John M Greally

List of Publications by Year
in descending order

227 papers	13,908 citations	19657 61 h-index	24982 109 g-index
252 all docs	252 docs citations	252 times ranked	21946 citing authors

#	Article	IF	Citations
1	Distinct Factors Control Histone Variant H3.3 Localization at Specific Genomic Regions. Cell, 2010, 140, 678-691.	28.9	1,069
2	DNA Methylation Signatures Identify Biologically Distinct Subtypes in Acute Myeloid Leukemia. Cancer Cell, 2010, 17, 13-27.	16.8	737
3	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	27.8	661
4	Comparative isoschizomer profiling of cytosine methylation: The HELP assay. Genome Research, 2006, 16, 1046-1055.	5.5	355
5	Recommendations for the design and analysis of epigenome-wide association studies. Nature Methods, 2013, 10, 949-955.	19.0	345
6	Epigenomics: beyond CpG islands. Nature Reviews Genetics, 2004, 5, 446-455.	16.3	314
7	LINE-1 Activity in Facultative Heterochromatin Formation during X Chromosome Inactivation. Cell, 2010, 141, 956-969.	28.9	296
8	MDS and secondary AML display unique patterns and abundance of aberrant DNA methylation. Blood, 2009, 114, 3448-3458.	1.4	292
9	Associating cellular epigenetic models with human phenotypes. Nature Reviews Genetics, 2017, 18, 441-451.	16.3	257
10	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.	14.5	231
11	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.	1.3	216
12	Redistribution of H3K27me3 upon DNA hypomethylation results in de-repression of Polycomb target genes. Genome Biology, 2013, 14, R25.	9.6	200
13	Genetic Recombination Is Targeted towards Gene Promoter Regions in Dogs. PLoS Genetics, 2013, 9, e1003984.	3.5	198
14	Identification of Four Highly Conserved Genes between Breakpoint Hotspots BP1 and BP2 of the Prader-Willi/Angelman Syndromes Deletion Region That Have Undergone Evolutionary Transposition Mediated by Flanking Duplicons. American Journal of Human Genetics, 2003, 73, 898-925.	6.2	197
15	Epigenome-wide Association Studies and the Interpretation of Disease -Omics. PLoS Genetics, 2016, 12, e1006105.	3.5	194
16	Cytosine methylation changes in enhancer regions of core pro-fibrotic genes characterize kidney fibrosis development. Genome Biology, 2013, 14, R108.	9.6	187
17	Tissueâ€specific dysregulation of DNA methylation in aging. Aging Cell, 2010, 9, 506-518.	6.7	185
18	Stem and progenitor cells in myelodysplastic syndromes show aberrant stage-specific expansion and harbor genetic and epigenetic alterations. Blood, 2012, 120, 2076-2086.	1.4	181

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19	Moving AHEAD with an international human epigenome project. Nature, 2008, 454, 711-715.	27.8	177
20	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.	7.1	162
21	Transposable element expression in tumors is associated with immune infiltration and increased antigenicity. Nature Communications, 2019, 10, 5228.	12.8	154
22	Epigenetics, cellular memory and gene regulation. Current Biology, 2016, 26, R644-R648.	3.9	148
23	A stain upon the silence: genes escaping X inactivation. Trends in Genetics, 2003, 19, 432-438.	6.7	146
24	Short interspersed transposable elements (SINEs) are excluded from imprinted regions in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 327-332.	7.1	145
25	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.	14.5	141
26	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.	3.4	140
27	DNA methylation signatures define molecular subtypes of diffuse large B-cell lymphoma. Blood, 2010, 116, e81-e89.	1.4	138
28	RNA:DNA hybrids in the human genome have distinctive nucleotide characteristics, chromatin composition, and transcriptional relationships. Epigenetics and Chromatin, 2015, 8, 46.	3.9	134
29	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.	7.1	130
30	Localization of MMR proteins on meiotic chromosomes in mice indicates distinct functions during prophase I. Journal of Cell Biology, 2005, 171, 447-458.	5.2	123
31	Cytosine Methylation Dysregulation in Neonates Following Intrauterine Growth Restriction. PLoS ONE, 2010, 5, e8887.	2.5	120
32	A user's guide to the ambiguous word 'epigenetics'. Nature Reviews Molecular Cell Biology, 2018, 19, 207-208.	37.0	117
33	Widespread Hypomethylation Occurs Early and Synergizes with Gene Amplification during Esophageal Carcinogenesis. PLoS Genetics, 2011, 7, e1001356.	3.5	112
34	Geneticâ€“epigenetic interactions in cis: a major focus in the post-GWAS era. Genome Biology, 2017, 18, 120.	8.8	109
35	Lactate-mediated epigenetic reprogramming regulates formation of human pancreatic cancer-associated fibroblasts. ELife, 2019, 8, .	6.0	103
36	Epigenomic Modifications Predict Active Promoters and Gene Structure in Toxoplasma gondii. PLoS Pathogens, 2007, 3, e77.	4.7	102

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37	Applying 'omics technologies in chemicals risk assessment: Report of an ECETOC workshop. Regulatory Toxicology and Pharmacology, 2017, 91, S3-S13.	2.7	102
38	Kaiso Contributes to DNA Methylation-Dependent Silencing of Tumor Suppressor Genes in Colon Cancer Cell Lines. Cancer Research, 2008, 68, 7258-7263.	0.9	101
39	The potential role of epigenomic dysregulation in complex human disease. Trends in Genetics, 2007, 23, 588-595.	6.7	100
40	Epigenetic Functions of Smchd1 Repress Gene Clusters on the Inactive X Chromosome and on Autosomes. Molecular and Cellular Biology, 2013, 33, 3150-3165.	2.3	99
41	Mammalian linker-histone subtypes differentially affect gene expression in vivo. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5920-5925.	7.1	96
42	Aberrant DNA hypermethylation signature in acute myeloid leukemia directed by EVI1. Blood, 2011, 117, 234-241.	1.4	94
43	Differential epigenome-wide DNA methylation patterns in childhood obesity-associated asthma. Scientific Reports, 2013, 3, 2164.	3.3	94
44	Mosaic Epigenetic Dysregulation of Ectodermal Cells in Autism Spectrum Disorder. PLoS Genetics, 2014, 10, e1004402.	3.5	93
45	Myeloma Is Characterized by Stage-Specific Alterations in DNA Methylation That Occur Early during Myelomagenesis. Journal of Immunology, 2013, 190, 2966-2975.	0.8	90
46	Aberrant DNA methylation in malignant melanoma. Melanoma Research, 2010, 20, 253-265.	1.2	88
47	Genome-wide epigenetic analysis delineates a biologically distinct immature acute leukemia with myeloid/T-lymphoid features. Blood, 2009, 113, 2795-2804.	1.4	83
48	Genome-wide and locus-specific DNA hypomethylation in G9a deficient mouse embryonic stem cells. Genes To Cells, 2007, 12, 1-11.	1.2	79
49	An Integrative Genomic and Epigenomic Approach for the Study of Transcriptional Regulation. PLoS ONE, 2008, 3, e1882.	2.5	77
50	Optimized design and data analysis of tag-based cytosine methylation assays. Genome Biology, 2010, 11, R36.	9.6	76
51	CG dinucleotide clustering is a species-specific property of the genome. Nucleic Acids Research, 2007, 35, 6798-6807.	14.5	74
52	Engineering a haematopoietic stem cell niche by revitalizing mesenchymal stromal cells. Nature Cell Biology, 2019, 21, 560-567.	10.3	74
53	Position Effects Are Influenced by the Orientation of a Transgene with Respect to Flanking Chromatin. Molecular and Cellular Biology, 2001, 21, 298-309.	2.3	73
54	Epigenetic abnormalities associated with a chromosome 18(q21-q22) inversion and a Gilles de la Tourette syndrome phenotype. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 4684-4689.	7.1	73

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55	Phase II trial of the histone deacetylase inhibitor romidepsin in patients with recurrent/metastatic head and neck cancer. Oral Oncology, 2012, 48, 1281-1288.	1.5	71
56	DNA Methylation is Developmentally Regulated for Genes Essential for Cardiogenesis. Journal of the American Heart Association, 2014, 3, e000976.	3.7	71
57	beta-globin YAC transgenes exhibit uniform expression levels but position effect variegation in mice. Human Molecular Genetics, 2000, 9, 631-636.	2.9	69
58	A pipeline for the quantitative analysis of CG dinucleotide methylation using mass spectrometry. Bioinformatics, 2009, 25, 2164-2170.	4.1	69
59	Genome-wide hydroxymethylation tested using the HELP-GT assay shows redistribution in cancer. Nucleic Acids Research, 2013, 41, e157-e157.	14.5	69
60	Chromatin organization in the female mouse brain fluctuates across the oestrous cycle. Nature Communications, 2019, 10, 2851.	12.8	68
61	Pediatric Obesity-Related Asthma: The Role of Metabolic Dysregulation. Pediatrics, 2016, 137, .	2.1	66
62	Recommendations for clinical interpretation of variants found in non-coding regions of the genome. Genome Medicine, 2022, 14, .	8.2	65
63	Whole-genome bisulfite sequencing with improved accuracy and cost. Genome Research, 2018, 28, 1364-1371.	5.5	64
64	Ascorbic acidâ€“induced TET activation mitigates adverse hydroxymethylcytosine loss in renal cell carcinoma. Journal of Clinical Investigation, 2019, 129, 1612-1625.	8.2	64
65	Epigenetic changes in B lymphocytes associated with house dust mite allergic asthma. Epigenetics, 2011, 6, 1131-1137.	2.7	62
66	Post-conversion targeted capture of modified cytosines in mammalian and plant genomes. Nucleic Acids Research, 2015, 43, e81-e81.	14.5	62
67	Epigenetically Aberrant Stroma in MDS Propagates Disease via Wnt/Î²-Catenin Activation. Cancer Research, 2017, 77, 4846-4857.	0.9	61
68	Comparative Sequence and X-Inactivation Analyses of a Domain of Escape in Human Xp11.2 and the Conserved Segment in Mouse. Genome Research, 2004, 14, 1275-1284.	5.5	60
69	Introduction to Epigenomics and Epigenome-Wide Analysis. Methods in Molecular Biology, 2010, 620, 243-265.	0.9	60
70	Kidney Cancer Is Characterized by Aberrant Methylation of Tissue-Specific Enhancers That Are Prognostic for Overall Survival. Clinical Cancer Research, 2014, 20, 4349-4360.	7.0	60
71	Toxoplasma gondii and Cryptosporidium parvum Lack Detectable DNA Cytosine Methylation. Eukaryotic Cell, 2008, 7, 537-540.	3.4	57
72	Retrotransposed genes such as Frat3 in the mouse Chromosome 7C Prader-Willi syndrome region acquire the imprinted status of their insertion site. Mammalian Genome, 2001, 12, 813-821.	2.2	54

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73	Applying whole-genome studies of epigenetic regulation to study human disease. Cytogenetic and Genome Research, 2006, 114, 1-15.	1.1	54
74	Lsh regulates LTR retrotransposon repression independently of Dnmt3b function. Genome Biology, 2013, 14, R146.	9.6	54
75	Unusual Characteristics of the DNA Binding Domain of Epigenetic Regulatory Protein MeCP2 Determine Its Binding Specificity. Biochemistry, 2014, 53, 3379-3391.	2.5	54
76	In vitro and in vivo testing methods of epigenomic endpoints for evaluating endocrine disruptors. ALTEX: Alternatives To Animal Experimentation, 2013, 30, 445-471.	1.5	52
77	Senescence and epigenetic dysregulation in cancer. International Journal of Biochemistry and Cell Biology, 2002, 34, 1475-1490.	2.8	51
78	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.	6.2	51
79	Altered hydroxymethylation is seen at regulatory regions in pancreatic cancer and regulates oncogenic pathways. Genome Research, 2017, 27, 1830-1842.	5.5	51
80	Methylome Profiling Reveals Distinct Alterations in Phenotypic and Mutational Subgroups of Myeloproliferative Neoplasms. Cancer Research, 2013, 73, 1076-1085.	0.9	50
81	An analytical pipeline for genomic representations used for cytosine methylation studies. Bioinformatics, 2008, 24, 1161-1167.	4.1	49
82	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
83	Non-CpG methylation by DNMT3B facilitates REST binding and gene silencing in developing mouse hearts. Nucleic Acids Research, 2017, 45, 3102-3115.	14.5	45
84	Epigenetic Silencing of the Circadian Clock Gene CRY1 is Associated with an Indolent Clinical Course in Chronic Lymphocytic Leukemia. PLoS ONE, 2012, 7, e34347.	2.5	44
85	Perceptive enzymes. Nature, 2007, 449, 148-149.	27.8	43
86	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.	3.4	43
87	A pre-neoplastic epigenetic field defect in HCV-infected liver at transcription factor binding sites and polycomb targets. Oncogene, 2017, 36, 2030-2044.	5.9	43
88	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.	2.8	42
89	Cell type-specific methylation profiles occurring disproportionately in CpG-less regions that delineate developmental similarity. Genes To Cells, 2007, 12, 1123-1132.	1.2	41
90	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.	3.4	41

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91	Inflammation-associated DNA methylation patterns in epithelium of ulcerative colitis. Epigenetics, 2017, 12, 591-606.	2.7	40
92	The mouse H19 locus mediates a transition between imprinted and non-imprinted DNA replication patterns. Human Molecular Genetics, 1998, 7, 91-95.	2.9	39
93	Functional genetic variants can mediate their regulatory effects through alteration of transcription factor binding. Nature Communications, 2019, 10, 3472.	12.8	39
94	Late-replicating heterochromatin is characterized by decreased cytosine methylation in the human genome. Genome Research, 2011, 21, 1833-1840.	5.5	38
95	DNA demethylation by 5-aza-2â€²-deoxycytidine is imprinted, targeted to euchromatin, and has limited transcriptional consequences. Epigenetics and Chromatin, 2015, 8, 11.	3.9	38
96	HSC commitmentâ€“associated epigenetic signature is prognostic in acute myeloid leukemia. Journal of Clinical Investigation, 2014, 124, 1158-1167.	8.2	38
97	Lack of Evidence for Green Tea Polyphenols as DNA Methylation Inhibitors in Murine Prostate. Cancer Prevention Research, 2009, 2, 1065-1075.	1.5	37
98	High Resolution Methylome Analysis Reveals Widespread Functional Hypomethylation during Adult Human Erythropoiesis. Journal of Biological Chemistry, 2013, 288, 8805-8814.	3.4	37
99	The meta-epigenomic structure of purified human stem cell populations is defined at cis-regulatory sequences. Nature Communications, 2014, 5, 5195.	12.8	37
100	Conserved characteristics of heterochromatin-forming DNA at the 15q11-q13 imprinting center. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 14430-14435.	7.1	36
101	Genomic Organization of the Genes Gtf2ird1, Gtf2i, and Ncf1 at the Mouse Chromosome 5 Region Syntenic to the Human Chromosome 7q11.23 Williams Syndrome Critical Region. Genomics, 2002, 79, 137-143.	2.9	34
102	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.	0.9	34
103	Opposing Roles of Dnmt1 in Early- and Late-Stage Murine Prostate Cancer. Molecular and Cellular Biology, 2010, 30, 4159-4174.	2.3	33
104	CDC42-related genes are upregulated in helper TÂcells from obese asthmatic children. Journal of Allergy and Clinical Immunology, 2018, 141, 539-548.e7.	2.9	32
105	Identification of a Candidate Regulatory Region in the HumanCD8Gene Complex by Colocalization of DNase I Hypersensitive Sites and Matrix Attachment Regions Which Bind SATB1 and GATA-3. Journal of Immunology, 2002, 168, 3915-3922.	0.8	31
106	Sexual dimorphism in epigenomic responses of stem cells to extreme fetal growth. Nature Communications, 2014, 5, 5187.	12.8	31
107	Genome-wide assays that identify and quantify modified cytosines in human disease studies. Epigenetics and Chromatin, 2015, 8, 5.	3.9	31
108	Cryptic Translocation Identification in Human and Mouse Using Several Telomeric Multiplex FISH (TM-FISH) Strategies. Laboratory Investigation, 2001, 81, 483-491.	3.7	30

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109	Ischemic stroke and intracranial multifocal cerebral arteriopathy in Williams syndrome. Journal of Pediatrics, 1995, 126, 945-948.	1.8	29
110	CG dinucleotide periodicities recognized by the Dnmt3aâ€“Dnmt3L complex are distinctive at retroelements and imprinted domains. Mammalian Genome, 2009, 20, 633-643.	2.2	29
111	The RUNX1/IL-34/CSF-1R axis is an autocrinally regulated modulator of resistance to BRAF-V600E inhibition in melanoma. JCI Insight, 2018, 3, .	5.0	29
112	Identification, Chromosomal Assignment, and Expression Analysis of the Human Homeodomain-Containing Gene Orthopedia (OTP). Genomics, 1999, 60, 96-104.	2.9	28
113	MEN1 tumor-suppressor protein localizes to telomeres during meiosis. Genes Chromosomes and Cancer, 2002, 35, 81-85.	2.8	28
114	Encyclopaedia of humble DNA. Nature, 2007, 447, 782-783.	27.8	28
115	Novel epigenetic changes in CDKN2A are associated with progression of cervical intraepithelial neoplasia. Gynecologic Oncology, 2016, 142, 566-573.	1.4	28
116	The Genomics of Colorectal Cancer in Populations with African and European Ancestry. Cancer Discovery, 2022, 12, 1282-1293.	9.4	28
117	A new class of tissueâ€specifically methylated regions involving entire CpG islands in the mouse. Genes To Cells, 2007, 12, 1305-1314.	1.2	27
118	Reduced-representation methylation mapping. Genome Biology, 2008, 9, 231.	9.6	26
119	DNA methylation profiling using HpaII tiny fragment enrichment by ligation-mediated PCR (HELP). Methods, 2010, 52, 218-222.	3.8	26
120	New insights and updated guidelines for epigenome-wide association studies. Neuroepigenetics, 2015, 1, 14-19.	2.8	26
121	Predictive properties of DNA methylation patterns in primary tumor samples for osteosarcoma relapse status. Epigenetics, 2015, 10, 31-39.	2.7	26
122	A novel approach to modelling transcriptional heterogeneity identifies the oncogene candidate CBX2 in invasive breast carcinoma. British Journal of Cancer, 2019, 120, 746-753.	6.4	26
123	Loss of MEN1 activates DNMT1 implicating DNA hypermethylation as a driver of MEN1 tumorigenesis. Oncotarget, 2016, 7, 12633-12650.	1.8	25
124	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.	1.8	25
125	The Wasp System: An open source environment for managing and analyzing genomic data. Genomics, 2012, 100, 345-351.	2.9	24
126	Convergent and divergent evolution of genomic imprinting in the marsupial Monodelphis domestica. BMC Genomics, 2012, 13, 394.	2.8	24

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127	SMITE: an R/Bioconductor package that identifies network modules by integrating genomic and epigenomic information. BMC Bioinformatics, 2017, 18, 41.	2.6	24
128	Matrix-attachment regions in the mouse Chromosome 7F imprinted domain. Mammalian Genome, 1997, 8, 805-810.	2.2	22
129	A Blueprint for an International Cancer Epigenome Consortium. A Report from the AACR Cancer Epigenome Task Force. Cancer Research, 2012, 72, 6319-6324.	0.9	22
130	Insights from deconvolution of cell subtype proportions enhance the interpretation of functional genomic data. PLoS ONE, 2019, 14, e0215987.	2.5	21
131	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.	2.5	20
132	Genome-wide expression profiling of B lymphocytes reveals IL4R increase in allergic asthma. Journal of Allergy and Clinical Immunology, 2014, 134, 972-975.	2.9	20
133	GUÃA: a digital platform to facilitate result disclosure in genetic counseling. Genetics in Medicine, 2021, 23, 942-949.	2.4	20
134	The SEQC2 epigenomics quality control (EpiQC) study. Genome Biology, 2021, 22, 332.	8.8	20
135	The shape of gene expression distributions matter: how incorporating distribution shape improves the interpretation of cancer transcriptomic data. BMC Bioinformatics, 2020, 21, 562.	2.6	19
136	Experimental approaches to the study of epigenomic dysregulation in ageing. Experimental Gerontology, 2010, 45, 255-268.	2.8	18
137	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.	2.9	18
138	The Help Assay. Methods in Molecular Biology, 2009, 507, 77-87.	0.9	18
139	Homez, a homeobox leucine zipper gene specific to the vertebrate lineage. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 10358-10363.	7.1	17
140	How might epigenetic dysregulation in early embryonic life contribute to autism spectrum disorder?. Epigenomics, 2015, 7, 1-4.	2.1	17
141	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.	5.6	17
142	A triple color FISH technique for mouse chromosome identification. Mammalian Genome, 2001, 12, 462-465.	2.2	15
143	Genetic mapping of putative Chrna7 and Luzp2 neuronal transcriptional enhancers due to impact of a transgene-insertion and 6.8 Mb deletion in a mouse model of Prader-Willi and Angelman syndromes. BMC Genomics, 2005, 6, 157.	2.8	15
144	Development of a Targeted Multi-Disorder High-Throughput Sequencing Assay for the Effective Identification of Disease-Causing Variants. PLoS ONE, 2015, 10, e0133742.	2.5	15

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145	MeCP2 Binding Cooperativity Inhibits DNA Modification-Specific Recognition. Biochemistry, 2016, 55, 4275-4285.	2.5	15
146	Mechanisms of establishment and functional significance of DNA demethylation during erythroid differentiation. Blood Advances, 2018, 2, 1833-1852.	5.2	15
147	A molecular anatomical analysis of mosaic trisomy 16. Human Genetics, 1996, 98, 86-90.	3.8	14
148	Population epigenetics. Current Opinion in Systems Biology, 2017, 1, 84-89.	2.6	13
149	The Current State of Epigenetic Research in Humans. JAMA Pediatrics, 2017, 171, 103.	6.2	13
150	Cell type-specific chromatin accessibility analysis in the mouse and human brain. Epigenetics, 2022, 17, 202-219.	2.7	13
151	Automated Computational Analysis of Genome-Wide DNA Methylation Profiling Data from HELP-Tagging Assays. Methods in Molecular Biology, 2012, 815, 79-87.	0.9	13
152	DNA methylation changes in murine breast adenocarcinomas allow the identification of candidate genes for human breast carcinogenesis. Mammalian Genome, 2011, 22, 249-259.	2.2	11
153	Astrogenomics: big data, old problems, old solutions?. Genome Biology, 2013, 14, 129.	8.8	11
154	Genome-wide DNA Methylation Analysis Using Massively Parallel Sequencing Technologies. Seminars in Hematology, 2013, 50, 70-77.	3.4	11
155	AptCompare: optimizedde novomotif discovery of RNA aptamers via HTS-SELEX. Bioinformatics, 2020, 36, 2905-2906.	4.1	11
156	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.	3.4	10
157	Intrauterine Hyperglycemia Is Associated with an Impaired Postnatal Response to Oxidative Damage. Stem Cells and Development, 2018, 27, 683-691.	2.1	10
158	Amnion as a surrogate tissue reporter of the effects of maternal preeclampsia on the fetus. Clinical Epigenetics, 2016, 8, 67.	4.1	9
159	LPA receptor activity is basal specific and coincident with early pregnancy and involution during mammary gland postnatal development. Scientific Reports, 2016, 6, 35810.	3.3	9
160	Preleukemic and leukemic evolution at the stem cell level. Blood, 2021, 137, 1013-1018.	1.4	9
161	Increased Global Gene Promoter Methylation after Relapse (Rel) of Acute Promyelocytic Leukemia (APL) from All-trans Retinoic Acid (ATRA)-Containing Treatment Is Dissociated from Concurrent Gene Expression Changes.. Blood, 2007, 110, 2121-2121.	1.4	9
162	Disproportionate Vitamin A Deficiency in Women of Specific Ethnicities Linked to Differences in Allele Frequencies of Vitamin A-Related Polymorphisms. Nutrients, 2021, 13, 1743.	4.1	8

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163	Genetics of Childhood Disorders: XIII. Genomic Imprinting: The Indelible Mark of the Gamete. Journal of the American Academy of Child and Adolescent Psychiatry, 2000, 39, 532-535.	0.5	7
164	Allele-specific transcriptional elongation regulates monoallelic expression of the IGF2BP1 gene. Epigenetics and Chromatin, 2011, 4, 14.	3.9	7
165	A polycomb-mediated epigenetic field defect precedes invasive cervical carcinoma. Oncotarget, 2016, 7, 62133-62143.	1.8	7
166	Bidding the CpG island goodbye. ELife, 2013, 2, e00593.	6.0	7
167	Differential DNA methylation patterns of homeobox genes in proximal and distal colon epithelial cells. Physiological Genomics, 2016, 48, 257-273.	2.3	6
168	DNA methylation haplotypes as cancer markers. Nature Genetics, 2018, 50, 1062-1063.	21.4	6
169	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.	2.6	6
170	Downregulation of Ribosomal Proteins Is Seen in Non 5q- MDS. Blood, 2008, 112, 854-854.	1.4	6
171	The physiology of anti-idiotypic interactions: From clonal to paratopic selection. Clinical Immunology and Immunopathology, 1991, 60, 1-12.	2.0	5
172	Genomic imprinting and chromatin insulation in beckwith-wiedemann syndrome. Molecular Biotechnology, 1999, 11, 159-173.	2.4	5
173	LINE-1 Activity in Facultative Heterochromatin Formation during X Chromosome Inactivation. Cell, 2016, 166, 782.	28.9	5
174	High-efficiency genomic editing in Epstein-Barr virus-transformed lymphoblastoid B cells using a single-stranded donor oligonucleotide strategy. Communications Biology, 2019, 2, 312.	4.4	5
175	Misidentification of MLL3 and other mutations in cancer due to highly homologous genomic regions. Leukemia and Lymphoma, 2019, 60, 3132-3137.	1.3	5
176	Retargeting of macroH2A following mitosis to cytogenetic-scale heterochromatic domains. Journal of Cell Biology, 2019, 218, 1810-1823.	5.2	5
177	The HELP-Based DNA Methylation Assays. Methods in Molecular Biology, 2018, 1708, 191-207.	0.9	4
178	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.	2.8	4
179	MDS Marrow Stroma Is Characterized by Distinct Epigenetic Alterations. Blood, 2008, 112, 3635-3635.	1.4	4
180	Genetics of Childhood Disorders: VIII. Making Sense Out of Nonsense. Journal of the American Academy of Child and Adolescent Psychiatry, 1999, 38, 1458-1461.	0.5	3

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