific PCR. <i>Methods in Molecular Biology</i> , 2018, 1708, 447-472.	0.4	22
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1740	Alterations in DNA methylation patterns and gene expression in spermatozoa of subfertile males. <i>Andrologia</i> , 2018, 50, e12934.	1.0	12
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1743	Associations Between <i>MAOA</i> \times <i>VNTR</i> Genotype, Maltreatment, <i>MAOA</i> Methylation, and Alcohol Consumption in Young Adult Males. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 508-519.	1.4	15
1744	Epigenetic profiles associated with major depression in the human brain. <i>Psychiatry Research</i> , 2018, 260, 439-442.	1.7	15
1745	Welcome to the 10th volume of <i>Epigenomics</i> . <i>Epigenomics</i> , 2018, 10, 1-3.	1.0	0
1746	Vitamin B ₁₂ supplementation influences methylation of genes associated with Type 2 diabetes and its intermediate traits. <i>Epigenomics</i> , 2018, 10, 71-90.	1.0	42
1747	Epigenetic Regulation of Biological Rhythms: An Evolutionary Ancient Molecular Timer. <i>Trends in Genetics</i> , 2018, 34, 90-100.	2.9	36
1748	Mechano-adaptation of the stem cell nucleus. <i>Nucleus</i> , 2018, 9, 9-19.	0.6	31
1749	Orphan CpG islands as alternative promoters. <i>Transcription</i> , 2018, 9, 171-176.	1.7	11
1750	Genetic and epigenetic regulation of major histocompatibility complex class I gene expression in bovine trophoblast cells. <i>American Journal of Reproductive Immunology</i> , 2018, 79, e12779.	1.2	17
1751	Genomic and Epigenomic Aberrations in Esophageal Squamous Cell Carcinoma and Implications for Patients. <i>Gastroenterology</i> , 2018, 154, 374-389.	0.6	188
1752	Epigenetic drivers of tumourigenesis and cancer metastasis. <i>Seminars in Cancer Biology</i> , 2018, 51, 149-159.	4.3	246
1753	Novel epigenetic therapies in hematological malignancies: Current status and beyond. <i>Seminars in Cancer Biology</i> , 2018, 51, 198-210.	4.3	22
1754	Epigenetic dysregulation in chronic myeloid leukaemia: A myriad of mechanisms and therapeutic options. <i>Seminars in Cancer Biology</i> , 2018, 51, 180-197.	4.3	53
1755	Neuroimaging Epigenetics: Challenges and Recommendations for Best Practices. <i>Neuroscience</i> , 2018, 370, 88-100.	1.1	19
1756	Renal transplantation increases angiotensin II receptor-mediated vascular contractility associated with changes of epigenetic mechanisms. <i>International Journal of Molecular Medicine</i> , 2018, 41, 2375-2388.	1.8	5
1757	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
1758	Gene methylation in liquid biopsy and risk of recurrence in lung cancer. <i>Journal of Thoracic Disease</i> , 2018, 10, 1286-1289.	0.6	2
1759	DNA Methylation and Chromatin: Role(s) of Methyl-CpG-Binding Protein ZBTB38. <i>Epigenetics Insights</i> , 2018, 11, 251686571881111.	0.6	17

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1767	Methylation profiles of <i>IL33</i> and <i>CCL26</i> in bronchial epithelial cells are associated with asthma. Epigenomics, 2018, 10, 1555-1568.	1.0	9
1768	Hepatic gene body hypermethylation is a shared epigenetic signature of murine longevity. PLoS Genetics, 2018, 14, e1007766.	1.5	8
1769	Methylome profiling of healthy and central precocious puberty girls. Clinical Epigenetics, 2018, 10, 146.	1.8	34
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1771	Epigenetic Heterogeneity in Human Colorectal Tumors Reveals Preferential Conservation And Evidence of Immune Surveillance. Scientific Reports, 2018, 8, 17292.	1.6	17
1772	Molecular Processes Connecting DNA Methylation Patterns with DNA Methyltransferases and Histone Modifications in Mammalian Genomes. Genes, 2018, 9, 566.	1.0	55
1773	Potential Epigenetic-Based Therapeutic Targets for Glioma. Frontiers in Molecular Neuroscience, 2018, 11, 408.	1.4	64
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1776	Epigenetic mechanisms and implications in tendon inflammation (Review). International Journal of Molecular Medicine, 2019, 43, 3-14.	1.8	10
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1780	Aberrant DNA methylation of <i>Tgfb1</i> in diabetic kidney mesangial cells. <i>Scientific Reports</i> , 2018, 8, 16338.	1.6	18
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1786	The Epigenome in Multiple Myeloma: Impact on Tumor Cell Plasticity and Drug Response. <i>Frontiers in Oncology</i> , 2018, 8, 566.	1.3	39
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1788	Blood-Based DNA Methylation Biomarkers for Type 2 Diabetes: Potential for Clinical Applications. <i>Frontiers in Endocrinology</i> , 2018, 9, 744.	1.5	56
1789	Data-Driven-Based Approach to Identifying Differentially Methylated Regions Using Modified 1D Ising Model. <i>BioMed Research International</i> , 2018, 2018, 1-8.	0.9	6
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1798	Investigation of allele-specific expression of genes involved in adipogenesis and lipid metabolism suggests complex regulatory mechanisms of PPARGC1A expression in porcine fat tissues. <i>BMC Genetics</i> , 2018, 19, 107.	2.7	7
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1800	High PITX1 expression in lung adenocarcinoma patients is associated with DNA methylation and poor prognosis. <i>Pathology Research and Practice</i> , 2018, 214, 2046-2053.	1.0	24
1801	Exposure to Polycyclic Aromatic Hydrocarbons and Accelerated DNA Methylation Aging. <i>Environmental Health Perspectives</i> , 2018, 126, 067005.	2.8	62
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1804	Dynamic DNA methylation: In the right place at the right time. <i>Science</i> , 2018, 361, 1336-1340.	6.0	469
1805	Transgenerational transmission of maternal stimulatory experience in domesticated birds. <i>FASEB Journal</i> , 2018, 32, 7002-7017.	0.2	10
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1807	Epigenetics and Carcinogenesis. , 2018, , 271-288.		0
1808	Dynamic DNA Methylation Changes of <i>Tbx21</i> and <i>Rorc</i> during Experimental Autoimmune Uveitis in Mice. <i>Mediators of Inflammation</i> , 2018, 2018, 1-13.	1.4	16
1809	DNA G-quadruplex structures mold the DNA methylome. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 951-957.	3.6	185
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1813	In Utero Heat Stress Alters the Offspring Epigenome. <i>Scientific Reports</i> , 2018, 8, 14609.	1.6	78
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1816	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
1817	Circularly permuted variants of two CG-specific prokaryotic DNA methyltransferases. <i>PLoS ONE</i> , 2018, 13, e0197232.	1.1	5
1818	A Novel Computational Method for Detecting DNA Methylation Sites with DNA Sequence Information and Physicochemical Properties. <i>International Journal of Molecular Sciences</i> , 2018, 19, 511.	1.8	38
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1824	Dynamic Methylation Changes of DNA and H3K4 by RG108 Improve Epigenetic Reprogramming of Somatic Cell Nuclear Transfer Embryos in Pigs. <i>Cellular Physiology and Biochemistry</i> , 2018, 50, 1376-1397.	1.1	17
1825	Phytophthora methylomes are modulated by 6mA methyltransferases and associated with adaptive genome regions. <i>Genome Biology</i> , 2018, 19, 181.	3.8	61
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1996	Expanding the Chemical Space of Nonribosomal Peptide Synthetase-like Enzymes by Domain and Tailoring Enzyme Recombination. <i>Organic Letters</i> , 2018, 20, 5082-5085.	2.4	7
1997	Hypermethylation of gene body CpG islands predicts high dosage of functional oncogenes in liver cancer. <i>Nature Communications</i> , 2018, 9, 3164.	5.8	134
1998	Memory Function in Feeding Habit Transformation of Mandarin Fish (<i>Siniperca chuatsi</i>). <i>International Journal of Molecular Sciences</i> , 2018, 19, 1254.	1.8	15
1999	Dietary intake of one-carbon metabolism nutrients and DNA methylation in peripheral blood. <i>American Journal of Clinical Nutrition</i> , 2018, 108, 611-621.	2.2	35
2000	Characterizing genetic and environmental influences on variable DNA methylation using monozygotic and dizygotic twins. <i>PLoS Genetics</i> , 2018, 14, e1007544.	1.5	153
2001	Fluorescent copper nanoclusters as a nano-dye for DNA methyltransferase activity analysis and inhibitor screening. <i>Analytical Biochemistry</i> , 2018, 559, 5-10.	1.1	6
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2003	DNA methylation regulates transcriptional homeostasis of algal endosymbiosis in the coral model <i>Aiptasia</i> . <i>Science Advances</i> , 2018, 4, eaat2142.	4.7	77
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2005	Nerve Injury-Induced Chronic Pain Is Associated with Persistent DNA Methylation Reprogramming in Dorsal Root Ganglion. <i>Journal of Neuroscience</i> , 2018, 38, 6090-6101.	1.7	66
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2007	Hydrophobic Modifications of Biomolecules: An Introduction. , 2018, , 477-486.		0
2008	DNA Methylation in Eukaryotes: Regulation and Function. , 2018, , 509-570.		0
2009	Promoter methylation of <i>PGC1A</i> and <i>PGC1B</i> predicts cancer incidence in a veteran cohort. <i>Epigenomics</i> , 2018, 10, 733-743.	1.0	12
2010	Tracking age-correlated DNA methylation markers in the young. <i>Forensic Science International: Genetics</i> , 2018, 36, 50-59.	1.6	41
2011	Combined SOM-portrayal of gene expression and DNA methylation landscapes disentangles modes of epigenetic regulation in glioblastoma. <i>Epigenomics</i> , 2018, 10, 745-764.	1.0	34
2012	Association of mitofusin 2 methylation and essential hypertension: a case-control study in a Chinese population. <i>Hypertension Research</i> , 2018, 41, 605-613.	1.5	7

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2015	Central Nervous System Development. , 2018, , 852-856.e1.		0
2016	Genome-wide DNA methylation signatures of infection status in Trinidadian guppies (<i>Poecilia</i>). <i>Tj ETQq1 1 0.784314 rgBTJ /Overl</i>	2.0	34
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2038	Profiling DNA methylation patterns of zebrafish liver associated with parental high dietary arachidonic acid. <i>PLoS ONE</i> , 2019, 14, e0220934.	1.1	19
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2061	<i>Systems-Level Understanding of Single-Cell Omics</i> , 2019, , 433-456.		0
2062	Tobacco smoking induces changes in true DNA methylation, hydroxymethylation and gene expression in bronchoalveolar lavage cells. <i>EBioMedicine</i> , 2019, 46, 290-304.	2.7	48
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2067	Epigenetic regulation of POMC; implications for nutritional programming, obesity and metabolic disease. <i>Frontiers in Neuroendocrinology</i> , 2019, 54, 100773.	2.5	48

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2073	Integrative analysis of DNA methylation and gene expression profiles identifies MIR4435-2HG as an oncogenic lncRNA for glioma progression. <i>Gene</i> , 2019, 715, 144012.	1.0	23
2074	Transcriptional networks in acute myeloid leukemia. <i>Genes Chromosomes and Cancer</i> , 2019, 58, 859-874.	1.5	20
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2077	Maternal and Post-weaning High-Fat Diets Produce Distinct DNA Methylation Patterns in Hepatic Metabolic Pathways within Specific Genomic Contexts. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3229.	1.8	10
2078	Chromatin Architecture as an Essential Determinant of Dendritic Cell Function. <i>Frontiers in Immunology</i> , 2019, 10, 1119.	2.2	14
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2082	<i>IRX1</i> hypermethylation promotes heart failure by inhibiting <i>CXCL14</i> expression. <i>Cell Cycle</i> , 2019, 18, 3251-3262.	1.3	9
2083	DNA methylation and behavioral changes induced by neonatal spinal transection. , 2019, 57, 101381.		3
2084	Differential COMT DNA methylation in patients with Borderline Personality Disorder: Genotype matters. <i>European Neuropsychopharmacology</i> , 2019, 29, 1295-1300.	0.3	8
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2088	Epigenetic signatures of smoking associate with cognitive function, brain structure, and mental and physical health outcomes in the Lothian Birth Cohort 1936. <i>Translational Psychiatry</i> , 2019, 9, 248.	2.4	34
2089	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
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2091	DNA Methylation: Toward Crop Disease Resistance Improvement. <i>Trends in Plant Science</i> , 2019, 24, 1137-1150.	4.3	76
2092	Early-life DNA methylation profiles are indicative of age-related transcriptome changes. <i>Epigenetics and Chromatin</i> , 2019, 12, 58.	1.8	22
2093	Methylation and gene expression differences between reproductive and sterile bumblebee workers. <i>Evolution Letters</i> , 2019, 3, 485-499.	1.6	48
2094	Differentially methylated gene patterns between age-matched sarcopenic and non-sarcopenic women. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2019, 10, 1295-1306.	2.9	19
2095	Preliminary Analysis of Within-Sample Co-methylation Patterns in Normal and Cancerous Breast Samples. <i>Cancer Informatics</i> , 2019, 18, 117693511988051.	0.9	3
2096	Transcriptome and DNA Methylome Signatures Associated With Retinal Müller Glia Development, Injury Response, and Aging. , 2019, 60, 4436.		13
2097	A review of computational algorithms for CpG islands detection. <i>Journal of Biosciences</i> , 2019, 44, 1.	0.5	6
2098	Cell-Free DNA Methylation Profiling Analysis Technologies and Bioinformatics. <i>Cancers</i> , 2019, 11, 1741.	1.7	37
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2109	Perinatal Bisphenol A Exposure and Reprogramming of Imprinted Gene Expression in the Adult Mouse Brain. <i>Frontiers in Genetics</i> , 2019, 10, 951.	1.1	13
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2122	Epigenetic downregulation of STAT6 increases HIF-1 α expression via mTOR/S6K/S6, leading to enhanced hypoxic viability of glioma cells. <i>Acta Neuropathologica Communications</i> , 2019, 7, 149.	2.4	14
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2126	Dynamic changes of muscle insulin sensitivity after metabolic surgery. <i>Nature Communications</i> , 2019, 10, 4179.	5.8	47
2127	Identification of bovine CpG SNPs as potential targets for epigenetic regulation via DNA methylation. <i>PLoS ONE</i> , 2019, 14, e0222329.	1.1	8
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2129	Perspectives of personalized weight loss interventions based on exercise genomics, nutrigenetic, epigenetic, and metagenomic data in fitness and sport. , 2019, , 487-508.		1
2130	Mechanism of ectopic hormone receptors in adrenal tumors and hyperplasia. <i>Current Opinion in Endocrine and Metabolic Research</i> , 2019, 8, 206-212.	0.6	4
2131	Artificial Light Pollution at Night: A Risk for Normal Circadian Rhythm and Physiological Functions in Humans. <i>Current Environmental Engineering</i> , 2019, 6, 111-125.	0.6	13
2132	Molecular Signature of CAID Syndrome: Noncanonical Roles of SGO1 in Regulation of TGF- β 2 Signaling and Epigenomics. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2019, 7, 411-431.	2.3	11
2133	DNA methylation in mice is influenced by genetics as well as sex and life experience. <i>Nature Communications</i> , 2019, 10, 305.	5.8	40
2134	Prenatal Bisphenol A Exposure in Mice Induces Multitissue Multiomics Disruptions Linking to Cardiometabolic Disorders. <i>Endocrinology</i> , 2019, 160, 409-429.	1.4	35
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2136	Challenges in Quantifying Cytosine Methylation in the HIV Provirus. <i>MBio</i> , 2019, 10, .	1.8	11
2137	BRIF-Seq: Bisulfite-Converted Randomly Integrated Fragments Sequencing at the Single-Cell Level. <i>Molecular Plant</i> , 2019, 12, 438-446.	3.9	17
2139	A Pilot Study Using a Multistaged Integrated Analysis of Gene Expression and Methylation to Evaluate Mechanisms for Evening Fatigue in Women Who Received Chemotherapy for Breast Cancer. <i>Biological Research for Nursing</i> , 2019, 21, 142-156.	1.0	10
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2141	Highly methylated Xist in SCNT embryos was retained in deceased cloned female goats. <i>Reproduction, Fertility and Development</i> , 2019, 31, 855.	0.1	12
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2145	MyD88 hypermethylation mediated by DNMT1 is associated with LTA-induced inflammatory response in human odontoblast-like cells. <i>Cell and Tissue Research</i> , 2019, 376, 413-423.	1.5	18
2146	CpG traffic lights are markers of regulatory regions in human genome. <i>BMC Genomics</i> , 2019, 20, 102.	1.2	43
2147	Predicting resistance to endocrine therapy in breast cancer: It's time for epigenetic biomarkers (Review). <i>Oncology Reports</i> , 2019, 41, 1431-1438.	1.2	13
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2149	Epigenetic Mechanisms in Hepatic Stellate Cell Activation During Liver Fibrosis and Carcinogenesis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2507.	1.8	45
2150	Effect of CREB1 promoter non-CpG island methylation on its differential expression profile on sheep ovaries associated with prolificacy. <i>Tissue and Cell</i> , 2019, 58, 61-69.	1.0	2
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2152	Effect of Disease-Associated Germline Mutations on Structure Function Relationship of DNA Methyltransferases. <i>Genes</i> , 2019, 10, 369.	1.0	23
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