

Manel Esteller

List of Publications by Year in descending order

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599
papers

86,043
citations

484

129
h-index

460

272
g-index

626
all docs

626
docs citations

626
times ranked

87051
citing authors

#	ARTICLE	IF	CITATIONS
1	Non-coding RNAs in human disease. <i>Nature Reviews Genetics</i> , 2011, 12, 861-874.	7.7	4,159
2	Epigenetics in Cancer. <i>New England Journal of Medicine</i> , 2008, 358, 1148-1159.	13.9	3,251
3	From The Cover: Epigenetic differences arise during the lifetime of monozygotic twins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10604-10609.	3.3	3,169
4	Epigenetic modifications and human disease. <i>Nature Biotechnology</i> , 2010, 28, 1057-1068.	9.4	2,328
5	Inactivation of the DNA-Repair Gene MGMT and the Clinical Response of Gliomas to Alkylating Agents. <i>New England Journal of Medicine</i> , 2000, 343, 1350-1354.	13.9	2,323
6	The Polycomb group protein EZH2 directly controls DNA methylation. <i>Nature</i> , 2006, 439, 871-874.	13.7	1,964
7	Cancer epigenomics: DNA methylomes and histone-modification maps. <i>Nature Reviews Genetics</i> , 2007, 8, 286-298.	7.7	1,916
8	Loss of acetylation at Lys16 and trimethylation at Lys20 of histone H4 is a common hallmark of human cancer. <i>Nature Genetics</i> , 2005, 37, 391-400.	9.4	1,710
9	Gene-Expression Profiles in Hereditary Breast Cancer. <i>New England Journal of Medicine</i> , 2001, 344, 539-548.	13.9	1,669
10	Global Epigenomic Reconfiguration During Mammalian Brain Development. <i>Science</i> , 2013, 341, 1237-905.	6.0	1,609
11	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016, 166, 740-754.	13.5	1,518
12	DNA Methylation and Cancer. <i>Advances in Genetics</i> , 2010, 70, 27-56.	0.8	1,238
13	CpG island hypermethylation and tumor suppressor genes: a booming present, a brighter future. <i>Oncogene</i> , 2002, 21, 5427-5440.	2.6	1,103
14	Cancer epigenetics reaches mainstream oncology. <i>Nature Medicine</i> , 2011, 17, 330-339.	15.2	1,102
15	The transcription factor Slug represses E-cadherin expression and induces epithelial to mesenchymal transitions: a comparison with Snail and E47 repressors. <i>Journal of Cell Science</i> , 2003, 116, 499-511.	1.2	1,021
16	A microRNA DNA methylation signature for human cancer metastasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13556-13561.	3.3	990
17	Validation of a DNA methylation microarray for 450,000 CpG sites in the human genome. <i>Epigenetics</i> , 2011, 6, 692-702.	1.3	908
18	Inactivation of the apoptosis effector Apaf-1 in malignant melanoma. <i>Nature</i> , 2001, 409, 207-211.	13.7	901

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19	Genetic Unmasking of an Epigenetically Silenced microRNA in Human Cancer Cells. <i>Cancer Research</i> , 2007, 67, 1424-1429.	0.4	883
20	The role of histone deacetylases (HDACs) in human cancer. <i>Molecular Oncology</i> , 2007, 1, 19-25.	2.1	796
21	Distinct DNA methylomes of newborns and centenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10522-10527.	3.3	687
22	Cancer as an epigenetic disease: DNA methylation and chromatin alterations in human tumours. <i>Journal of Pathology</i> , 2002, 196, 1-7.	2.1	679
23	DNA methylation profiling in the clinic: applications and challenges. <i>Nature Reviews Genetics</i> , 2012, 13, 679-692.	7.7	675
24	Snail Mediates E-Cadherin Repression by the Recruitment of the Sin3A/Histone Deacetylase 1 (HDAC1)/HDAC2 Complex. <i>Molecular and Cellular Biology</i> , 2004, 24, 306-319.	1.1	672
25	Identification of an Immune-specific Class of Hepatocellular Carcinoma, Based on Molecular Features. <i>Gastroenterology</i> , 2017, 153, 812-826.	0.6	650
26	Epigenetics and aging: the targets and the marks. <i>Trends in Genetics</i> , 2007, 23, 413-418.	2.9	611
27	Epigenetic gene silencing in cancer: the DNA hypermethylome. <i>Human Molecular Genetics</i> , 2007, 16, R50-R59.	1.4	604
28	Toward understanding and exploiting tumor heterogeneity. <i>Nature Medicine</i> , 2015, 21, 846-853.	15.2	604
29	Changes in the pattern of DNA methylation associate with twin discordance in systemic lupus erythematosus. <i>Genome Research</i> , 2010, 20, 170-179.	2.4	569
30	DNA methyltransferases control telomere length and telomere recombination in mammalian cells. <i>Nature Cell Biology</i> , 2006, 8, 416-424.	4.6	538
31	Aberrant Epigenetic Landscape in Cancer: How Cellular Identity Goes Awry. <i>Developmental Cell</i> , 2010, 19, 698-711.	3.1	529
32	Validation of a DNA methylation microarray for 850,000 CpG sites of the human genome enriched in enhancer sequences. <i>Epigenomics</i> , 2016, 8, 389-399.	1.0	529
33	Epigenetic mechanisms in neurological diseases: genes, syndromes, and therapies. <i>Lancet Neurology</i> , 2009, 8, 1056-1072.	4.9	528
34	CpG Island Hypermethylation of the DNA Repair Enzyme Methyltransferase Predicts Response to Temozolomide in Primary Gliomas. <i>Clinical Cancer Research</i> , 2004, 10, 4933-4938.	3.2	523
35	ABERRANT DNA METHYLATION AS A CANCER-INDUCING MECHANISM. <i>Annual Review of Pharmacology and Toxicology</i> , 2005, 45, 629-656.	4.2	490
36	lncRNAs and microRNAs with a role in cancer development. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 169-176.	0.9	449

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37	MLH1 promoter hypermethylation is associated with the microsatellite instability phenotype in sporadic endometrial carcinomas. <i>Oncogene</i> , 1998, 17, 2413-2417.	2.6	442
38	Notch Signaling Is Essential for Ventricular Chamber Development. <i>Developmental Cell</i> , 2007, 12, 415-429.	3.1	422
39	Cancer epigenomics: beyond genomics. <i>Current Opinion in Genetics and Development</i> , 2012, 22, 50-55.	1.5	421
40	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
41	Cis-acting noncoding RNAs: friends and foes. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1068-1075.	3.6	384
42	DNA methylation-based prognosis and epidrivers in hepatocellular carcinoma. <i>Hepatology</i> , 2015, 61, 1945-1956.	3.6	367
43	DNA Methylation: A Profile of Methods and Applications. <i>BioTechniques</i> , 2002, 33, 632-649.	0.8	359
44	Epigenetic profiling to classify cancer of unknown primary: a multicentre, retrospective analysis. <i>Lancet Oncology</i> , The, 2016, 17, 1386-1395.	5.1	357
45	A TARBP2 mutation in human cancer impairs microRNA processing and DICER1 function. <i>Nature Genetics</i> , 2009, 41, 365-370.	9.4	355
46	DNA methylation contributes to natural human variation. <i>Genome Research</i> , 2013, 23, 1363-1372.	2.4	353
47	Clinical epigenetics: seizing opportunities for translation. <i>Nature Reviews Genetics</i> , 2019, 20, 109-127.	7.7	353
48	A DNA methylation fingerprint of 1628 human samples. <i>Genome Research</i> , 2012, 22, 407-419.	2.4	341
49	A Role for RNAi in the Selective Correction of DNA Methylation Defects. <i>Science</i> , 2009, 323, 1600-1604.	6.0	338
50	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226.	9.4	323
51	Role of the RB1 family in stabilizing histone methylation at constitutive heterochromatin. <i>Nature Cell Biology</i> , 2005, 7, 420-428.	4.6	314
52	Genome-wide parent-of-origin DNA methylation analysis reveals the intricacies of human imprinting and suggests a germline methylation-independent mechanism of establishment. <i>Genome Research</i> , 2014, 24, 554-569.	2.4	311
53	A Genetic Defect in Exportin-5 Traps Precursor MicroRNAs in the Nucleus of Cancer Cells. <i>Cancer Cell</i> , 2010, 18, 303-315.	7.7	299
54	Methyl-CpG binding proteins identify novel sites of epigenetic inactivation in human cancer. <i>EMBO Journal</i> , 2003, 22, 6335-6345.	3.5	294

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55	Relevance of DNA methylation in the management of cancer. <i>Lancet Oncology</i> , The, 2003, 4, 351-358.	5.1	293
56	Generating mutations but providing chemosensitivity: the role of O6-methylguanine DNA methyltransferase in human cancer. <i>Oncogene</i> , 2004, 23, 1-8.	2.6	289
57	Chromosomal Instability Correlates with Genome-wide DNA Demethylation in Human Primary Colorectal Cancers. <i>Cancer Research</i> , 2006, 66, 8462-9468.	0.4	286
58	SOCS-1, a negative regulator of cytokine signaling, is frequently silenced by methylation in multiple myeloma. <i>Blood</i> , 2003, 101, 2784-2788.	0.6	285
59	DNA methylomes, histone codes and miRNAs: Tying it all together. <i>International Journal of Biochemistry and Cell Biology</i> , 2009, 41, 87-95.	1.2	283
60	hMLH1 Promoter Hypermethylation Is an Early Event in Human Endometrial Tumorigenesis. <i>American Journal of Pathology</i> , 1999, 155, 1767-1772.	1.9	280
61	DNA Methylation Polymorphisms Precede Any Histological Sign of Atherosclerosis in Mice Lacking Apolipoprotein E. <i>Journal of Biological Chemistry</i> , 2004, 279, 29147-29154.	1.6	279
62	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737.	9.4	270
63	Dysregulation of microRNAs in cancer: Playing with fire. <i>FEBS Letters</i> , 2011, 585, 2087-2099.	1.3	264
64	DNA methylation loss promotes immune evasion of tumours with high mutation and copy number load. <i>Nature Communications</i> , 2019, 10, 4278.	5.8	263
65	Loss of the glycine N-methyltransferase gene leads to steatosis and hepatocellular carcinoma in mice. <i>Hepatology</i> , 2008, 47, 1191-1199.	3.6	262
66	Hypermethylation of the DNA Repair Gene O6-Methylguanine DNA Methyltransferase and Survival of Patients With Diffuse Large B-Cell Lymphoma. <i>Journal of the National Cancer Institute</i> , 2002, 94, 26-32.	3.0	261
67	Tumor Cell-Specific BRCA1 and RASSF1A Hypermethylation in Serum, Plasma, and Peritoneal Fluid from Ovarian Cancer Patients. <i>Cancer Research</i> , 2004, 64, 6476-6481.	0.4	259
68	A truncating mutation of HDAC2 in human cancers confers resistance to histone deacetylase inhibition. <i>Nature Genetics</i> , 2006, 38, 566-569.	9.4	254
69	Abnormalities of the APC/β-catenin pathway in endometrial cancer. <i>Oncogene</i> , 2002, 21, 7981-7990.	2.6	252
70	A Prognostic DNA Methylation Signature for Stage I Non-Small-Cell Lung Cancer. <i>Journal of Clinical Oncology</i> , 2013, 31, 4140-4147.	0.8	250
71	Histone deacetylase inhibitors: Understanding a new wave of anticancer agents. <i>International Journal of Cancer</i> , 2004, 112, 171-178.	2.3	241
72	Epigenetic inactivation of the premature aging Werner syndrome gene in human cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8822-8827.	3.3	240

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73	Bromodomain inhibitors and cancer therapy: From structures to applications. <i>Epigenetics</i> , 2017, 12, 323-339.	1.3	239
74	Tumor-Related Molecular Mechanisms of Oxaliplatin Resistance. <i>Molecular Cancer Therapeutics</i> , 2015, 14, 1767-1776.	1.9	237
75	Sarcoma classification by DNA methylation profiling. <i>Nature Communications</i> , 2021, 12, 498.	5.8	237
76	GATA-4 and GATA-5 Transcription Factor Genes and Potential Downstream Antitumor Target Genes Are Epigenetically Silenced in Colorectal and Gastric Cancer. <i>Molecular and Cellular Biology</i> , 2003, 23, 8429-8439.	1.1	234
77	RNA-RNA interactions in gene regulation: the coding and noncoding players. <i>Trends in Biochemical Sciences</i> , 2015, 40, 248-256.	3.7	230
78	Small molecule enoxacin is a cancer-specific growth inhibitor that acts by enhancing TAR RNA-binding protein 2-mediated microRNA processing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4394-4399.	3.3	222
79	Cross-Talk between Aging and Cancer: The Epigenetic Language. <i>Annals of the New York Academy of Sciences</i> , 2007, 1100, 60-74.	1.8	221
80	The dynamic DNA methylomes of double-stranded DNA viruses associated with human cancer. <i>Genome Research</i> , 2009, 19, 438-451.	2.4	218
81	Genetic analysis of p38 MAP kinases in myogenesis: fundamental role of p38 β in abrogating myoblast proliferation. <i>EMBO Journal</i> , 2007, 26, 1245-1256.	3.5	217
82	Genomic DNA hypomethylation as a biomarker for bladder cancer susceptibility in the Spanish Bladder Cancer Study: a case-control study. <i>Lancet Oncology</i> , The, 2008, 9, 359-366.	5.1	211
83	DNA Methylation Map of Human Atherosclerosis. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 692-700.	5.1	207
84	The Epigenetic Face of Systemic Lupus Erythematosus. <i>Journal of Immunology</i> , 2006, 176, 7143-7147.	0.4	203
85	The affinity of different MBD proteins for a specific methylated locus depends on their intrinsic binding properties. <i>Nucleic Acids Research</i> , 2003, 31, 1765-1774.	6.5	202
86	Lung cancer epigenetics: From knowledge to applications. <i>Seminars in Cancer Biology</i> , 2018, 51, 116-128.	4.3	202
87	Heterozygous disruption of Hic1 predisposes mice to a gender-dependent spectrum of malignant tumors. <i>Nature Genetics</i> , 2003, 33, 197-202.	9.4	200
88	Allele-specific histone lysine methylation marks regulatory regions at imprinted mouse genes. <i>EMBO Journal</i> , 2002, 21, 6560-6570.	3.5	198
89	Epigenetic biomarkers for human cancer: The time is now. <i>Critical Reviews in Oncology/Hematology</i> , 2008, 68, 1-11.	2.0	197
90	Head-to-head antisense transcription and R-loop formation promotes transcriptional activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5785-5790.	3.3	194

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91	A Mouse Skin Multistage Carcinogenesis Model Reflects the Aberrant DNA Methylation Patterns of Human Tumors. <i>Cancer Research</i> , 2004, 64, 5527-5534.	0.4	193
92	Epigenetic inactivation of the Sotos overgrowth syndrome gene histone methyltransferase NSD1 in human neuroblastoma and glioma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21830-21835.	3.3	190
93	Discovery of methylated circulating DNA biomarkers for comprehensive non-invasive monitoring of treatment response in metastatic colorectal cancer. <i>Gut</i> , 2018, 67, 1995-2005.	6.1	188
94	Epigenetic and genetic alterations of APC and CDH1 genes in lobular breast cancer: Relationships with abnormal E-cadherin and catenin expression and microsatellite instability. <i>International Journal of Cancer</i> , 2003, 106, 208-215.	2.3	186
95	Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. <i>Genome Biology</i> , 2016, 17, 11.	3.8	184
96	The Epigenetic Basis of Twin Discordance in Age-Related Diseases. <i>Pediatric Research</i> , 2007, 61, 38R-42R.	1.1	183
97	Point mutation and homozygous deletion of PTEN/MMAC1 in primary bladder cancers. <i>Oncogene</i> , 1998, 16, 3215-3218.	2.6	175
98	Methyl-DNA immunoprecipitation (MeDIP): Hunting down the DNA methylome. <i>BioTechniques</i> , 2008, 44, 35-43.	0.8	175
99	Epigenetic inactivation of LKB1 in primary tumors associated with the Peutz-Jeghers syndrome. <i>Oncogene</i> , 2000, 19, 164-168.	2.6	171
100	Human DNA Methyltransferase 1 Is Required for Maintenance of the Histone H3 Modification Pattern. <i>Journal of Biological Chemistry</i> , 2004, 279, 37175-37184.	1.6	171
101	Genome-Wide Analysis of DNA Methylation Differences in Muscle and Fat from Monozygotic Twins Discordant for Type 2 Diabetes. <i>PLoS ONE</i> , 2012, 7, e51302.	1.1	171
102	Breast Cancer Epigenetics: From DNA Methylation to microRNAs. <i>Journal of Mammary Gland Biology and Neoplasia</i> , 2010, 15, 5-17.	1.0	167
103	Epigenetic alterations involved in cancer stem cell reprogramming. <i>Molecular Oncology</i> , 2012, 6, 620-636.	2.1	167
104	An Adenine Code for DNA: A Second Life for N6-Methyladenine. <i>Cell</i> , 2015, 161, 710-713.	13.5	167
105	Epigenetic prediction of response to anti-PD-1 treatment in non-small-cell lung cancer: a multicentre, retrospective analysis. <i>Lancet Respiratory Medicine</i> , 2018, 6, 771-781.	5.2	167
106	The Wnt antagonist DICKKOPF-1 gene is induced by 1 α ,25-dihydroxyvitamin D3 associated to the differentiation of human colon cancer cells. <i>Carcinogenesis</i> , 2007, 28, 1877-1884.	1.3	166
107	E47 phosphorylation by p38 MAPK promotes MyoD/E47 association and muscle-specific gene transcription. <i>EMBO Journal</i> , 2005, 24, 974-984.	3.5	165
108	Epigenetic Inactivation of the Circadian Clock Gene <i>BMAL1</i> in Hematologic Malignancies. <i>Cancer Research</i> , 2009, 69, 8447-8454.	0.4	161

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109	DNA methylation and cancer therapy: new developments and expectations. <i>Current Opinion in Oncology</i> , 2005, 17, 55-60.	1.1	159
110	Intronic RNAs mediate EZH2 regulation of epigenetic targets. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 664-670.	3.6	159
111	Mechanisms of Therapy Resistance in Patient-Derived Xenograft Models of BRCA1-Deficient Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2016, 108, djw148.	3.0	157
112	A DNA methylation-based definition of biologically distinct breast cancer subtypes. <i>Molecular Oncology</i> , 2015, 9, 555-568.	2.1	156
113	A microarray-based DNA methylation study of glioblastoma multiforme. <i>Epigenetics</i> , 2009, 4, 255-264.	1.3	155
114	EMP3, a Myelin-Related Gene Located in the Critical 19q13.3 Region, Is Epigenetically Silenced and Exhibits Features of a Candidate Tumor Suppressor in Glioma and Neuroblastoma. <i>Cancer Research</i> , 2005, 65, 2565-2571.	0.4	154
115	Sirtuin 1 regulation of developmental genes during differentiation of stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 13736-13741.	3.3	154
116	<i>BRCA1</i> CpG Island Hypermethylation Predicts Sensitivity to Poly(Adenosine Diphosphate)- Ribose Polymerase Inhibitors. <i>Journal of Clinical Oncology</i> , 2010, 28, e563-e564.	0.8	152
117	Towards the Human Cancer Epigenome: A First Draft of Histone Modifications. <i>Cell Cycle</i> , 2005, 4, 1377-1381.	1.3	149
118	The necessity of a human epigenome project. <i>Carcinogenesis</i> , 2006, 27, 1121-1125.	1.3	149
119	Genome-wide profiling of p53-regulated enhancer RNAs uncovers a subset of enhancers controlled by a lncRNA. <i>Nature Communications</i> , 2015, 6, 6520.	5.8	149
120	CSL-MAML-dependent Notch1 signaling controls T lineage-specific IL-7R α gene expression in early human thymopoiesis and leukemia. <i>Journal of Experimental Medicine</i> , 2009, 206, 779-791.	4.2	145
121	How epigenetics can explain human metastasis: A new role for microRNAs. <i>Cell Cycle</i> , 2009, 8, 377-382.	1.3	143
122	Whole-Exome Sequencing Identifies MDH2 as a New Familial Paraganglioma Gene. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	143
123	High-performance capillary electrophoretic method for the quantification of 5-methyl 2'-deoxycytidine in genomic DNA: Application to plant, animal and human cancer tissues. <i>Electrophoresis</i> , 2002, 23, 1677.	1.3	142
124	Genetic syndromes caused by mutations in epigenetic genes. <i>Human Genetics</i> , 2013, 132, 359-383.	1.8	141
125	A CpG island hypermethylation profile of primary colorectal carcinomas and colon cancer cell lines. <i>Molecular Cancer</i> , 2004, 3, 28.	7.9	140
126	Epigenetic inactivation of the p53-induced long noncoding RNA TP53 target 1 in human cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7535-E7544.	3.3	140

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127	Differential DNA hypermethylation and hypomethylation signatures in colorectal cancer. <i>Human Molecular Genetics</i> , 2005, 14, 319-326.	1.4	138
128	MGMT hypermethylation: A prognostic foe, a predictive friend. <i>DNA Repair</i> , 2007, 6, 1155-1160.	1.3	138
129	Characterization of 8p21.3 chromosomal deletions in B-cell lymphoma: TRAIL-R1 and TRAIL-R2 as candidate dosage-dependent tumor suppressor genes. <i>Blood</i> , 2005, 106, 3214-3222.	0.6	137
130	Regulation of pri-miRNA Processing by a Long Noncoding RNA Transcribed from an Ultraconserved Region. <i>Molecular Cell</i> , 2014, 55, 138-147.	4.5	137
131	Human DNA methylomes of neurodegenerative diseases show common epigenomic patterns. <i>Translational Psychiatry</i> , 2016, 6, e718-e718.	2.4	137
132	Putative cis-regulatory drivers in colorectal cancer. <i>Nature</i> , 2014, 512, 87-90.	13.7	136
133	DNA methylation profiling in breast cancer discordant identical twins identifies DOK7 as novel epigenetic biomarker. <i>Carcinogenesis</i> , 2013, 34, 102-108.	1.3	135
134	New insights into the biology and origin of mature aggressive B-cell lymphomas by combined epigenomic, genomic, and transcriptional profiling. <i>Blood</i> , 2009, 113, 2488-2497.	0.6	133
135	The Contribution of Epigenetics to Cancer Immunotherapy. <i>Trends in Immunology</i> , 2020, 41, 676-691.	2.9	133
136	The Epitranscriptome of Noncoding RNAs in Cancer. <i>Cancer Discovery</i> , 2017, 7, 359-368.	7.7	132
137	DNA methylation map of mouse and human brain identifies target genes in Alzheimer's disease. <i>Brain</i> , 2013, 136, 3018-3027.	3.7	129
138	Epigenetic disruption of ribosomal RNA genes and nucleolar architecture in DNA methyltransferase 1 (Dnmt1) deficient cells. <i>Nucleic Acids Research</i> , 2007, 35, 2191-2198.	6.5	128
139	Normative Data on Angular Vestibulo-Ocular Responses in the Yaw Axis Measured Using the Video Head Impulse Test. <i>Otology and Neurotology</i> , 2015, 36, 466-471.	0.7	128
140	Disrupted microRNA expression caused by Mecp2 loss in a mouse model of Rett syndrome. <i>Epigenetics</i> , 2010, 5, 656-663.	1.3	125
141	A mutation in the POT1 gene is responsible for cardiac angiosarcoma in TP53-negative Li-Fraumeni-like families. <i>Nature Communications</i> , 2015, 6, 8383.	5.8	124
142	Mutator pathways unleashed by epigenetic silencing in human cancer. <i>Mutagenesis</i> , 2007, 22, 247-253.	1.0	123
143	Identification of inflammatory mediators in patients with Crohn's disease unresponsive to anti-TNF α therapy. <i>Gut</i> , 2015, 64, 233-242.	6.1	123
144	IL-4 orchestrates STAT6-mediated DNA demethylation leading to dendritic cell differentiation. <i>Genome Biology</i> , 2016, 17, 4.	3.8	122

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145	Abnormalities of E- and P-cadherin and catenin (β -, γ -catenin, and p120 ^{ctn}) expression in endometrial cancer and endometrial atypical hyperplasia. <i>Journal of Pathology</i> , 2003, 199, 471-478.	2.1	121
146	MicroRNAs and cancer epigenetics: a macrorevolution. <i>Current Opinion in Oncology</i> , 2010, 22, 35-45.	1.1	121
147	Profiling aberrant DNA methylation in hematologic neoplasms: a view from the tip of the iceberg. <i>Clinical Immunology</i> , 2003, 109, 80-88.	1.4	120
148	Epigenetic inactivation of the putative DNA/RNA helicase SLFN11 in human cancer confers resistance to platinum drugs. <i>Oncotarget</i> , 2016, 7, 3084-3097.	0.8	120
149	Clustering of Gene Hypermethylation Associated With Clinical Risk Groups in Neuroblastoma. <i>Journal of the National Cancer Institute</i> , 2004, 96, 1208-1219.	3.0	119
150	Inactivation of the Lamin A/C Gene by CpG Island Promoter Hypermethylation in Hematologic Malignancies, and Its Association With Poor Survival in Nodal Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2005, 23, 3940-3947.	0.8	119
151	H3K4me1 marks DNA regions hypomethylated during aging in human stem and differentiated cells. <i>Genome Research</i> , 2015, 25, 27-40.	2.4	119
152	Dynamics of DNA Methylation in Recent Human and Great Ape Evolution. <i>PLoS Genetics</i> , 2013, 9, e1003763.	1.5	118
153	Cancer Epigenetics: Dna Methylation and Chromatin Alterations in Human Cancer. <i>Advances in Experimental Medicine and Biology</i> , 2003, 532, 39-49.	0.8	118
154	Genetic unmasking of epigenetically silenced tumor suppressor genes in colon cancer cells deficient in DNA methyltransferases. <i>Human Molecular Genetics</i> , 2003, 12, 2209-2219.	1.4	117
155	The impact of proinflammatory cytokines on the β -cell regulatory landscape provides insights into the genetics of type 1 diabetes. <i>Nature Genetics</i> , 2019, 51, 1588-1595.	9.4	117
156	Cancer Epigenetics and Methylation. <i>Science</i> , 2002, 297, 1807d-1808.	6.0	116
157	A Profile of Methyl-CpG Binding Domain Protein Occupancy of Hypermethylated Promoter CpG Islands of Tumor Suppressor Genes in Human Cancer. <i>Cancer Research</i> , 2006, 66, 8342-8346.	0.4	116
158	Hypermethylation of the hMLH1 gene promoter is associated with microsatellite instability in early human gastric neoplasia. <i>Oncogene</i> , 2001, 20, 329-335.	2.6	115
159	<i>BRCA1</i> epigenetic inactivation predicts sensitivity to platinum-based chemotherapy in breast and ovarian cancer. <i>Epigenetics</i> , 2012, 7, 1225-1229.	1.3	113
160	A Novel Epigenetic Signature for Early Diagnosis in Lung Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 3361-3371.	3.2	113
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