John M Greally

List of Publications by Year
in descending order

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227	13,908	22548 61	28425 109
papers	citations	h-index	g-index

252	252	252	24413
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Cell type-specific chromatin accessibility analysis in the mouse and human brain. Epigenetics, 2022, 17, 202-219.	1.3	13
2	eP236: TeleKidSeq: Incorporating telehealth into clinical care of children from diverse backgrounds undergoing clinical genome sequencing. Genetics in Medicine, 2022, 24, S150.	1.1	2
3	eP067: Diagnostic yield of genome sequencing versus targeted gene panel testing in diverse pediatric patients in the NYCKidSeq study. Genetics in Medicine, 2022, 24, S45.	1.1	0
4	The Genomics of Colorectal Cancer in Populations with African and European Ancestry. Cancer Discovery, 2022, 12, 1282-1293.	7.7	28
5	Vitamin D Deficiency During Development Permanently Alters Liver Cell Composition and Function. Frontiers in Endocrinology, 2022, 13, .	1.5	2
6	Role of a Preconception Maternal Nutrition Supplement and Pre-pregnancy BMI on Amnion DNA Methylation at Birth in Guatemalan Mother-Infant Dyads: The Women First Trial. Current Developments in Nutrition, 2022, 6, 625.	0.1	0
7	Epigenetic and Transcriptomic Programming of HSC Quiescence Signaling in Large for Gestational Age Neonates. International Journal of Molecular Sciences, 2022, 23, 7323.	1.8	2
8	Recommendations for clinical interpretation of variants found in non-coding regions of the genome. Genome Medicine, 2022, 14, .	3.6	65
9	Preleukemic and leukemic evolution at the stem cell level. Blood, 2021, 137, 1013-1018.	0.6	9
10	GUÃ: a digital platform to facilitate result disclosure in genetic counseling. Genetics in Medicine, 2021, 23, 942-949.	1.1	20
11	Disproportionate Vitamin A Deficiency in Women of Specific Ethnicities Linked to Differences in Allele Frequencies of Vitamin A-Related Polymorphisms. Nutrients, 2021, 13, 1743.	1.7	8
12	GenomeDiver: a platform for phenotype-guided medical genomic diagnosis. Genetics in Medicine, 2021, 23, 1998-2002.	1.1	3
13	The SEQC2 epigenomics quality control (EpiQC) study. Genome Biology, 2021, 22, 332.	3.8	20
14	A Cellular Stress Response Induced by the CRISPR-dCas9 Activation System Is Not Heritable Through Cell Divisions. CRISPR Journal, 2020, 3, 188-197.	1.4	2
15	Identification of a novel subgroup of endometrial cancer patients with loss of thyroid hormone receptor beta expression and improved survival. BMC Cancer, 2020, 20, 857.	1.1	6
16	Variant Classification Concordance using the ACMG-AMP Variant Interpretation Guidelines across Nine Genomic Implementation Research Studies. American Journal of Human Genetics, 2020, 107, 932-941.	2.6	51
17	AptCompare: optimizedde novomotif discovery of RNA aptamers via HTS-SELEX. Bioinformatics, 2020, 36, 2905-2906.	1.8	11
18	Functional Genomics of the Pediatric Obese Asthma Phenotype Reveal Enrichment of Rho-GTPase Pathways. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 259-274.	2.5	17

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19	The shape of gene expression distributions matter: how incorporating distribution shape improves the interpretation of cancer transcriptomic data. BMC Bioinformatics, 2020, 21, 562.	1.2	19
20	Quantitative Kinetic Analyses of Histone Turnover Using Imaging and Flow Cytometry. Bio-protocol, 2020, 10, .	0.2	0
21	Functional genetic variants can mediate their regulatory effects through alteration of transcription factor binding. Nature Communications, 2019, 10, 3472.	5.8	39
22	High-efficiency genomic editing in Epstein-Barr virus-transformed lymphoblastoid B cells using a single-stranded donor oligonucleotide strategy. Communications Biology, 2019, 2, 312.	2.0	5
23	Misidentification of MLL3 and other mutations in cancer due to highly homologous genomic regions. Leukemia and Lymphoma, 2019, 60, 3132-3137.	0.6	5
24	Chromatin organization in the female mouse brain fluctuates across the oestrous cycle. Nature Communications, 2019, 10, 2851.	5.8	68
25	Aneuvis: web-based exploration of numerical chromosomal variation in single cells. BMC Bioinformatics, 2019, 20, 336.	1.2	2
26	Retargeting of macroH2A following mitosis to cytogenetic-scale heterochromatic domains. Journal of Cell Biology, 2019, 218, 1810-1823.	2.3	5
27	Insights from deconvolution of cell subtype proportions enhance the interpretation of functional genomic data. PLoS ONE, 2019, 14, e0215987.	1.1	21
28	Engineering a haematopoietic stem cell niche by revitalizing mesenchymal stromal cells. Nature Cell Biology, 2019, 21, 560-567.	4.6	74
29	A novel approach to modelling transcriptional heterogeneity identifies the oncogene candidate CBX2 in invasive breast carcinoma. British Journal of Cancer, 2019, 120, 746-753.	2.9	26
30	Transposable element expression in tumors is associated with immune infiltration and increased antigenicity. Nature Communications, 2019, 10, 5228.	5.8	154
31	Ascorbic acidâ€“induced TET activation mitigates adverse hydroxymethylcytosine loss in renal cell carcinoma. Journal of Clinical Investigation, 2019, 129, 1612-1625.	3.9	64
32	Lactate-mediated epigenetic reprogramming regulates formation of human pancreatic cancer-associated fibroblasts. ELife, 2019, 8, .	2.8	103
33	Engineering a Hematopoietic Stem Cell Niche By Revitalizing Mesenchymal Stem Cells with Five Transcription Factors. Blood, 2019, 134, 5004-5004.	0.6	0
34	Intrauterine Hyperglycemia Is Associated with an Impaired Postnatal Response to Oxidative Damage. Stem Cells and Development, 2018, 27, 683-691.	1.1	10
35	A user's guide to the ambiguous word 'epigenetics'. Nature Reviews Molecular Cell Biology, 2018, 19, 207-208.	16.1	117
36	CDC42-related genes are upregulated in helper TÂcells from obese asthmatic children. Journal of Allergy and Clinical Immunology, 2018, 141, 539-548.e7.	1.5	32

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37	The HELP-Based DNA Methylation Assays. Methods in Molecular Biology, 2018, 1708, 191-207.	0.4	4
38	Mechanisms of establishment and functional significance of DNA demethylation during erythroid differentiation. Blood Advances, 2018, 2, 1833-1852.	2.5	15
39	Detecting, quantifying, and discriminating the mechanism of mosaic chromosomal aneuploidies using MAD-seq. Genome Research, 2018, 28, 1039-1052.	2.4	3
40	Genome Wide Mapping of Methylated and Hydroxyl-Methylated Cytosines Using a Modified HpaII Tiny Fragment Enrichment by Ligation Mediated PCR Tagged Sequencing Protocol. Methods in Molecular Biology, 2018, 1792, 167-177.	0.4	1
41	O10. Neuronal Chromatin Dynamics and Anxiety-Related Phenotypes Across the Estrous Cycle. Biological Psychiatry, 2018, 83, S112.	0.7	0
42	DNA methylation haplotypes as cancer markers. Nature Genetics, 2018, 50, 1062-1063.	9.4	6
43	Selective modulation of local linkages between active transcription and oxidative demethylation activity shapes cardiomyocyte-specific gene-body epigenetic status in mice. BMC Genomics, 2018, 19, 349.	1.2	4
44	Whole-genome bisulfite sequencing with improved accuracy and cost. Genome Research, 2018, 28, 1364-1371.	2.4	64
45	The RUNX1/IL-34/CSF-1R axis is an autocrinally regulated modulator of resistance to BRAF-V600E inhibition in melanoma. JCI Insight, 2018, 3, .	2.3	29
46	Population epigenetics. Current Opinion in Systems Biology, 2017, 1, 84-89.	1.3	13
47	Notch Pathway Is Activated via Genetic and Epigenetic Alterations and Is a Therapeutic Target in Clear Cell Renal Cancer. Journal of Biological Chemistry, 2017, 292, 837-846.	1.6	43
48	Geneticâ€“epigenetic interactions in cis: a major focus in the post-GWAS era. Genome Biology, 2017, 18, 120.	3.8	109
49	Non-CpG methylation by DNMT3B facilitates REST binding and gene silencing in developing mouse hearts. Nucleic Acids Research, 2017, 45, 3102-3115.	6.5	45
50	Associating cellular epigenetic models with human phenotypes. Nature Reviews Genetics, 2017, 18, 441-451.	7.7	257
51	Inflammation-associated DNA methylation patterns in epithelium of ulcerative colitis. Epigenetics, 2017, 12, 591-606.	1.3	40
52	The Current State of Epigenetic Research in Humans. JAMA Pediatrics, 2017, 171, 103.	3.3	13
53	Applying 'omics technologies in chemicals risk assessment: Report of an ECETOC workshop. Regulatory Toxicology and Pharmacology, 2017, 91, S3-S13.	1.3	102
54	In Utero Exposure to a High-Fat Diet Programs Hepatic Hypermethylation and Gene Dysregulation and Development of Metabolic Syndrome in Male Mice. Endocrinology, 2017, 158, 2860-2872.	1.4	42

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55	Epigenetically Aberrant Stroma in MDS Propagates Disease via Wnt/Î²-Catenin Activation. Cancer Research, 2017, 77, 4846-4857.	0.4	61
56	SMITE: an R/Bioconductor package that identifies network modules by integrating genomic and epigenomic information. BMC Bioinformatics, 2017, 18, 41.	1.2	24
57	A pre-neoplastic epigenetic field defect in HCV-infected liver at transcription factor binding sites and polycomb targets. Oncogene, 2017, 36, 2030-2044.	2.6	43
58	Development and validation of a targeted next generation DNA sequencing panel outperforming whole exome sequencing for the identification of clinically relevant genetic variants. Oncotarget, 2017, 8, 102033-102045.	0.8	25
59	Altered hydroxymethylation is seen at regulatory regions in pancreatic cancer and regulates oncogenic pathways. Genome Research, 2017, 27, 1830-1842.	2.4	51
60	Abstract 3332: Aberrant expression of CSF1R in melanoma is driven through an endogenous viral promoter and it contributes to malignant growth and the acquisition of resistance against BRAF inhibition. , 2017, , .		0
61	Loss of MEN1 activates DNMT1 implicating DNA hypermethylation as a driver of MEN1 tumorigenesis. Oncotarget, 2016, 7, 12633-12650.	0.8	25
62	Amnion as a surrogate tissue reporter of the effects of maternal preeclampsia on the fetus. Clinical Epigenetics, 2016, 8, 67.	1.8	9
63	LPA receptor activity is basal specific and coincident with early pregnancy and involution during mammary gland postnatal development. Scientific Reports, 2016, 6, 35810.	1.6	9
64	Pediatric Obesity-Related Asthma: The Role of Metabolic Dysregulation. Pediatrics, 2016, 137, .	1.0	66
65	Differential DNA methylation patterns of homeobox genes in proximal and distal colon epithelial cells. Physiological Genomics, 2016, 48, 257-273.	1.0	6
66	Novel epigenetic changes in CDKN2A are associated with progression of cervical intraepithelial neoplasia. Gynecologic Oncology, 2016, 142, 566-573.	0.6	28
67	LINE-1 Activity in Facultative Heterochromatin Formation during X Chromosome Inactivation. Cell, 2016, 166, 782.	13.5	5
68	Neuroepigenomics and Human Disease. , 2016, , 73-91.		0
69	Epigenetics, cellular memory and gene regulation. Current Biology, 2016, 26, R644-R648.	1.8	148
70	MeCP2 Binding Cooperativity Inhibits DNA Modification-Specific Recognition. Biochemistry, 2016, 55, 4275-4285.	1.2	15
71	Epigenome-wide Association Studies and the Interpretation of Disease -Omics. PLoS Genetics, 2016, 12, e1006105.	1.5	194
72	A polycomb-mediated epigenetic field defect precedes invasive cervical carcinoma. Oncotarget, 2016, 7, 62133-62143.	0.8	7

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73	Abstract 1885: Integrated epigenomic profiling reveals widespread demethylation in melanoma and points to the role of CSF1R-RUNX1 axis in resistance against BRAF inhibition. , 2016, , .		0
74	RNA:DNA hybrids in the human genome have distinctive nucleotide characteristics, chromatin composition, and transcriptional relationships. Epigenetics and Chromatin, 2015, 8, 46.	1.8	134
75	Development of a Targeted Multi-Disorder High-Throughput Sequencing Assay for the Effective Identification of Disease-Causing Variants. PLoS ONE, 2015, 10, e0133742.	1.1	15
76	New insights and updated guidelines for epigenome-wide association studies. Neuroepigenetics, 2015, 1, 14-19.	2.8	26
77	Predictive properties of DNA methylation patterns in primary tumor samples for osteosarcoma relapse status. Epigenetics, 2015, 10, 31-39.	1.3	26
78	Post-conversion targeted capture of modified cytosines in mammalian and plant genomes. Nucleic Acids Research, 2015, 43, e81-e81.	6.5	62
79	Genome-wide assays that identify and quantify modified cytosines in human disease studies. Epigenetics and Chromatin, 2015, 8, 5.	1.8	31
80	DNA demethylation by 5-aza-2â€²-deoxycytidine is imprinted, targeted to euchromatin, and has limited transcriptional consequences. Epigenetics and Chromatin, 2015, 8, 11.	1.8	38
81	How might epigenetic dysregulation in early embryonic life contribute to autism spectrum disorder?. Epigenomics, 2015, 7, 1-4.	1.0	17
82	Abstract PR06: Integrated epigenomic profiling reveals widespread demethylation in melanoma and reveals CSF-1 Receptor as an aberrant regulator of malignant growth and invasion. , 2015, , .		0
83	Kidney Cancer Is Characterized by Aberrant Methylation of Tissue-Specific Enhancers That Are Prognostic for Overall Survival. Clinical Cancer Research, 2014, 20, 4349-4360.	3.2	60
84	Mosaic Epigenetic Dysregulation of Ectodermal Cells in Autism Spectrum Disorder. PLoS Genetics, 2014, 10, e1004402.	1.5	93
85	The meta-epigenomic structure of purified human stem cell populations is defined at cis-regulatory sequences. Nature Communications, 2014, 5, 5195.	5.8	37
86	Sexual dimorphism in epigenomic responses of stem cells to extreme fetal growth. Nature Communications, 2014, 5, 5187.	5.8	31
87	Genome-wide expression profiling of B lymphocytes reveals IL4R increase in allergic asthma. Journal of Allergy and Clinical Immunology, 2014, 134, 972-975.	1.5	20
88	DNA Methylation is Developmentally Regulated for Genes Essential for Cardiogenesis. Journal of the American Heart Association, 2014, 3, e000976.	1.6	71
89	Unusual Characteristics of the DNA Binding Domain of Epigenetic Regulatory Protein MeCP2 Determine Its Binding Specificity. Biochemistry, 2014, 53, 3379-3391.	1.2	54
90	HSC commitmentâ€“associated epigenetic signature is prognostic in acute myeloid leukemia. Journal of Clinical Investigation, 2014, 124, 1158-1167.	3.9	38

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91	Myelodysplastic Syndrome Marrow Stroma Shows Widespread Aberrant Hypermethylation That Is Abrogated By Treatment with Dnmt Inhibitors. Blood, 2014, 124, 4379-4379.	0.6	2
92	Epigenetic Effects of Extreme Intrauterine Growth in Humans. Research and Perspectives in Endocrine Interactions, 2014, , 131-138.	0.2	0
93	Abstract 4781: Integrated epigenomic profiling reveals widespread demethylation in melanoma and reveals CSF-1 receptor as an aberrant regulator of malignant growth and invasion. , 2014, , .		0
94	Redistribution of H3K27me3 upon DNA hypomethylation results in de-repression of Polycomb target genes. Genome Biology, 2013, 14, R25.	13.9	200
95	Cytosine methylation changes in enhancer regions of core pro-fibrotic genes characterize kidney fibrosis development. Genome Biology, 2013, 14, R108.	13.9	187
96	Recommendations for the design and analysis of epigenome-wide association studies. Nature Methods, 2013, 10, 949-955.	9.0	345
97	Astrogenomics: big data, old problems, old solutions?. Genome Biology, 2013, 14, 129.	3.8	11
98	Hypomethylation of Noncoding DNA Regions and Overexpression of the Long Noncoding RNA, AFAP1-AS1, in Barrett's Esophagus and Esophageal Adenocarcinoma. Gastroenterology, 2013, 144, 956-966.e4.	0.6	216
99	Myeloma Is Characterized by Stage-Specific Alterations in DNA Methylation That Occur Early during Myelomagenesis. Journal of Immunology, 2013, 190, 2966-2975.	0.4	90
100	Genome-wide DNA Methylation Analysis Using Massively Parallel Sequencing Technologies. Seminars in Hematology, 2013, 50, 70-77.	1.8	11
101	Epigenetic Functions of Smchd1 Repress Gene Clusters on the Inactive X Chromosome and on Autosomes. Molecular and Cellular Biology, 2013, 33, 3150-3165.	1.1	99
102	Genetic Recombination Is Targeted towards Gene Promoter Regions in Dogs. PLoS Genetics, 2013, 9, e1003984.	1.5	198
103	Large, Male Germ Cell-Specific Hypomethylated DNA Domains With Unique Genomic and Epigenomic Features on the Mouse X Chromosome. DNA Research, 2013, 20, 549-565.	1.5	10
104	Methylome Profiling Reveals Distinct Alterations in Phenotypic and Mutational Subgroups of Myeloproliferative Neoplasms. Cancer Research, 2013, 73, 1076-1085.	0.4	50
105	High Resolution Methylome Analysis Reveals Widespread Functional Hypomethylation during Adult Human Erythropoiesis. Journal of Biological Chemistry, 2013, 288, 8805-8814.	1.6	37
106	Genome-wide hydroxymethylation tested using the HELP-GT assay shows redistribution in cancer. Nucleic Acids Research, 2013, 41, e157-e157.	6.5	69
107	Differential epigenome-wide DNA methylation patterns in childhood obesity-associated asthma. Scientific Reports, 2013, 3, 2164.	1.6	94
108	Lsh regulates LTR retrotransposon repression independently of Dnmt3b function. Genome Biology, 2013, 14, R146.	13.9	54

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109	Abstract A26: Integrated epigenomic profiling reveals widespread demethylation in melanoma, and reveals aberrant CSF-1 receptor expression as a regulator of malignant growth and invasion inhibited by PLX3397. Cancer Research, 2013, 73, A26-A26.	0.4	1
110	In vitro and in vivo testing methods of epigenomic endpoints for evaluating endocrine disruptors. ALTEX: Alternatives To Animal Experimentation, 2013, 30, 445-471.	0.9	52
111	Bidding the CpG island goodbye. ELife, 2013, 2, e00593.	2.8	7
112	A Blueprint for an International Cancer Epigenome Consortium. A Report from the AACR Cancer Epigenome Task Force. Cancer Research, 2012, 72, 6319-6324.	0.4	22
113	Repressor element-1 silencing transcription factor (REST)-dependent epigenetic remodeling is critical to ischemia-induced neuronal death. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E962-71.	3.3	162
114	Stem and progenitor cells in myelodysplastic syndromes show aberrant stage-specific expansion and harbor genetic and epigenetic alterations. Blood, 2012, 120, 2076-2086.	0.6	181
115	The Wasp System: An open source environment for managing and analyzing genomic data. Genomics, 2012, 100, 345-351.	1.3	24
116	Maternal gametic transmission of translocations or inversions of human chromosome 11p15.5 results in regional DNA hypermethylation and downregulation of CDKN1C expression. Genomics, 2012, 99, 25-35.	1.3	18
117	Convergent and divergent evolution of genomic imprinting in the marsupial Monodelphis domestica. BMC Genomics, 2012, 13, 394.	1.2	24
118	Phase II trial of the histone deacetylase inhibitor romidepsin in patients with recurrent/metastatic head and neck cancer. Oral Oncology, 2012, 48, 1281-1288.	0.8	71
119	Epigenetic Silencing of the Circadian Clock Gene CRY1 is Associated with an Indolent Clinical Course in Chronic Lymphocytic Leukemia. PLoS ONE, 2012, 7, e34347.	1.1	44
120	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
121	Aberrant DNA hypermethylation signature in acute myeloid leukemia directed by EVI1. Blood, 2011, 117, 234-241.	0.6	94
122	DNA methylation changes in murine breast adenocarcinomas allow the identification of candidate genes for human breast carcinogenesis. Mammalian Genome, 2011, 22, 249-259.	1.0	11
123	Allele-specific transcriptional elongation regulates monoallelic expression of the IGF2BP1 gene. Epigenetics and Chromatin, 2011, 4, 14.	1.8	7
124	Epigenetic changes in B lymphocytes associated with house dust mite allergic asthma. Epigenetics, 2011, 6, 1131-1137.	1.3	62
125	Late-replicating heterochromatin is characterized by decreased cytosine methylation in the human genome. Genome Research, 2011, 21, 1833-1840.	2.4	38
126	Aberrant Epigenetic and Genetic Marks Are Seen in Myelodysplastic Leukocytes and Reveal Dock4 as a Candidate Pathogenic Gene on Chromosome 7q. Journal of Biological Chemistry, 2011, 286, 25211-25223.	1.6	41

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127	Widespread Hypomethylation Occurs Early and Synergizes with Gene Amplification during Esophageal Carcinogenesis. PLoS Genetics, 2011, 7, e1001356.	1.5	112
128	Aberrant DNA methylation in malignant melanoma. Melanoma Research, 2010, 20, 253-265.	0.6	88
129	DNA methylation signatures define molecular subtypes of diffuse large B-cell lymphoma. Blood, 2010, 116, e81-e89.	0.6	138
130	Experimental approaches to the study of epigenomic dysregulation in ageing. Experimental Gerontology, 2010, 45, 255-268.	1.2	18
131	DNA Methylation Signatures Identify Biologically Distinct Subtypes in Acute Myeloid Leukemia. Cancer Cell, 2010, 17, 13-27.	7.7	737
132	DNA methylation alterations in multiple myeloma as a model for epigenetic changes in cancer. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 654-669.	6.6	46
133	Tissueâ€specific dysregulation of DNA methylation in aging. Aging Cell, 2010, 9, 506-518.	3.0	185
134	Cytosine Methylation Dysregulation in Neonates Following Intrauterine Growth Restriction. PLoS ONE, 2010, 5, e8887.	1.1	120
135	Experimental Intrauterine Growth Restriction Induces Alterations in DNA Methylation and Gene Expression in Pancreatic Islets of Rats. Journal of Biological Chemistry, 2010, 285, 15111-15118.	1.6	140
136	Opposing Roles of Dnmt1 in Early- and Late-Stage Murine Prostate Cancer. Molecular and Cellular Biology, 2010, 30, 4159-4174.	1.1	33
137	Introduction to Epigenomics and Epigenome-Wide Analysis. Methods in Molecular Biology, 2010, 620, 243-265.	0.4	60
138	Distinct Factors Control Histone Variant H3.3 Localization at Specific Genomic Regions. Cell, 2010, 140, 678-691.	13.5	1,069
139	LINE-1 Activity in Facultative Heterochromatin Formation during X Chromosome Inactivation. Cell, 2010, 141, 956-969.	13.5	296
140	DNA methylation profiling using HpaII tiny fragment enrichment by ligation-mediated PCR (HELP). Methods, 2010, 52, 218-222.	1.9	26
141	Optimized design and data analysis of tag-based cytosine methylation assays. Genome Biology, 2010, 11, R36.	13.9	76
142	Epigenomic Profiling of Myeloproliferative Diseases Reveal Idiopathic Myelofibrosis as An Epigenetically Distinct Subgroup and Highlights the Epigenetic Effects of Jak2V617F Mutation. Blood, 2010, 116, 627-627.	0.6	2
143	Lack of Evidence for Green Tea Polyphenols as DNA Methylation Inhibitors in Murine Prostate. Cancer Prevention Research, 2009, 2, 1065-1075.	0.7	37
144	A pipeline for the quantitative analysis of CG dinucleotide methylation using mass spectrometry. Bioinformatics, 2009, 25, 2164-2170.	1.8	69

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145	High-resolution genome-wide cytosine methylation profiling with simultaneous copy number analysis and optimization for limited cell numbers. Nucleic Acids Research, 2009, 37, 3829-3839.	6.5	141
146	Institutional Profile: The Einstein Center for Epigenomics: studying the role of epigenomic dysregulation in human disease. Epigenomics, 2009, 1, 33-38.	1.0	1
147	CG dinucleotide periodicities recognized by the Dnmt3aâ€"Dnmt3L complex are distinctive at retroelements and imprinted domains. Mammalian Genome, 2009, 20, 633-643.	1.0	29
148	Genome-Wide Determination of DNA Methylation by Hpa II Tiny Fragment Enrichment by Ligation-Mediated PCR (HELP) for the Study of Acute Leukemias. Methods in Molecular Biology, 2009, 538, 395-407.	0.4	34
149	Genome-wide epigenetic analysis delineates a biologically distinct immature acute leukemia with myeloid/T-lymphoid features. Blood, 2009, 113, 2795-2804.	0.6	83
150	MDS and secondary AML display unique patterns and abundance of aberrant DNA methylation. Blood, 2009, 114, 3448-3458.	0.6	292
151	The Help Assay. Methods in Molecular Biology, 2009, 507, 77-87.	0.4	18
152	DNA Methylation Profiling Predicts Clinical Outcomes and Reveals Unique Insights Into the Molecular Complexity of Acute Myeloid Leukemia.. Blood, 2009, 114, 707-707.	0.6	0
153	600: Abnormal intrauterine growth induces global epigenetic changes in human stem cells. American Journal of Obstetrics and Gynecology, 2008, 199, S173.	0.7	0
154	Moving AHEAD with an international human epigenome project. Nature, 2008, 454, 711-715.	13.7	177
155	Journal club. Nature, 2008, 456, 549-549.	13.7	0
156	Reduced-representation methylation mapping. Genome Biology, 2008, 9, 231.	13.9	26
157	Toxoplasma gondii and Cryptosporidium parvum Lack Detectable DNA Cytosine Methylation. Eukaryotic Cell, 2008, 7, 537-540.	3.4	57
158	An analytical pipeline for genomic representations used for cytosine methylation studies. Bioinformatics, 2008, 24, 1161-1167.	1.8	49
159	Kaiso Contributes to DNA Methylation-Dependent Silencing of Tumor Suppressor Genes in Colon Cancer Cell Lines. Cancer Research, 2008, 68, 7258-7263.	0.4	101
160	Meta-Analysis of Microarray Studies Reveals a Novel Hematopoietic Progenitor Cell Signature and Demonstrates Feasibility of Inter-Platform Data Integration. PLoS ONE, 2008, 3, e2965.	1.1	20
161	MDS Marrow Stroma Is Characterized by Distinct Epigenetic Alterations. Blood, 2008, 112, 3635-3635.	0.6	4
162	Integrative Genomic Analysis Reveals Aberrant Epigenetic Marks in MDS That Can Be Seen in Peripheral Blood Leucocytes. Blood, 2008, 112, 595-595.	0.6	3

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163	Epigenetic Signatures Identify New Clinically Relevant Subtypes and Define Gene Regulatory Patterns in Patients with Acute Myeloid Leukemia (AML). Blood, 2008, 112, 756-756.	0.6	2
164	Two Different EVI1 Expressing Poor-Risk AML Subgroups with Distinct Epigenetic Signatures Uncovered by Genome Wide DNA Methylation Profiling. Blood, 2008, 112, 757-757.	0.6	3
165	Downregulation of Ribosomal Proteins Is Seen in Non 5q- MDS. Blood, 2008, 112, 854-854.	0.6	6
166	An Integrative Genomic and Epigenomic Approach for the Study of Transcriptional Regulation. PLoS ONE, 2008, 3, e1882.	1.1	77
167	Genome-Wide Epigenetics in Myeloid Leukemias.. Blood, 2008, 112, sci-35-sci-35.	0.6	0
168	Transcriptional signature with differential expression of BCL6 target genes accurately identifies BCL6-dependent diffuse large B cell lymphomas. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3207-3212.	3.3	130
169	Epigenomic Modifications Predict Active Promoters and Gene Structure in Toxoplasma gondii. PLoS Pathogens, 2007, 3, e77.	2.1	102
170	CG dinucleotide clustering is a species-specific property of the genome. Nucleic Acids Research, 2007, 35, 6798-6807.	6.5	74
171	Encyclopaedia of humble DNA. Nature, 2007, 447, 782-783.	13.7	28
172	Perceptive enzymes. Nature, 2007, 449, 148-149.	13.7	43
173	Bcl-6 mediates the germinal center B cell phenotype and lymphomagenesis through transcriptional repression of the DNA-damage sensor ATR. Nature Immunology, 2007, 8, 705-714.	7.0	231
174	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	13.7	661
175	Genome-wide and locus-specific DNA hypomethylation in G9a deficient mouse embryonic stem cells. Genes To Cells, 2007, 12, 1-11.	0.5	79
176	Cell type-specific methylation profiles occurring disproportionately in CpG-less regions that delineate developmental similarity. Genes To Cells, 2007, 12, 1123-1132.	0.5	41
177	A new class of tissueâ€specifically methylated regions involving entire CpG islands in the mouse. Genes To Cells, 2007, 12, 1305-1314.	0.5	27
178	The potential role of epigenomic dysregulation in complex human disease. Trends in Genetics, 2007, 23, 588-595.	2.9	100
179	Global DNA Methylation Profiling Demonstrates That Idiopathic Myelofibrosis Is Characterized by a Distinct Epigenetic Signature with Aberrant Methylation Changes in Genes Involved in Inflammation and Hematopoiesis. Blood, 2007, 110, 1536-1536.	0.6	2
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