

Manel Esteller

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

560
papers

69,612
citations

119
h-index

251
g-index

626
ext. papers

79,278
ext. citations

10
avg, IF

8.48
L-index

#	Paper	IF	Citations
560	DNA methylation-associated dysregulation of transfer RNA expression in human cancer.. <i>Molecular Cancer</i> , 2022 , 21, 48	42.1	1
559	Experimental and Bioinformatic Approaches to Studying DNA Methylation in Cancer.. <i>Cancers</i> , 2022 , 14,	6.6	1
558	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	10.7	1
557	Validation of a DNA methylation microarray for 285,000 CpG sites in the mouse genome.. <i>Epigenetics</i> , 2022 ,	5.7	3
556	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	8.8	0
555	Accelerated biological aging in COVID-19 patients.. <i>Nature Communications</i> , 2022 , 13, 2135	17.4	4
554	Dynamic epigenetic age mosaicism in the human atherosclerotic artery. <i>PLoS ONE</i> , 2022 , 17, e0269501	3.7	0
553	The transcribed ultraconserved region uc.160+ enhances processing and A-to-I editing of the miR-376 cluster: hypermethylation improves glioma prognosis. <i>Molecular Oncology</i> , 2021 ,	7.9	2
552	DNA Methylation Profiling of Human Hepatocarcinogenesis. <i>Hepatology</i> , 2021 , 74, 183-199	11.2	10
551	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	7.9	1
550	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,	6.6	1
549	Epigenome-wide association study of COVID-19 severity with respiratory failure. <i>EBioMedicine</i> , 2021 , 66, 103339	8.8	33
548	DNA methylation biomarkers of myocardial infarction and cardiovascular disease. <i>Clinical Epigenetics</i> , 2021 , 13, 86	7.7	9
547	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	9.8	5
546	Extramedullary multiple myeloma patient-derived orthotopic xenograft with a highly altered genome: combined molecular and therapeutic studies. <i>DMM Disease Models and Mechanisms</i> , 2021 , 14,	4.1	2
545	Genetic Predisposition to Alzheimer β Disease Is Associated with Enlargement of Perivascular Spaces in Centrum Semiovale Region. <i>Genes</i> , 2021 , 12,	4.2	1
544	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	4.5	1

543	methylation is associated with bipolar disorder and the isoform expression and methylation of myelin genes. <i>Epigenomics</i> , 2021 , 13, 845-858	4.4	1
542	Single-cell technologies and analyses in hematopoiesis and hematological malignancies. <i>Experimental Hematology</i> , 2021 , 98, 1-13	3.1	2
541	DNA methylation in cancer: From mouse to human and back again. <i>EBioMedicine</i> , 2021 , 68, 103393	8.8	0
540	DNA methylome in visceral adipose tissue can discriminate patients with and without colorectal cancer. <i>Epigenetics</i> , 2021 , 1-12	5.7	0
539	The Exceptional Responders Initiative: Feasibility of a National Cancer Institute Pilot Study. <i>Journal of the National Cancer Institute</i> , 2021 , 113, 27-37	9.7	9
538	Synthetic Conjugates of Ursodeoxycholic Acid Inhibit Cystogenesis in Experimental Models of Polycystic Liver Disease. <i>Hepatology</i> , 2021 , 73, 186-203	11.2	1
537	Discovery of novel DNA methylation biomarkers for non-invasive sporadic breast cancer detection in the Latino population. <i>Molecular Oncology</i> , 2021 , 15, 473-486	7.9	4
536	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. <i>Cancer Cell</i> , 2021 , 39, 38-53.e7	24.3	18
535	Triple negative breast cancer in the era of miRNA. <i>Critical Reviews in Oncology/Hematology</i> , 2021 , 157, 103196	7	10
534	A Tumor Suppressor Enhancer of in T-cell development and leukemia. <i>Blood Cancer Discovery</i> , 2021 , 2, 92-109	7	4
533	Epigenetic loss of m1A RNA demethylase ALKBH3 in Hodgkin lymphoma targets collagen, conferring poor clinical outcome. <i>Blood</i> , 2021 , 137, 994-999	2.2	7
532	Targeting aberrant DNA methylation in mesenchymal stromal cells as a treatment for myeloma bone disease. <i>Nature Communications</i> , 2021 , 12, 421	17.4	11
531	Disruption of NIPBL/Sccl in Cornelia de Lange Syndrome provokes cohesin genome-wide redistribution with an impact in the transcriptome. <i>Nature Communications</i> , 2021 , 12, 4551	17.4	2
530	Towards a druggable epitranscriptome: Compounds that target RNA modifications in cancer. <i>British Journal of Pharmacology</i> , 2021 ,	8.6	2
529	Stabilization Effect of Intrinsically Disordered Regions on Multidomain Proteins: The Case of the Methyl-CpG Protein 2, MeCP2. <i>Biomolecules</i> , 2021 , 11,	5.9	1
528	Impact of the Epigenetically Regulated Hoxa-5 Gene in Neural Differentiation from Human Adipose-Derived Stem Cells. <i>Biology</i> , 2021 , 10,	4.9	1
527	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	12.9	3
526	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,	11.5	2

525	Epigenetic Profiling and Response to CD19 Chimeric Antigen Receptor T-Cell Therapy in B-Cell Malignancies. <i>Journal of the National Cancer Institute</i> , 2021 ,	9.7	4
524	Sarcoma classification by DNA methylation profiling. <i>Nature Communications</i> , 2021 , 12, 498	17.4	74
523	The DNA methylation landscape of human cancer organoids available at the American type culture collection. <i>Epigenetics</i> , 2020 , 15, 1167-1177	5.7	10
522	Towards a more precise therapy in cancer: Exploring epigenetic complexity. <i>Current Opinion in Chemical Biology</i> , 2020 , 57, 41-49	9.7	20
521	The DNA methylation landscape of hematological malignancies: an update. <i>Molecular Oncology</i> , 2020 , 14, 1616-1639	7.9	8
520	Epitranscriptomics in Hematopoiesis and Hematologic Malignancies. <i>Blood Cancer Discovery</i> , 2020 , 1, 26-31	7	11
519	Identification of 20 novel loci associated with ischaemic stroke. Epigenome-wide association study. <i>Epigenetics</i> , 2020 , 15, 988-997	5.7	9
518	Disruption of the RNA modifications that target the ribosome translation machinery in human cancer. <i>Molecular Cancer</i> , 2020 , 19, 70	42.1	12
517	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	5.3	10
516	The Contribution of Epigenetics to Cancer Immunotherapy. <i>Trends in Immunology</i> , 2020 , 41, 676-691	14.4	50
515	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	1.3	1
514	Writers, readers and erasers of RNA modifications in cancer. <i>Cancer Letters</i> , 2020 , 474, 127-137	9.9	47
513	MethCORR modelling of methylomes from formalin-fixed paraffin-embedded tissue enables characterization and prognostication of colorectal cancer. <i>Nature Communications</i> , 2020 , 11, 2025	17.4	2
512	Epigenome-wide gene-age interaction analysis reveals reversed effects of DNA methylation on survival between young and elderly early-stage NSCLC patients. <i>Aging</i> , 2020 , 12, 10642-10662	5.6	2
511	DNA methylation of MMPs and TIMPs in atherothrombosis process in carotid plaques and blood tissues. <i>Oncotarget</i> , 2020 , 11, 905-912	3.3	4
510	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	8.9	4
509	B-cell leukemia transdifferentiation to macrophage involves reconfiguration of DNA methylation for long-range regulation. <i>Leukemia</i> , 2020 , 34, 1158-1162	10.7	7
508	Epigenetic Gene Repression Confers Sensitivity to Therapeutic BRAFV600E Blockade in Colon Neuroendocrine Carcinomas. <i>Clinical Cancer Research</i> , 2020 , 26, 902-909	12.9	13

507	Physical Activity and Genome-wide DNA Methylation: The REgistre GlronDel COR Study. <i>Medicine and Science in Sports and Exercise</i> , 2020 , 52, 589-597	1.2	5
506	Molecular Context-Dependent Effects Induced by Rett Syndrome-Associated Mutations in MeCP2. <i>Biomolecules</i> , 2020 , 10,	5.9	3
505	The human epigenomeImplications for the understanding of human disease 2020 , 139-148		
504	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	7.6	17
503	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 ^{11,5}	11.5	12
502	Sirt7 auto-ADP-ribosylation regulates glucose starvation response through mH2A1. <i>Science Advances</i> , 2020 , 6, eaaz2590	14.3	13
501	Epigenetic Awakening of Viral Mimicry in Cancer. <i>Cancer Discovery</i> , 2020 , 10, 1258-1260	24.4	2
500	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	5.3	8
499	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	7.7	7
498	Effect of BDNF Val66Met on hippocampal subfields volumes and compensatory interaction with APOE-ε in middle-age cognitively unimpaired individuals from the ALFA study. <i>Brain Structure and Function</i> , 2020 , 225, 2331-2345	4	3
497	Use of DNA methylation profiling in translational oncology. <i>Seminars in Cancer Biology</i> , 2020 ,	12.7	13
496	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	17.4	29
495	DNA methylation loss promotes immune evasion of tumours with high mutation and copy number load. <i>Nature Communications</i> , 2019 , 10, 4278	17.4	109
494	Interactive effect of age and APOE-ε allele load on white matter myelin content in cognitively normal middle-aged subjects. <i>NeuroImage: Clinical</i> , 2019 , 24, 101983	5.3	6
493	Germline variation in O-methylguanine-DNA methyltransferase (MGMT) as cause of hereditary colorectal cancer. <i>Cancer Letters</i> , 2019 , 447, 86-92	9.9	12
492	EGLN2 DNA methylation and expression interact with HIF1A to affect survival of early-stage NSCLC. <i>Epigenetics</i> , 2019 , 14, 118-129	5.7	17
491	Disruption of Long Noncoding RNAs Targets Cancer Hallmark Pathways in Lung Tumorigenesis. <i>Cancer Research</i> , 2019 , 79, 3028-3030	10.1	18
490	Walking pathways with positive feedback loops reveal DNA methylation biomarkers of colorectal cancer. <i>BMC Bioinformatics</i> , 2019 , 20, 119	3.6	17

489	APOE- ϵ 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	5.3	10
488	Differences in expression rather than methylation at placenta-specific imprinted loci is associated with intrauterine growth restriction. <i>Clinical Epigenetics</i> , 2019 , 11, 35	7.7	13
487	SIPA1L3 methylation modifies the benefit of smoking cessation on lung adenocarcinoma survival: an epigenomic-smoking interaction analysis. <i>Molecular Oncology</i> , 2019 , 13, 1235-1248	7.9	11
486	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	7.7	25
485	Epigenetic inactivation of the splicing RNA-binding protein CELF2 in human breast cancer. <i>Oncogene</i> , 2019 , 38, 7106-7112	9.2	29
484	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	14.3	55
483	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	8.7	29
482	The Altered Transcriptome and DNA Methylation Profiles of Docetaxel Resistance in Breast Cancer PDX Models. <i>Molecular Cancer Research</i> , 2019 , 17, 2063-2076	6.6	12
481	MicroRNA-654-5p suppresses ovarian cancer development impacting on MYC, WNT and AKT pathways. <i>Oncogene</i> , 2019 , 38, 6035-6050	9.2	34
480	Epigenetic silencing of TGFBI confers resistance to trastuzumab in human breast cancer. <i>Breast Cancer Research</i> , 2019 , 21, 79	8.3	20
479	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	4.9	11
478	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	5.8	23
477	The impact of proinflammatory cytokines on the cell regulatory landscape provides insights into the genetics of type 1 diabetes. <i>Nature Genetics</i> , 2019 , 51, 1588-1595	36.3	55
476	Epigenetic loss of the endoplasmic reticulum-associated degradation inhibitor SVIP induces cancer cell metabolic reprogramming. <i>JCI Insight</i> , 2019 , 5,	9.9	8
475	Trans-omics biomarker model improves prognostic prediction accuracy for early-stage lung adenocarcinoma. <i>Aging</i> , 2019 , 11, 6312-6335	5.6	8
474	Altered Long Non-coding RNA Expression in Cancer: Potential Biomarkers and Therapeutic Targets?. <i>Topics in Medicinal Chemistry</i> , 2019 , 401-428	0.4	3
473	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	5.8	5
472	Clinical epigenetics: seizing opportunities for translation. <i>Nature Reviews Genetics</i> , 2019 , 20, 109-127	30.1	222

471	Identification of an episiature of human colorectal cancer associated with obesity by genome-wide DNA methylation analysis. <i>International Journal of Obesity</i> , 2019 , 43, 176-188	5.5	32
470	Epigenomic signature of adrenoleukodystrophy predicts compromised oligodendrocyte differentiation. <i>Brain Pathology</i> , 2018 , 28, 902-919	6	15
469	A multi-omic study reveals BTG2 as a reliable prognostic marker for early-stage non-small cell lung cancer. <i>Molecular Oncology</i> , 2018 , 12, 913-924	7.9	23
468	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	12.9	11
467	Non-coding RNAs, epigenetics, and cancer: tying it all together. <i>Cancer and Metastasis Reviews</i> , 2018 , 37, 55-73	9.6	61
466	Epigenetic control of influenza virus: role of H3K79 methylation in interferon-induced antiviral response. <i>Scientific Reports</i> , 2018 , 8, 1230	4.9	30
465	SIRT6-dependent cysteine monoubiquitination in the PRE-SET domain of Suv39h1 regulates the NF- κ B pathway. <i>Nature Communications</i> , 2018 , 9, 101	17.4	30
464	The Human Epigenome Implications for the Understanding of Human Disease 2018 , 165-182		1
463	Epigenetic modifications in lysine demethylases associate with survival of early-stage NSCLC. <i>Clinical Epigenetics</i> , 2018 , 10, 41	7.7	11
462	A multiplatform approach identifies miR-152-3p as a common epigenetically regulated onco-suppressor in prostate cancer targeting. <i>Clinical Epigenetics</i> , 2018 , 10, 40	7.7	27
461	An Epigenetic Signature in Adipose Tissue Is Linked to Nicotinamide N-Methyltransferase Gene Expression. <i>Molecular Nutrition and Food Research</i> , 2018 , 62, e1700933	5.9	14
460	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,	5.8	76
459	CpG Islands in Cancer: Heads, Tails, and Sides. <i>Methods in Molecular Biology</i> , 2018 , 1766, 49-80	1.4	13
458	Infinium DNA Methylation Microarrays on Formalin-Fixed, Paraffin-Embedded Samples. <i>Methods in Molecular Biology</i> , 2018 , 1766, 83-107	1.4	3
457	Effects of APOE- ϵ 4 allele load on brain morphology in a cohort of middle-aged healthy individuals with enriched genetic risk for Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2018 , 14, 902-912	1.2	64
456	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	9.8	58
455	Higher prevalence of cerebral white matter hyperintensities in homozygous APOE-e4 allele carriers aged 45-75: Results from the ALFA study. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2018 , 38, 250-261	7.3	17
454	Profiling of oxBS-450K 5-hydroxymethylcytosine in human placenta and brain reveals enrichment at imprinted loci. <i>Epigenetics</i> , 2018 , 13, 182-191	5.7	12

453	Lung cancer epigenetics: From knowledge to applications. <i>Seminars in Cancer Biology</i> , 2018 , 51, 116-128	12.7	142
452	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	7.7	27
451	PM20D1 is a quantitative trait locus associated with Alzheimer's disease. <i>Nature Medicine</i> , 2018 , 24, 598-603	5.3	38
450	Label-free DNA-methylation detection by direct ds-DNA fragment screening using poly-purine hairpins. <i>Biosensors and Bioelectronics</i> , 2018 , 120, 47-54	11.8	23
449	White matter microstructure is altered in cognitively normal middle-aged APOE- $\epsilon 4$ homozygotes. <i>Alzheimer's Research and Therapy</i> , 2018 , 10, 48	9	27
448	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	35.1	107
447	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	14.3	63
446	Inhibition of Gsk3b 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	10.6	20
445	and activity of a new small-molecule inhibitor of HDAC6 in mantle cell lymphoma. <i>Haematologica</i> , 2018 , 103, e537-e540	6.6	11
444	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	19.2	119
443	CD137 (4-1BB) Costimulation Modifies DNA Methylation in CD8 T Cell-Relevant Genes. <i>Cancer Immunology Research</i> , 2018 , 6, 69-78	12.5	26
442	SnapShot: Messenger RNA Modifications. <i>Cell</i> , 2018 , 174, 498-498.e1	56.2	31
441	Mod Squad: Altered Histone Modifications in Cancer 2018 , 481-481		
440	Circular RNA CpG island hypermethylation-associated silencing in human cancer. <i>Oncotarget</i> , 2018 , 9, 29208-29219	3.3	22
439	An integrated genomic analysis of anaplastic meningioma identifies prognostic molecular signatures. <i>Scientific Reports</i> , 2018 , 8, 13537	4.9	29
438	DNA Methylation of : A Biomarker for Survival of Early-Stage Non-Small Cell Lung Cancer Patients. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018 , 27, 1527-1535	4	7
437	Characterization of parent-of-origin methylation using the Illumina Infinium MethylationEPIC array platform. <i>Epigenomics</i> , 2018 , 10, 941-954	4.4	13
436	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	42.1	45

435	Whole genome grey and white matter DNA methylation profiles in dorsolateral prefrontal cortex. <i>Synapse</i> , 2017 , 71, e21959	2.4	10
434	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	4.9	59
433	Journal club: epigenetic profiling to classify cancer of unknown primary - AuthorsPreply. <i>Lancet Oncology, The</i> , 2017 , 18, e131	21.7	1
432	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	4.9	11
431	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	22.4	37
430	Risk aversion and inequity aversion in demand for unemployment benefits. <i>International Tax and Public Finance</i> , 2017 , 24, 198-220	1	3
429	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	6.1	19
428	Is Decentralization Really Welfare Enhancing? Empirical Evidence from Survey Data (1994-2011). <i>Kyklos</i> , 2017 , 70, 189-219	1.7	9
427	Molecular-Subtype-Specific Biomarkers Improve Prediction of Prognosis in Colorectal Cancer. <i>Cell Reports</i> , 2017 , 19, 1268-1280	10.6	55
426	Obesity and menopause modify the epigenomic profile of breast cancer. <i>Endocrine-Related Cancer</i> , 2017 , 24, 351-363	5.7	23
425	Resistance to Taxanes in Triple-Negative Breast Cancer Associates with the Dynamics of a CD49f+ Tumor-Initiating Population. <i>Stem Cell Reports</i> , 2017 , 8, 1392-1407	8	53
424	Bromodomain inhibitors and cancer therapy: From structures to applications. <i>Epigenetics</i> , 2017 , 12, 323-339	3.7	171
423	Identification of an Immune-specific Class of Hepatocellular Carcinoma, Based on Molecular Features. <i>Gastroenterology</i> , 2017 , 153, 812-826	13.3	371
422	Stem Cell Technology for (Epi)genetic Brain Disorders. <i>Advances in Experimental Medicine and Biology</i> , 2017 , 978, 443-475	3.6	4
421	Hydrogeochemical characteristics of a volcanic-sedimentary aquifer with special emphasis on Fe and Mn content: A case study in Mexico. <i>Journal of Geochemical Exploration</i> , 2017 , 180, 113-126	3.8	15
420	A DNA methylation map of human cancer at single base-pair resolution. <i>Oncogene</i> , 2017 , 36, 5648-5657	9.2	52
419	N-BLR, a primate-specific non-coding transcript leads to colorectal cancer invasion and migration. <i>Genome Biology</i> , 2017 , 18, 98	18.3	75
418	Fiscal equalization and lobbying. <i>International Tax and Public Finance</i> , 2017 , 24, 221-247	1	2

4 ¹⁷	Epigenetic loss of the RNA decapping enzyme NUDT16 mediates C-MYC activation in T-cell acute lymphoblastic leukemia. <i>Leukemia</i> , 2017 , 31, 1622-1625	10.7	12
4 ¹⁶	Stepwise analysis of MIR9 loci identifies miR-9-5p to be involved in Oestrogen regulated pathways in breast cancer patients. <i>Scientific Reports</i> , 2017 , 7, 45283	4.9	31
4 ¹⁵	The Epitranscriptome of Noncoding RNAs in Cancer. <i>Cancer Discovery</i> , 2017 , 7, 359-368	24.4	104
4 ¹⁴	The NCI-60 Methylome and Its Integration into CellMiner. <i>Cancer Research</i> , 2017 , 77, 601-612	10.1	34
4 ¹³	Opening up the DNA methylome of dementia. <i>Molecular Psychiatry</i> , 2017 , 22, 485-496	15.1	41
4 ¹²	Stem cell-like transcriptional reprogramming mediates metastatic resistance to mTOR inhibition. <i>Oncogene</i> , 2017 , 36, 2737-2749	9.2	27
4 ¹¹	The epigenetic landscape of Alu repeats delineates the structural and functional genomic architecture of colon cancer cells. <i>Genome Research</i> , 2017 , 27, 118-132	9.7	29
4 ¹⁰	Early-onset and classical forms of type 2 diabetes show impaired expression of genes involved in muscle branched-chain amino acids metabolism. <i>Scientific Reports</i> , 2017 , 7, 13850	4.9	28
4 ⁰⁹	Histone H1 depletion triggers an interferon response in cancer cells via activation of heterochromatic repeats. <i>Nucleic Acids Research</i> , 2017 , 45, 11622-11642	20.1	25
4 ⁰⁸	DNA methylation signal has a major role in the response of human breast cancer cells to the microenvironment. <i>Oncogenesis</i> , 2017 , 6, e390	6.6	22
4 ⁰⁷	Bromodomain inhibition shows antitumoral activity in mice and human luminal breast cancer. <i>Oncotarget</i> , 2017 , 8, 51621-51629	3.3	17
4 ⁰⁶	DNA Methylomes Reveal Biological Networks Involved in Human Eye Development, Functions and Associated Disorders. <i>Scientific Reports</i> , 2017 , 7, 11762	4.9	22
4 ⁰⁵	Epigenetic inactivation of tumour suppressor coding and non-coding genes in human cancer: an update. <i>Open Biology</i> , 2017 , 7,	7	51
4 ⁰⁴	Copy number rather than epigenetic alterations are the major dictator of imprinted methylation in tumors. <i>Nature Communications</i> , 2017 , 8, 467	17.4	18
4 ⁰³	Targeted Exome Sequencing of Krebs Cycle Genes Reveals Candidate Cancer-Predisposing Mutations in Pheochromocytomas and Paragangliomas. <i>Clinical Cancer Research</i> , 2017 , 23, 6315-6324	12.9	47
4 ⁰²	The Epigenomic Revolution in Breast Cancer: From Single-Gene to Genome-Wide Next-Generation Approaches. <i>American Journal of Pathology</i> , 2017 , 187, 2163-2174	5.8	18
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