

# Manel Esteller

## List of Publications by Year in descending order

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Version: 2024-02-01

599  
papers

86,043  
citations

492

129  
h-index

460

272  
g-index

626  
all docs

626  
docs citations

626  
times ranked

87051  
citing authors

#	ARTICLE	IF	CITATIONS
1	Use of DNA methylation profiling in translational oncology. <i>Seminars in Cancer Biology</i> , 2022, 83, 523-535.	9.6	36
2	DNA methylome in visceral adipose tissue can discriminate patients with and without colorectal cancer. <i>Epigenetics</i> , 2022, 17, 665-676.	2.7	9
3	Towards a druggable epitranscriptome: Compounds that target RNA modifications in cancer. <i>British Journal of Pharmacology</i> , 2022, 179, 2868-2889.	5.4	19
4	Epigenetic Profiling and Response to CD19 Chimeric Antigen Receptor T-Cell Therapy in B-Cell Malignancies. <i>Journal of the National Cancer Institute</i> , 2022, 114, 436-445.	6.3	29
5	The transcribed ultraconserved region <i>uc.160+</i> enhances processing and A-to-I editing of the <i>miR-376</i> cluster: hypermethylation improves glioma prognosis. <i>Molecular Oncology</i> , 2022, 16, 648-664.	4.6	5
6	Experimental and Bioinformatic Approaches to Studying DNA Methylation in Cancer. <i>Cancers</i> , 2022, 14, 349.	3.7	9
7	Analysis of the circRNA and T-UCR populations identifies convergent pathways in mouse and human models of Rett syndrome. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 27, 621-644.	5.1	9
8	Epigenome-wide three-way interaction study identifies a complex pattern between <i>TRIM27</i> , <i>KIAA0226</i> , and smoking associated with overall survival of early-stage NSCLC. <i>Molecular Oncology</i> , 2022, 16, 717-731.	4.6	4
9	DNA methylation-associated dysregulation of transfer RNA expression in human cancer. <i>Molecular Cancer</i> , 2022, 21, 48.	19.2	7
10	Validation of a DNA methylation microarray for 285,000 CpG sites in the mouse genome. <i>Epigenetics</i> , 2022, , 1-9.	2.7	9
11	Epigenetic landscape in the kick-and-kill therapeutic vaccine BCN02 clinical trial is associated with antiretroviral treatment interruption (ATI) outcome. <i>EBioMedicine</i> , 2022, 78, 103956.	6.1	5
12	Refinement of computational identification of somatic copy number alterations using DNA methylation microarrays illustrated in cancers of unknown primary. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	1
13	Biological and Molecular Factors Predicting Response to Adoptive Cell Therapies in Cancer. <i>Journal of the National Cancer Institute</i> , 2022, 114, 930-939.	6.3	10
14	Accelerated biological aging in COVID-19 patients. <i>Nature Communications</i> , 2022, 13, 2135.	12.8	87
15	Resistance to PI3K inhibitors in marginal zone lymphoma can be reverted by targeting the IL-6/PDGFR $\alpha$ axis. <i>Haematologica</i> , 2022, 107, 2685-2697.	3.5	10
16	Novel Targeting of DNA Methyltransferase Activity Inhibits Ewing Sarcoma Cell Proliferation and Enhances Tumor Cell Sensitivity to DNA Damaging Drugs by Activating the DNA Damage Response. <i>Frontiers in Endocrinology</i> , 2022, 13, .	3.5	4
17	Novel genetic variants of KHDC3L and other members of the subcortical maternal complex associated with Beckwith-Wiedemann syndrome or Pseudohypoparathyroidism 1B and multi-locus imprinting disturbances. <i>Clinical Epigenetics</i> , 2022, 14, .	4.1	7
18	Dynamic epigenetic age mosaicism in the human atherosclerotic artery. <i>PLoS ONE</i> , 2022, 17, e0269501.	2.5	1

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19	Remodeling of the m6A RNA landscape in the conversion of acute lymphoblastic leukemia cells to macrophages. <i>Leukemia</i> , 2022, 36, 2121-2124.	7.2	6
20	DNA Methylation and Ischemic Stroke Risk: An Epigenome-Wide Association Study. <i>Thrombosis and Haemostasis</i> , 2022, 122, 1767-1778.	3.4	12
21	Epigenetic profiling linked to multisystem inflammatory syndrome in children (MIS-C): A multicenter, retrospective study. <i>EClinicalMedicine</i> , 2022, 50, 101515.	7.1	11
22	A timely, user-friendly analysis of the mouse DNA methylome. <i>Cell Genomics</i> , 2022, 2, 100153.	6.5	1
23	Single cell cancer epigenetics. <i>Trends in Cancer</i> , 2022, 8, 820-838.	7.4	37
24	Noninvasive early detection of colorectal cancer by hypermethylation of the LINC00473 promoter in plasma cell-free DNA. <i>Clinical Epigenetics</i> , 2022, 14, .	4.1	8
25	DNA Methylation Profiling of Human Hepatocarcinogenesis. <i>Hepatology</i> , 2021, 74, 183-199.	7.3	42
26	The Exceptional Responders Initiative: Feasibility of a National Cancer Institute Pilot Study. <i>Journal of the National Cancer Institute</i> , 2021, 113, 27-37.	6.3	17
27	Synthetic Conjugates of Ursodeoxycholic Acid Inhibit Cystogenesis in Experimental Models of Polycystic Liver Disease. <i>Hepatology</i> , 2021, 73, 186-203.	7.3	7
28	Discovery of novel DNA methylation biomarkers for noninvasive sporadic breast cancer detection in the Latino population. <i>Molecular Oncology</i> , 2021, 15, 473-486.	4.6	8
29	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. <i>Cancer Cell</i> , 2021, 39, 38-53.e7.	16.8	65
30	Triple negative breast cancer in the era of miRNA. <i>Critical Reviews in Oncology/Hematology</i> , 2021, 157, 103196.	4.4	38
31	A Tumor Suppressor Enhancer of <i>PTEN</i> in T-cell Development and Leukemia. <i>Blood Cancer Discovery</i> , 2021, 2, 92-109.	5.0	15
32	Epigenetic loss of m1A RNA demethylase ALKBH3 in Hodgkin lymphoma targets collagen, conferring poor clinical outcome. <i>Blood</i> , 2021, 137, 994-999.	1.4	30
33	Targeting aberrant DNA methylation in mesenchymal stromal cells as a treatment for myeloma bone disease. <i>Nature Communications</i> , 2021, 12, 421.	12.8	29
34	Influence of the disordered domain structure of MeCP2 on its structural stability and dsDNA interaction. <i>International Journal of Biological Macromolecules</i> , 2021, 175, 58-66.	7.5	7
35	Gene Amplification-Associated Overexpression of the Selenoprotein tRNA Enzyme TRIT1 Confers Sensitivity to Arsenic Trioxide in Small-Cell Lung Cancer. <i>Cancers</i> , 2021, 13, 1869.	3.7	6
36	Epigenome-wide association study of COVID-19 severity with respiratory failure. <i>EBioMedicine</i> , 2021, 66, 103339.	6.1	90

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37	DNA methylation biomarkers of myocardial infarction and cardiovascular disease. <i>Clinical Epigenetics</i> , 2021, 13, 86.	4.1	42
38	Clinicopathologic and molecular analysis of embryonal rhabdomyosarcoma of the genitourinary tract: evidence for a distinct DICER1-associated subgroup. <i>Modern Pathology</i> , 2021, 34, 1558-1569.	5.5	28
39	Extramedullary multiple myeloma patient derived orthotopic xenograft with high disturbed genome: combined exhaustive molecular and therapeutic studies. <i>DMM Disease Models and Mechanisms</i> , 2021, 14, .	2.4	5
40	Genetic Predisposition to Alzheimer's Disease Is Associated with Enlargement of Perivascular Spaces in Centrum Semiovale Region. <i>Genes</i> , 2021, 12, 825.	2.4	7
41	Distinct Associations of BMI and Fatty Acids With DNA Methylation in Fasting and Postprandial States in Men. <i>Frontiers in Genetics</i> , 2021, 12, 665769.	2.3	7
42	DDR1 methylation is associated with bipolar disorder and the isoform expression and methylation of myelin genes. <i>Epigenomics</i> , 2021, 13, 845-858.	2.1	4
43	Single-cell technologies and analyses in hematopoiesis and hematological malignancies. <i>Experimental Hematology</i> , 2021, 98, 1-13.	0.4	11
44	Follow-Up Study Confirms the Presence of Gastric Cancer DNA Methylation Hallmarks in High-Risk Precursor Lesions. <i>Cancers</i> , 2021, 13, 2760.	3.7	4
45	DNA methylation in cancer: From mouse to human and back again. <i>EBioMedicine</i> , 2021, 68, 103393.	6.1	1
46	Disruption of NIPBL/Scp2 in Cornelia de Lange Syndrome provokes cohesin genome-wide redistribution with an impact in the transcriptome. <i>Nature Communications</i> , 2021, 12, 4551.	12.8	20
47	Stabilization Effect of Intrinsically Disordered Regions on Multidomain Proteins: The Case of the Methyl-CpG Protein 2, MeCP2. <i>Biomolecules</i> , 2021, 11, 1216.	4.0	9
48	Impact of the Epigenetically Regulated Hoxa-5 Gene in Neural Differentiation from Human Adipose-Derived Stem Cells. <i>Biology</i> , 2021, 10, 802.	2.8	2
49	Antitumor Activity of the Novel BTK Inhibitor TG-1701 Is Associated with Disruption of Ikaros Signaling in Patients with B-cell Non-Hodgkin Lymphoma. <i>Clinical Cancer Research</i> , 2021, 27, 6591-6601.	7.0	8
50	MAX mutant small-cell lung cancers exhibit impaired activities of MGA-dependent noncanonical polycomb repressive complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2024824118.	7.1	9
51	Modulation of Colorectal Tumor Behavior via lncRNA TP53TG1-Lipidic Nanosystem. <i>Pharmaceutics</i> , 2021, 13, 1507.	4.5	4
52	Sarcoma classification by DNA methylation profiling. <i>Nature Communications</i> , 2021, 12, 498.	12.8	237
53	Sex differences in genetic susceptibility of hippocampal subfields: A polygenic association study. <i>Alzheimer's and Dementia</i> , 2021, 17, .	0.8	0
54	B-cell leukemia transdifferentiation to macrophage involves reconfiguration of DNA methylation for long-range regulation. <i>Leukemia</i> , 2020, 34, 1158-1162.	7.2	13

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55	Epigenetic <i>EGFR</i> Gene Repression Confers Sensitivity to Therapeutic BRAFV600E Blockade in Colon Neuroendocrine Carcinomas. <i>Clinical Cancer Research</i> , 2020, 26, 902-909.	7.0	29
56	Physical Activity and Genome-wide DNA Methylation: The REgistre Glron del COR Study. <i>Medicine and Science in Sports and Exercise</i> , 2020, 52, 589-597.	0.4	12
57	Molecular Context-Dependent Effects Induced by Rett Syndrome-Associated Mutations in MeCP2. <i>Biomolecules</i> , 2020, 10, 1533.	4.0	8
58	The human epigenome's implications for the understanding of human disease. , 2020, , 139-148.		0
59	Methylation regulation of Antiviral host factors, Interferon Stimulated Genes (ISGs) and T-cell responses associated with natural HIV control. <i>PLoS Pathogens</i> , 2020, 16, e1008678.	4.7	25
60	Epigenetic loss of the transfer RNA-modifying enzyme TYW2 induces ribosome frameshifts in colon cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20785-20793.	7.1	31
61	Sirt7 auto-ADP-ribosylation regulates glucose starvation response through mH2A1. <i>Science Advances</i> , 2020, 6, eaaz2590.	10.3	33
62	Epigenetic Awakening of Viral Mimicry in Cancer. <i>Cancer Discovery</i> , 2020, 10, 1258-1260.	9.4	7
63	Hsa-miR-155-5p Up-Regulation in Breast Cancer and Its Relevance for Treatment With Poly[ADP-Ribose] Polymerase 1 (PARP-1) Inhibitors. <i>Frontiers in Oncology</i> , 2020, 10, 1415.	2.8	31
64	Epigenetic-smoking interaction reveals histologically heterogeneous effects of TRIM27 DNA methylation on overall survival among early-stage NSCLC patients. <i>Molecular Oncology</i> , 2020, 14, 2759-2774.	4.6	13
65	Effect of BDNF Val66Met on hippocampal subfields volumes and compensatory interaction with APOE- $\epsilon$ 4 in middle-age cognitively unimpaired individuals from the ALFA study. <i>Brain Structure and Function</i> , 2020, 225, 2331-2345.	2.3	5
66	The DNA methylation landscape of human cancer organoids available at the American type culture collection. <i>Epigenetics</i> , 2020, 15, 1167-1177.	2.7	20
67	Towards a more precise therapy in cancer: Exploring epigenetic complexity. <i>Current Opinion in Chemical Biology</i> , 2020, 57, 41-49.	6.1	38
68	The DNA methylation landscape of hematological malignancies: an update. <i>Molecular Oncology</i> , 2020, 14, 1616-1639.	4.6	26
69	Epitranscriptomics in Hematopoiesis and Hematologic Malignancies. <i>Blood Cancer Discovery</i> , 2020, 1, 26-31.	5.0	18
70	Identification of 20 novel loci associated with ischaemic stroke. Epigenome-wide association study. <i>Epigenetics</i> , 2020, 15, 988-997.	2.7	22
71	Disruption of the RNA modifications that target the ribosome translation machinery in human cancer. <i>Molecular Cancer</i> , 2020, 19, 70.	19.2	36
72	Independent Validation of Early-Stage Non-Small Cell Lung Cancer Prognostic Scores Incorporating Epigenetic and Transcriptional Biomarkers With Gene-Gene Interactions and Main Effects. <i>Chest</i> , 2020, 158, 808-819.	0.8	26

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73	The Contribution of Epigenetics to Cancer Immunotherapy. <i>Trends in Immunology</i> , 2020, 41, 676-691.	6.8	133
74	Genetics and epigenetics of leukemia and lymphoma: from knowledge to applications, meeting report of the Josep Carreras Leukaemia Research Institute. <i>Hematological Oncology</i> , 2020, 38, 432-438.	1.7	6
75	Writers, readers and erasers of RNA modifications in cancer. <i>Cancer Letters</i> , 2020, 474, 127-137.	7.2	104
76	MethCORR modelling of methylomes from formalin-fixed paraffin-embedded tissue enables characterization and prognostication of colorectal cancer. <i>Nature Communications</i> , 2020, 11, 2025.	12.8	5
77	Genome-Wide DNA Methylation Profiling in Early Stage I Lung Adenocarcinoma Reveals Predictive Aberrant Methylation in the Promoter Region of the Long Noncoding RNA PLUT: An Exploratory Study. <i>Journal of Thoracic Oncology</i> , 2020, 15, 1338-1350.	1.1	8
78	Insights from the genetic and transcriptional characterization of a cancer of unknown primary (CUP) Tj ETQq0 0 0 rBT /Overlock 10 Tf	8.9	4
79	Epigenome-wide geneâ€age interaction analysis reveals reversed effects of <i>PRODH</i> DNA methylation on survival between young and elderly early-stage NSCLC patients. <i>Aging</i> , 2020, 12, 10642-10662.	3.1	8
80	DNA methylation of MMPs and TIMPs in atherothrombosis process in carotid plaques and blood tissues. <i>Oncotarget</i> , 2020, 11, 905-912.	1.8	4
81	Epigenetic inactivation of the splicing RNA-binding protein CELF2 in human breast cancer. <i>Oncogene</i> , 2019, 38, 7106-7112.	5.9	48
82	Epigenetic loss of RNA-methyltransferase NSUN5 in glioma targets ribosomes to drive a stress adaptive translational program. <i>Acta Neuropathologica</i> , 2019, 138, 1053-1074.	7.7	106
83	Molecular portrait of high alpha-fetoprotein in hepatocellular carcinoma: implications for biomarker-driven clinical trials. <i>British Journal of Cancer</i> , 2019, 121, 340-343.	6.4	62
84	The Altered Transcriptome and DNA Methylation Profiles of Docetaxel Resistance in Breast Cancer PDX Models. <i>Molecular Cancer Research</i> , 2019, 17, 2063-2076.	3.4	20
85	MicroRNA-654-5p suppresses ovarian cancer development impacting on MYC, WNT and AKT pathways. <i>Oncogene</i> , 2019, 38, 6035-6050.	5.9	49
86	Epigenetic silencing of TGFBI confers resistance to trastuzumab in human breast cancer. <i>Breast Cancer Research</i> , 2019, 21, 79.	5.0	41
87	Hsa-miR-210-3p expression in breast cancer and its putative association with worse outcome in patients treated with Docetaxel. <i>Scientific Reports</i> , 2019, 9, 14913.	3.3	19
88	MeCP2-E1 isoform is a dynamically expressed, weakly DNA-bound protein with different protein and DNA interactions compared to MeCP2-E2. <i>Epigenetics and Chromatin</i> , 2019, 12, 63.	3.9	50
89	The impact of proinflammatory cytokines on the Î²-cell regulatory landscape provides insights into the genetics of type 1 diabetes. <i>Nature Genetics</i> , 2019, 51, 1588-1595.	21.4	117
90	The transcribed pseudogene RPSAP52 enhances the oncofetal HMGA2-IGF2BP2-RAS axis through LIN28B-dependent and independent let-7 inhibition. <i>Nature Communications</i> , 2019, 10, 3979.	12.8	51

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91	DNA methylation loss promotes immune evasion of tumours with high mutation and copy number load. <i>Nature Communications</i> , 2019, 10, 4278.	12.8	263
92	Interactive effect of age and APOE- $\epsilon$ 4 allele load on white matter myelin content in cognitively normal middle-aged subjects. <i>NeuroImage: Clinical</i> , 2019, 24, 101983.	2.7	30
93	Germline variation in O6-methylguanine-DNA methyltransferase (MGMT) as cause of hereditary colorectal cancer. <i>Cancer Letters</i> , 2019, 447, 86-92.	7.2	12
94	<i>EGLN2</i> DNA methylation and expression interact with <i>HIF1A</i> to affect survival of early-stage NSCLC. <i>Epigenetics</i> , 2019, 14, 118-129.	2.7	28
95	Disruption of Long Noncoding RNAs Targets Cancer Hallmark Pathways in Lung Tumorigenesis. <i>Cancer Research</i> , 2019, 79, 3028-3030.	0.9	25
96	Walking pathways with positive feedback loops reveal DNA methylation biomarkers of colorectal cancer. <i>BMC Bioinformatics</i> , 2019, 20, 119.	2.6	37
97	APOE- $\epsilon$ 4 risk variant for Alzheimer's disease modifies the association between cognitive performance and cerebral morphology in healthy middle-aged individuals. <i>NeuroImage: Clinical</i> , 2019, 23, 101818.	2.7	18
98	Differences in expression rather than methylation at placenta-specific imprinted loci is associated with intrauterine growth restriction. <i>Clinical Epigenetics</i> , 2019, 11, 35.	4.1	29
99	<i>SIPA1L3</i> methylation modifies the benefit of smoking cessation on lung adenocarcinoma survival: an epigenomic "smoking interaction analysis. <i>Molecular Oncology</i> , 2019, 13, 1235-1248.	4.6	19
100	A two-gene epigenetic signature for the prediction of response to neoadjuvant chemotherapy in triple-negative breast cancer patients. <i>Clinical Epigenetics</i> , 2019, 11, 33.	4.1	39
101	Altered Long Non-coding RNA Expression in Cancer: Potential Biomarkers and Therapeutic Targets?. <i>Topics in Medicinal Chemistry</i> , 2019, , 401-428.	0.8	4
102	Global Proteomic and Methylome Analysis in Human Induced Pluripotent Stem Cells Reveals Overexpression of a Human TLR3 Affecting Proper Innate Immune Response Signaling. <i>Stem Cells</i> , 2019, 37, 476-488.	3.2	7
103	Clinical epigenetics: seizing opportunities for translation. <i>Nature Reviews Genetics</i> , 2019, 20, 109-127.	16.3	353
104	Identification of an episingature of human colorectal cancer associated with obesity by genome-wide DNA methylation analysis. <i>International Journal of Obesity</i> , 2019, 43, 176-188.	3.4	42
105	Epigenetic loss of the endoplasmic reticulum-associated degradation inhibitor SVIP induces cancer cell metabolic reprogramming. <i>JCI Insight</i> , 2019, 4, .	5.0	14
106	Trans-omics biomarker model improves prognostic prediction accuracy for early-stage lung adenocarcinoma. <i>Aging</i> , 2019, 11, 6312-6335.	3.1	13
107	Epigenomic signature of adrenoleukodystrophy predicts compromised oligodendrocyte differentiation. <i>Brain Pathology</i> , 2018, 28, 902-919.	4.1	21
108	A multi-omic study reveals <i>BTG2</i> as a reliable prognostic marker for early-stage non-small cell lung cancer. <i>Molecular Oncology</i> , 2018, 12, 913-924.	4.6	31

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109	Orthoxenografts of Testicular Germ Cell Tumors Demonstrate Genomic Changes Associated with Cisplatin Resistance and Identify PDMP as a Resensitizing Agent. <i>Clinical Cancer Research</i> , 2018, 24, 3755-3766.	7.0	17
110	Non-coding RNAs, epigenetics, and cancer: tying it all together. <i>Cancer and Metastasis Reviews</i> , 2018, 37, 55-73.	5.9	87
111	Epigenetic control of influenza virus: role of H3K79 methylation in interferon-induced antiviral response. <i>Scientific Reports</i> , 2018, 8, 1230.	3.3	43
112	SIRT6-dependent cysteine monoubiquitination in the PRE-SET domain of Suv39h1 regulates the NF- $\kappa$ B pathway. <i>Nature Communications</i> , 2018, 9, 101.	12.8	46
113	The Human Epigenomeâ€™ Implications for the Understanding of Human Disease. , 2018, , 165-182.		1
114	Epigenetic modifications in KDM lysine demethylases associate with survival of early-stage NSCLC. <i>Clinical Epigenetics</i> , 2018, 10, 41.	4.1	12
115	A multiplatform approach identifies miR-152-3p as a common epigenetically regulated onco-suppressor in prostate cancer targeting TMEM97. <i>Clinical Epigenetics</i> , 2018, 10, 40.	4.1	39
116	An Epigenetic Signature in Adipose Tissue Is Linked to Nicotinamide Nâ€™Methyltransferase Gene Expression. <i>Molecular Nutrition and Food Research</i> , 2018, 62, e1700933.	3.3	26
117	Interplay between long non-coding RNAs and epigenetic machinery: emerging targets in cancer?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20170074.	4.0	112
118	CpG Islands in Cancer: Heads, Tails, and Sides. <i>Methods in Molecular Biology</i> , 2018, 1766, 49-80.	0.9	19
119	Infinium DNA Methylation Microarrays on Formalin-Fixed, Paraffin-Embedded Samples. <i>Methods in Molecular Biology</i> , 2018, 1766, 83-107.	0.9	3
120	Effects of <i>APOE</i> $\epsilon$ 4 allele load on brain morphology in a cohort of middleâ€™aged healthy individuals with enriched genetic risk for Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2018, 14, 902-912.	0.8	98
121	Array-based DNA-methylation profiling in sarcomas with small blue round cell histology provides valuable diagnostic information. <i>Modern Pathology</i> , 2018, 31, 1246-1256.	5.5	76
122	Higher prevalence of cerebral white matter hyperintensities in homozygous <i>APOE-É4</i> allele carriers aged 45â€™75: Results from the ALFA study. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2018, 38, 250-261.	4.3	29
123	Profiling of oxBS-450K 5-hydroxymethylcytosine in human placenta and brain reveals enrichment at imprinted loci. <i>Epigenetics</i> , 2018, 13, 182-191.	2.7	23
124	Lung cancer epigenetics: From knowledge to applications. <i>Seminars in Cancer Biology</i> , 2018, 51, 116-128.	9.6	202
125	CD137 (4-1BB) Costimulation Modifies DNA Methylation in CD8+ T Cellâ€™Relevant Genes. <i>Cancer Immunology Research</i> , 2018, 6, 69-78.	3.4	34
126	SnapShot: Messenger RNA Modifications. <i>Cell</i> , 2018, 174, 498-498.e1.	28.9	52



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127	Mod Squad: Altered Histone Modifications in Cancer. , 2018, , 481-481.		0
128	Circular RNA CpG island hypermethylation-associated silencing in human cancer. <i>Oncotarget</i> , 2018, 9, 29208-29219.	1.8	35
129	An integrated genomic analysis of anaplastic meningioma identifies prognostic molecular signatures. <i>Scientific Reports</i> , 2018, 8, 13537.	3.3	49
130	DNA Methylation of <i>LRRC3B</i> : A Biomarker for Survival of Early-Stage Non-Small Cell Lung Cancer Patients. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 1527-1535.	2.5	10
131	Characterization of parent-of-origin methylation using the Illumina Infinium MethylationEPIC array platform. <i>Epigenomics</i> , 2018, 10, 941-954.	2.1	31
132	Introduction: Epigenetics in cancer. <i>Seminars in Cancer Biology</i> , 2018, 51, iv-v.	9.6	6
133	A new approach to epigenome-wide discovery of non-invasive methylation biomarkers for colorectal cancer screening in circulating cell-free DNA using pooled samples. <i>Clinical Epigenetics</i> , 2018, 10, 53.	4.1	44
134	PM20D1 is a quantitative trait locus associated with Alzheimer's disease. <i>Nature Medicine</i> , 2018, 24, 598-603.	30.7	73
135	Label-free DNA-methylation detection by direct ds-DNA fragment screening using poly-purine hairpins. <i>Biosensors and Bioelectronics</i> , 2018, 120, 47-54.	10.1	34
136	White matter microstructure is altered in cognitively normal middle-aged APOE- $\epsilon$ 4 homozygotes. <i>Alzheimer's Research and Therapy</i> , 2018, 10, 48.	6.2	43
137	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.	10.7	167
138	Primary intracranial spindle cell sarcoma with rhabdomyosarcoma-like features share a highly distinct methylation profile and DICER1 mutations. <i>Acta Neuropathologica</i> , 2018, 136, 327-337.	7.7	104
139	Inhibition of Gsk3 $\beta$ Reduces Nfkb1 Signaling and Rescues Synaptic Activity to Improve the Rett Syndrome Phenotype in Mecp2-Knockout Mice. <i>Cell Reports</i> , 2018, 23, 1665-1677.	6.4	36
140	<i>In vitro</i> and <i>in vivo</i> activity of a new small-molecule inhibitor of HDAC6 in mantle cell lymphoma. <i>Haematologica</i> , 2018, 103, e537-e540.	3.5	15
141	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.	12.1	188
142	MIR-193b promoter methylation accurately detects prostate cancer in urine sediments and miR-34b/c or miR-129-2 promoter methylation define subsets of clinically aggressive tumors. <i>Molecular Cancer</i> , 2017, 16, 26.	19.2	64
143	Whole genome grey and white matter DNA methylation profiles in dorsolateral prefrontal cortex. <i>Synapse</i> , 2017, 71, e21959.	1.2	13
144	DNA methylation map in circulating leukocytes mirrors subcutaneous adipose tissue methylation pattern: a genome-wide analysis from non-obese and obese patients. <i>Scientific Reports</i> , 2017, 7, 41903.	3.3	88

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145	Journal club: epigenetic profiling to classify cancer of unknown primary – Authors' reply. <i>Lancet Oncology</i> , 2017, 18, e131.	10.7	1
146	The intervening domain from MeCP2 enhances the DNA affinity of the methyl binding domain and provides an independent DNA interaction site. <i>Scientific Reports</i> , 2017, 7, 41635.	3.3	19
147	Downregulation of miR-130b~301b cluster is mediated by aberrant promoter methylation and impairs cellular senescence in prostate cancer. <i>Journal of Hematology and Oncology</i> , 2017, 10, 43.	17.0	48
148	Risk aversion and inequity aversion in demand for unemployment benefits. <i>International Tax and Public Finance</i> , 2017, 24, 198-220.	1.0	3
149	Genomic and Molecular Screenings Identify Different Mechanisms for Acquired Resistance to MET Inhibitors in Lung Cancer Cells. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 1366-1376.	4.1	23
150	Is Decentralization Really Welfare Enhancing? Empirical Evidence from Survey Data (1994–2011). <i>Kyklos</i> , 2017, 70, 189-219.	1.4	16
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