

# Huidong Shi

## List of Publications by Year in descending order

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137  
papers

8,410  
citations

50170

46  
h-index

48187

88  
g-index

143  
all docs

143  
docs citations

143  
times ranked

14319  
citing authors

#	ARTICLE	IF	CITATIONS
1	Activation of Gpr109a, Receptor for Niacin and the Commensal Metabolite Butyrate, Suppresses Colonic Inflammation and Carcinogenesis. <i>Immunity</i> , 2014, 40, 128-139.	6.6	1,654
2	Combined epigenetic therapy with the histone methyltransferase EZH2 inhibitor 3-deazaneplanocin A and the histone deacetylase inhibitor panobinostat against human AML cells. <i>Blood</i> , 2009, 114, 2733-2743.	0.6	336
3	Ultradeep Bisulfite Sequencing Analysis of DNA Methylation Patterns in Multiple Gene Promoters by 454 Sequencing. <i>Cancer Research</i> , 2007, 67, 8511-8518.	0.4	252
4	Methylation-Specific Oligonucleotide Microarray: A New Potential for High-Throughput Methylation Analysis. <i>Genome Research</i> , 2002, 12, 158-164.	2.4	247
5	Butyrate suppresses colonic inflammation through HDAC1-dependent Fas upregulation and Fas-mediated apoptosis of T cells. <i>American Journal of Physiology - Renal Physiology</i> , 2012, 302, G1405-G1415.	1.6	218
6	DNMT1 is essential for mammary and cancer stem cell maintenance and tumorigenesis. <i>Nature Communications</i> , 2015, 6, 6910.	5.8	204
7	Obesity related methylation changes in DNA of peripheral blood leukocytes. <i>BMC Medicine</i> , 2010, 8, 87.	2.3	187
8	The MLL1-H3K4me3 Axis-Mediated PD-L1 Expression and Pancreatic Cancer Immune Evasion. <i>Journal of the National Cancer Institute</i> , 2017, 109, djw283.	3.0	182
9	A genome-wide methylation study on obesity. <i>Epigenetics</i> , 2013, 8, 522-533.	1.3	174
10	Metabolomic Profiling Reveals Potential Markers and Bioprocesses Altered in Bladder Cancer Progression. <i>Cancer Research</i> , 2011, 71, 7376-7386.	0.4	166
11	An Inherently Bifunctional Subset of Foxp3+ T Helper Cells Is Controlled by the Transcription Factor Eos. <i>Immunity</i> , 2013, 38, 998-1012.	6.6	159
12	Methylation microarray analysis of late-stage ovarian carcinomas distinguishes progression-free survival in patients and identifies candidate epigenetic markers. <i>Clinical Cancer Research</i> , 2002, 8, 2246-52.	3.2	156
13	Label-free quantitative DNA detection using the liquid core optical ring resonator. <i>Biosensors and Bioelectronics</i> , 2008, 23, 1003-1009.	5.3	145
14	Inhibiting DNA Methylation by 5-Aza-2-deoxycytidine Ameliorates Atherosclerosis Through Suppressing Macrophage Inflammation. <i>Endocrinology</i> , 2014, 155, 4925-4938.	1.4	138
15	Epigenetic regulation of macrophage polarization and inflammation by DNA methylation in obesity. <i>JCI Insight</i> , 2016, 1, e87748.	2.3	138
16	Large-Scale CpG Methylation Analysis Identifies Novel Candidate Genes and Reveals Methylation Hotspots in Acute Lymphoblastic Leukemia. <i>Cancer Research</i> , 2007, 67, 2617-2625.	0.4	134
17	Soy Isoflavones Have an Antiestrogenic Effect and Alter Mammary Promoter Hypermethylation in Healthy Premenopausal Women. <i>Nutrition and Cancer</i> , 2009, 61, 238-244.	0.9	126
18	Combined Inhibition of DNMT and HDAC Blocks the Tumorigenicity of Cancer Stem-like Cells and Attenuates Mammary Tumor Growth. <i>Cancer Research</i> , 2016, 76, 3224-3235.	0.4	122

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19	Oligonucleotide-based microarray for DNA methylation analysis: Principles and applications. <i>Journal of Cellular Biochemistry</i> , 2003, 88, 138-143.	1.2	119
20	A systematic evaluation of miRNA:mRNA interactions involved in the migration and invasion of breast cancer cells. <i>Journal of Translational Medicine</i> , 2013, 11, 57.	1.8	117
21	CD73 on cancer-associated fibroblasts enhanced by the A2B-mediated feedforward circuit enforces an immune checkpoint. <i>Nature Communications</i> , 2020, 11, 515.	5.8	117
22	Triple analysis of the cancer epigenome: an integrated microarray system for assessing gene expression, DNA methylation, and histone acetylation. <i>Cancer Research</i> , 2003, 63, 2164-71.	0.4	109
23	Double RNA interference of DNMT3b and DNMT1 enhances DNA demethylation and gene reactivation. <i>Cancer Research</i> , 2003, 63, 6110-5.	0.4	109
24	Loss of Methyl-CpGâ€“Binding Domain Protein 2 Enhances Endothelial Angiogenesis and Protects Mice Against Hind-Limb Ischemic Injury. <i>Circulation</i> , 2011, 123, 2964-2974.	1.6	104
25	Metabolic flux analysis for biosynthesis of poly(Î²-hydroxybutyric acid) in <i>Alcaligenes eutrophus</i> from various carbon sources. <i>Journal of Bioscience and Bioengineering</i> , 1997, 84, 579-587.	0.9	98
26	MBD3 Localizes at Promoters, Gene Bodies and Enhancers of Active Genes. <i>PLoS Genetics</i> , 2013, 9, e1004028.	1.5	97
27	Activation of p53 in Immature Myeloid Precursor Cells Controls Differentiation into Ly6c+CD103+ Monocytic Antigen-Presenting Cells in Tumors. <i>Immunity</i> , 2018, 48, 91-106.e6.	6.6	95
28	Methylation Target Array for Rapid Analysis of CpG Island Hypermethylation in Multiple Tissue Genomes. <i>American Journal of Pathology</i> , 2003, 163, 37-45.	1.9	92
29	Differential distribution of DNA methylation within the RASSF1A CpG island in breast cancer. <i>Cancer Research</i> , 2003, 63, 6178-86.	0.4	88
30	A Genome-Wide Methylation Study of Severe Vitamin D Deficiency in African American Adolescents. <i>Journal of Pediatrics</i> , 2013, 162, 1004-1009.e1.	0.9	87
31	Genome-wide DNA methylation analysis reveals novel epigenetic changes in chronic lymphocytic leukemia. <i>Epigenetics</i> , 2012, 7, 567-578.	1.3	85
32	Discovery of novel epigenetic markers in non-Hodgkin's lymphoma. <i>Carcinogenesis</i> , 2007, 28, 60-70.	1.3	83
33	Analyzing the cancer methylome through targeted bisulfite sequencing. <i>Cancer Letters</i> , 2013, 340, 171-178.	3.2	75
34	Predicting DNA Methylation State of CpG Dinucleotide Using Genome Topological Features and Deep Networks. <i>Scientific Reports</i> , 2016, 6, 19598.	1.6	75
35	Differential DNA methylation patterns of small B-cell lymphoma subclasses with different clinical behavior. <i>Leukemia</i> , 2006, 20, 1855-1862.	3.3	74
36	Applications of CpG Island Microarrays for High-Throughput Analysis of DNA Methylation. <i>Journal of Nutrition</i> , 2002, 132, 2430S-2434S.	1.3	73

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37	Large-Scale Characterization of DNA Methylation Changes in Human Gastric Carcinomas with and without Metastasis. <i>Clinical Cancer Research</i> , 2014, 20, 4598-4612.	3.2	73
38	SHOX2 Is a Direct miR-375 Target and a Novel Epithelial-to-Mesenchymal Transition Inducer in Breast Cancer Cells. <i>Neoplasia</i> , 2014, 16, 279-290.e5.	2.3	72
39	Display of green fluorescent protein on Escherichia coli cell surface. <i>Enzyme and Microbial Technology</i> , 2001, 28, 25-34.	1.6	68
40	Targeted bisulfite sequencing by solution hybrid selection and massively parallel sequencing. <i>Nucleic Acids Research</i> , 2011, 39, e127-e127.	6.5	61
41	Expressed CpG island sequence tag microarray for dual screening of DNA hypermethylation and gene silencing in cancer cells. <i>Cancer Research</i> , 2002, 62, 3214-20.	0.4	61
42	DNA hypermethylation accompanied by transcriptional repression in follicular lymphoma. <i>Genes Chromosomes and Cancer</i> , 2009, 48, 828-841.	1.5	59
43	Large-scale analysis of DNA methylation in chronic lymphocytic leukemia. <i>Epigenomics</i> , 2009, 1, 39-61.	1.0	57
44	A Genome-Wide Methylation Study on Essential Hypertension in Young African American Males. <i>PLoS ONE</i> , 2013, 8, e53938.	1.1	57
45	Dynamics and modeling on fermentative production of poly ( $\gamma$ -hydroxybutyric acid) from sugars via lactate by a mixed culture of <i>Lactobacillus delbrueckii</i> and <i>Alcaligenes eutrophus</i> . <i>Journal of Biotechnology</i> , 1999, 67, 113-134.	1.9	55
46	CpG islands: their potential as biomarkers for cancer. <i>Expert Review of Molecular Diagnostics</i> , 2007, 7, 519-531.	1.5	55
47	Label-free DNA methylation analysis using opto-fluidic ring resonators. <i>Biosensors and Bioelectronics</i> , 2010, 26, 1016-1020.	5.3	50
48	Identification of Global DNA Methylation Signatures in Glioblastoma-Derived Cancer Stem Cells. <i>Journal of Genetics and Genomics</i> , 2015, 42, 355-371.	1.7	47
49	Autocrine IL6-Mediated Activation of the STAT3-DNMT Axis Silences the TNF-RIP1 Necroptosis Pathway to Sustain Survival and Accumulation of Myeloid-Derived Suppressor Cells. <i>Cancer Research</i> , 2020, 80, 3145-3156.	0.4	47
50	Dual Therapeutic Utility of Proteasome Modulating Agents for Pharmacogeno-gene Therapy of the Cystic Fibrosis Airway. <i>Molecular Therapy</i> , 2004, 10, 990-1002.	3.7	46
51	Isolation and characterization of a population of stem-like progenitor cells from an atypical meningioma. <i>Experimental and Molecular Pathology</i> , 2011, 90, 179-188.	0.9	45
52	Stem Cells as Vectors to Deliver HSV/tk Gene Therapy for Malignant Gliomas. <i>Current Stem Cell Research and Therapy</i> , 2009, 4, 44-49.	0.6	43
53	DNA methylation protects against cisplatin-induced kidney injury by regulating specific genes, including interferon regulatory factor 8. <i>Kidney International</i> , 2017, 92, 1194-1205.	2.6	43
54	Effect of modifying metabolic network on poly-3-hydroxybutyrate biosynthesis in recombinant <i>Escherichia coli</i> . <i>Journal of Bioscience and Bioengineering</i> , 1999, 87, 666-677.	1.1	42

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55	Hypomethylation coordinates antagonistically with hypermethylation in cancer development: a case study of leukemia. <i>Human Genomics</i> , 2016, 10, 18.	1.4	40
56	Persistent STAT5 activation reprograms the epigenetic landscape in CD4 <sup>+</sup> T cells to drive polyfunctionality and antitumor immunity. <i>Science Immunology</i> , 2020, 5, .	5.6	40
57	WDR5-H3K4me3 epigenetic axis regulates OPN expression to compensate PD-L1 function to promote pancreatic cancer immune escape. , 2021, 9, e002624.		36
58	Genome-Wide DNA Methylation Maps in Follicular Lymphoma Cells Determined by Methylation-Enriched Bisulfite Sequencing. <i>PLoS ONE</i> , 2010, 5, e13020.	1.1	35
59	Inhibition of the BTK-IDO-mTOR axis promotes differentiation of monocyte-lineage dendritic cells and enhances anti-tumor T cell immunity. <i>Immunity</i> , 2021, 54, 2354-2371.e8.	6.6	34
60	An epigenome-wide study of obesity in African American youth and young adults: novel findings, replication in neutrophils, and relationship with gene expression. <i>Clinical Epigenetics</i> , 2018, 10, 3.	1.8	33
61	Long non-coding RNAs transcribed by ERV-9 LTR retrotransposon act in cis to modulate long-range LTR enhancer function. <i>Nucleic Acids Research</i> , 2017, 45, gkx055.	6.5	32
62	A novel immunohistochemical score to predict early mortality in acute myeloid leukemia patients based on indoleamine 2,3 dioxygenase expression. <i>Scientific Reports</i> , 2017, 7, 12892.	1.6	31
63	THZ1 suppresses human non-small-cell lung cancer cells in vitro through interference with cancer metabolism. <i>Acta Pharmacologica Sinica</i> , 2019, 40, 814-822.	2.8	31
64	Differential DNA Methylation of Gene Promoters in Small B-Cell Lymphomas. <i>American Journal of Clinical Pathology</i> , 2005, 124, 430-439.	0.4	30
65	Phenotypic alteration of CD8 <sup>+</sup> T cells in chronic lymphocytic leukemia is associated with epigenetic reprogramming. <i>Oncotarget</i> , 2016, 7, 40558-40570.	0.8	30
66	The androgen receptor gene is preferentially hypermethylated in follicular non-Hodgkin's lymphomas. <i>Clinical Cancer Research</i> , 2003, 9, 4034-42.	3.2	29
67	Targeting HSF1 disrupts HSP90 chaperone function in chronic lymphocytic leukemia. <i>Oncotarget</i> , 2015, 6, 31767-31779.	0.8	28
68	Promoter Methylation Modulates Indoleamine 2,3-Dioxygenase 1 Induction by Activated T Cells in Human Breast Cancers. <i>Cancer Immunology Research</i> , 2017, 5, 330-344.	1.6	28
69	The co-chaperone UNC45A is essential for the expression of mitotic kinase NEK7 and tumorigenesis. <i>Journal of Biological Chemistry</i> , 2019, 294, 5246-5260.	1.6	27
70	Adipose tissue-derived neurotrophic factor 3 regulates sympathetic innervation and thermogenesis in adipose tissue. <i>Nature Communications</i> , 2021, 12, 5362.	5.8	27
71	HOXC9 directly regulates distinct sets of genes to coordinate diverse cellular processes during neuronal differentiation. <i>BMC Genomics</i> , 2013, 14, 830.	1.2	24
72	Epigenetic Hypothesis Tests for Methylation and Acetylation in a Triple Microarray System. <i>Journal of Computational Biology</i> , 2005, 12, 370-390.	0.8	21

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73	Developmental cues and persistent neurogenic potential within an in vitro neural niche. BMC Developmental Biology, 2010, 10, 5.	2.1	21
74	PRIMEGENS-v2: genome-wide primer design for analyzing DNA methylation patterns of CpG islands. Bioinformatics, 2008, 24, 1837-1842.	1.8	19
75	Roles of Distal and Genic Methylation in the Development of Prostate Tumorigenesis Revealed by Genome-wide DNA Methylation Analysis. Scientific Reports, 2016, 6, 22051.	1.6	19
76	Discovery and Validation of a Novel Neutrophil Activation Marker Associated with Obesity. Scientific Reports, 2019, 9, 3433.	1.6	19
77	RPPA-based protein profiling reveals eIF4G overexpression and 4E-BP1 serine 65 phosphorylation as molecular events that correspond with a pro-survival phenotype in chronic lymphocytic leukemia. Oncotarget, 2015, 6, 14632-14645.	0.8	19
78	A survey of computational methods in transcriptome-wide alternative splicing analysis. Biomolecular Concepts, 2015, 6, 59-66.	1.0	18
79	CD38 Deficiency Promotes Inflammatory Response through Activating Sirt1/NF- $\kappa$ B-Mediated Inhibition of TLR2 Expression in Macrophages. Mediators of Inflammation, 2018, 2018, 1-13.	1.4	18
80	Aberrant Epigenetic Gene Regulation in Lymphoid Malignancies. Seminars in Hematology, 2013, 50, 38-47.	1.8	17
81	Sequencing the Cancer Methylome. Methods in Molecular Biology, 2015, 1238, 627-651.	0.4	15
82	On-line metabolic pathway analysis based on metabolic signal flow diagram. , 1998, 58, 139-148.		14
83	A Method to Detect Differentially Methylated Loci With Next-Generation Sequencing. Genetic Epidemiology, 2013, 37, 377-382.	0.6	14
84	Hypermethylated LTR retrotransposon exhibits enhancer activity. Epigenetics, 2017, 12, 226-237.	1.3	14
85	Differential DNA methylation of gene promoters in small B-cell lymphomas. American Journal of Clinical Pathology, 2005, 124, 430-9.	0.4	14
86	FKBP12.6 protects heart from AngII-induced hypertrophy through inhibiting Ca <sup>2+</sup> /calmodulin-mediated signalling pathways in vivo and in vitro. Journal of Cellular and Molecular Medicine, 2018, 22, 3638-3651.	1.6	13
87	Computational Methods and Correlation of Exon-skipping Events with Splicing, Transcription, and Epigenetic Factors. Methods in Molecular Biology, 2017, 1513, 163-170.	0.4	12
88	Unlocking the epigenetic code of T cell exhaustion. Translational Cancer Research, 2017, 6, S384-S387.	0.4	12
89	The expression of RUNDC3B is associated with promoter methylation in lymphoid malignancies. Hematological Oncology, 2017, 35, 25-33.	0.8	11
90	Epigenetic interaction between UTX and DNMT1 regulates diet-induced myogenic remodeling in brown fat. Nature Communications, 2021, 12, 6838.	5.8	11

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91	Novel low-avidity glypican-3 specific CARTs resist exhaustion and mediate durable antitumor effects against HCC. <i>Hepatology</i> , 2022, 76, 330-344.	3.6	11
92	Promoter DNA methylation of CD10 in lymphoid malignancies. <i>Leukemia</i> , 2006, 20, 1910-1912.	3.3	10
93	G6PD functions as a metabolic checkpoint to regulate granzyme B expression in tumor-specific cytotoxic T lymphocytes. , 2022, 10, e003543.		10
94	H3K9me3 represses G6PD expression to suppress the pentose phosphate pathway and ROS production to promote human mesothelioma growth. <i>Oncogene</i> , 2022, , .	2.6	10
95	Recruitment of monocytes and epigenetic silencing of intratumoral CYP7B1 primarily contribute to the accumulation of 27-hydroxycholesterol in breast cancer. <i>American Journal of Cancer Research</i> , 2019, 9, 2194-2208.	1.4	9
96	Complete genome sequence and analysis of the industrial <i>Saccharomyces cerevisiae</i> strain N85 used in Chinese rice wine production. <i>DNA Research</i> , 2018, 25, 297-306.	1.5	8
97	Dnmt3b Deficiency in Myf5+-Brown Fat Precursor Cells Promotes Obesity in Female Mice. <i>Biomolecules</i> , 2021, 11, 1087.	1.8	8
98	Restoring FAS Expression via Lipid-Encapsulated FAS DNA Nanoparticle Delivery Is Sufficient to Suppress Colon Tumor Growth In Vivo. <i>Cancers</i> , 2022, 14, 361.	1.7	8
99	Temperature-induced expression of phb genes in <i>Escherichia coli</i> and the effect of temperature patterns on the production of poly-3-hydroxybutyrate. <i>Journal of Bioscience and Bioengineering</i> , 2001, 91, 21-26.	1.1	7
100	Indoximod Combined with Standard Induction Chemotherapy Is Well Tolerated and Induces a High Rate of Complete Remission with MRD-Negativity in Patients with Newly Diagnosed AML: Results from a Phase I Trial. <i>Blood</i> , 2018, 132, 332-332.	0.6	7
101	Molecular detection of B-cell neoplasms by specific DNA methylation biomarkers. <i>International Journal of Clinical and Experimental Pathology</i> , 2010, 3, 265-79.	0.5	7
102	An integrated metabolic pathway analysis based on metabolic signal flow diagram and cellular energetics for <i>Saccharomyces cerevisiae</i> . <i>Journal of Bioscience and Bioengineering</i> , 1997, 83, 275-280.	0.9	6
103	A similar effect of P16 hydroxymethylation and true-methylation on the prediction of malignant transformation of oral epithelial dysplasia: observation from a prospective study. <i>BMC Cancer</i> , 2018, 18, 918.	1.1	6
104	The Monocytes That Repopulate in Mice After Cyclophosphamide Treatment Acquire a Neutrophil Precursor Gene Signature and Immunosuppressive Activity. <i>Frontiers in Immunology</i> , 2020, 11, 594540.	2.2	6
105	Relational Analysis of CpG Islands Methylation and Gene Expression in Human Lymphomas Using Possibilistic C-Means Clustering and Modified Cluster Fuzzy Density. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 176-189.	1.9	5
106	Differential methylation tests of regulatory regions. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2016, 15, 237-251.	0.2	5
107	NRF2 mediates $\beta$ -globin gene regulation through epigenetic modifications in a $\beta$ -YAC transgenic mouse model. <i>Experimental Biology and Medicine</i> , 2020, 245, 1308-1318.	1.1	5
108	DNA Hypomethylation within B-Cell Enhancers and Super Enhancers Reveal a Dependency on Immune and Metabolic Mechanisms in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2016, 128, 1049-1049.	0.6	5

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109	Next Generation Sequencing: Advances in Characterizing the Methylome. <i>Genes</i> , 2010, 1, 143-165.	1.0	4
110	CAME: identification of chromatin accessibility from nucleosome occupancy and methylome sequencing. <i>Bioinformatics</i> , 2017, 33, 1139-1146.	1.8	4
111	Genome wide DNA differential methylation regions in colorectal cancer patients in relation to blood related family members, obese and non-obese controls - a preliminary report. <i>Oncotarget</i> , 2018, 9, 25557-25571.	0.8	3
112	Haemophagocytic lymphohistiocytosis occurred during induction chemotherapy in an acute monocytic leukemia patient with FLT3-ITD and DNMT3A mutations. <i>BMC Cancer</i> , 2018, 18, 604.	1.1	2
113	Detection of Differentially Methylated Regions Using Bayes Factor for Ordinal Group Responses. <i>Genes</i> , 2019, 10, 721.	1.0	2
114	Brown Fat Dnmt3b Deficiency Ameliorates Obesity in Female Mice. <i>Life</i> , 2021, 11, 1325.	1.1	2
115	Label-free DNA detection using liquid core optical ring resonators. <i>Proceedings of SPIE</i> , 2007, , .	0.8	1
116	New approaches to identify cancer heterogeneity in DNA methylation studies using the lepage test and multinomial logistic regression. , 2015, , .		1
117	Computational Methods for Detection of Differentially Methylated Regions Using Kernel Distance and Scan Statistics. <i>Genes</i> , 2019, 10, 298.	1.0	1
118	DNA Hypomethylation Leads to Aberrant Expression of PD-1 in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2012, 120, 3504-3504.	0.6	1
119	Heat Shock Factor 1 Promotes NF-Kb and B-Cell Signaling in a Preclinical Model of Chronic Lymphocytic Leukemia. <i>Blood</i> , 2015, 126, 5297-5297.	0.6	1
120	A Metabolic Model for On-Line Estimation of Poly- $\hat{1}^2$ -Hydroxybutyrate (PHB) Production. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 1998, 31, 343-348.	0.4	0
121	Fermentation Characteristics in Conversion of Organic Acids Obtained by Oxidation of Low-Rank Coals to Poly(.BETA.-hydroxybutyrate) Using <i>A. eutrophus</i> Cells with Some Analysis on Metabolic Flux Distribution.. <i>Kagaku Kogaku Ronbunshu</i> , 1999, 25, 226-232.	0.1	0
122	Label-free analysis of DNA methylation using optofluidic ring resonators. , 2009, 2009, 2760-2.		0
123	Label-free DNA methylation analysis using the optofluidic ring resonator sensor. <i>Proceedings of SPIE</i> , 2009, , .	0.8	0
124	Relational Analysis of CpG Islands Methylation and Gene Expression in Human Lymphomas Using Possibilistic C-Means Clustering and Modified Cluster Fuzzy Density. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, , .	1.9	0
125	Future Directions in Research on the Epigenetics of Aging. , 2010, , 433-446.		0
126	A software package for next-gen bisulfite sequencing data analysis. , 2011, , .		0



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127	Presence of an Early Lineage Stem Cell Phenotype in Meningioma-Initiating Cells. , 2013, , 211-218.		0
128	Mediator complex components are frequent targets for genetic alterations in various types of human cancer. Journal of Genetics and Genomics, 2017, 44, 587-591.	1.7	0
129	Integrative analysis of multiple types of genomic data using an accelerated failure time frailty model. Computational Statistics, 2021, 36, 1499-1532.	0.8	0
130	Detection of Minimal Residual Disease in Precursor B Lymphoblastic Leukemia (B-ALL) Patients by a Novel Epigenetic DNA Methylation Biomarker.. Blood, 2005, 106, 4524-4524.	0.6	0
131	A Sensitive Molecular Method for Detection of Disseminating Hematopoietic Tumor Cells by Using Specific Epigenetic DNA Methylation Biomarkers. Blood, 2008, 112, 4850-4850.	0.6	0
132	The Epigenetics of Age-Related Cancers. , 2010, , 285-313.		0
133	A genome-wide methylation study of vitamin D deficiency in African American adolescents. FASEB Journal, 2012, 26, 116.7.	0.2	0
134	Genome-Wide DNA Methylation Landscape Defines IGHV Mutated and Unmutated B Cell Chronic Lymphocytic Leukemias. Blood, 2012, 120, 526-526.	0.6	0
135	Genome-Wide DNA Methylation Analysis Identifies Aberrant Epigenetic Changes in CD8+ T Cells from Chronic Lymphocytic Leukemia Patients. Blood, 2014, 124, 3552-3552.	0.6	0
136	ALPL, A Novel Marker Of Neutrophil Activation In Response To Obesity. FASEB Journal, 2018, 32, lb477.	0.2	0
137	Transcriptome Sequencing Reveals Alternative Splicing Patterns and an Increased Sensitivity to Spliceosome Inhibition Associated MYD88 L265P Mutation in Chronic Lymphocytic Leukemia. Blood, 2018, 132, 5535-5535.	0.6	0