

Manel Esteller

List of Publications by Citations

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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	Non-coding RNAs in human disease. <i>Nature Reviews Genetics</i> , 2011 , 12, 861-74	30.1	3300
559	Epigenetics in cancer. <i>New England Journal of Medicine</i> , 2008 , 358, 1148-59	59.2	2783
558	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, 10604-9	11.5	2645
557	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, 1350-4	59.2	1984
556	Epigenetic modifications and human disease. <i>Nature Biotechnology</i> , 2010 , 28, 1057-68	44.5	1922
555	The Polycomb group protein EZH2 directly controls DNA methylation. <i>Nature</i> , 2006 , 439, 871-4	50.4	1721
554	Cancer epigenomics: DNA methylomes and histone-modification maps. <i>Nature Reviews Genetics</i> , 2007 , 8, 286-98	30.1	1674
553	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	36.3	1492
552	Gene-expression profiles in hereditary breast cancer. <i>New England Journal of Medicine</i> , 2001 , 344, 539-48	59.2	1462
551	Global epigenomic reconfiguration during mammalian brain development. <i>Science</i> , 2013 , 341, 1237905	33.3	1283
550	CpG island hypermethylation and tumor suppressor genes: a booming present, a brighter future. <i>Oncogene</i> , 2002 , 21, 5427-40	9.2	952
549	Cancer epigenetics reaches mainstream oncology. <i>Nature Medicine</i> , 2011 , 17, 330-9	50.5	920
548	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	5.3	912
547	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016 , 166, 740-754	56.2	892
546	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, 13556-61	11.5	890
545	DNA methylation and cancer. <i>Advances in Genetics</i> , 2010 , 70, 27-56	3.3	861
544	Inactivation of the apoptosis effector Apaf-1 in malignant melanoma. <i>Nature</i> , 2001 , 409, 207-11	50.4	831

543	Genetic unmasking of an epigenetically silenced microRNA in human cancer cells. <i>Cancer Research</i> , 2007 , 67, 1424-9	10.1	795
542	Validation of a DNA methylation microarray for 450,000 CpG sites in the human genome. <i>Epigenetics</i> , 2011 , 6, 692-702	5.7	767
541	The role of histone deacetylases (HDACs) in human cancer. <i>Molecular Oncology</i> , 2007 , 1, 19-25	7.9	646
540	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, 306-19	4.8	591
539	Cancer as an epigenetic disease: DNA methylation and chromatin alterations in human tumours. <i>Journal of Pathology</i> , 2002 , 196, 1-7	9.4	583
538	DNA methylation profiling in the clinic: applications and challenges. <i>Nature Reviews Genetics</i> , 2012 , 13, 679-92	30.1	579
537	Distinct DNA methylomes of newborns and centenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 10522-7	11.5	563
536	Epigenetics and aging: the targets and the marks. <i>Trends in Genetics</i> , 2007 , 23, 413-8	8.5	518
535	Epigenetic gene silencing in cancer: the DNA hypermethylome. <i>Human Molecular Genetics</i> , 2007 , 16 Spec No 1, R50-9	5.6	515
534	Changes in the pattern of DNA methylation associate with twin discordance in systemic lupus erythematosus. <i>Genome Research</i> , 2010 , 20, 170-9	9.7	486
533	Epigenetic mechanisms in neurological diseases: genes, syndromes, and therapies. <i>Lancet Neurology</i> , 2009 , 8, 1056-72	24.1	473
532	DNA methyltransferases control telomere length and telomere recombination in mammalian cells. <i>Nature Cell Biology</i> , 2006 , 8, 416-24	23.4	471
531	CpG island hypermethylation of the DNA repair enzyme methyltransferase predicts response to temozolomide in primary gliomas. <i>Clinical Cancer Research</i> , 2004 , 10, 4933-8	12.9	457
530	Toward understanding and exploiting tumor heterogeneity. <i>Nature Medicine</i> , 2015 , 21, 846-53	50.5	441
529	Aberrant epigenetic landscape in cancer: how cellular identity goes awry. <i>Developmental Cell</i> , 2010 , 19, 698-711	10.2	440
528	Aberrant DNA methylation as a cancer-inducing mechanism. <i>Annual Review of Pharmacology and Toxicology</i> , 2005 , 45, 629-56	17.9	426
527	MLH1 promoter hypermethylation is associated with the microsatellite instability phenotype in sporadic endometrial carcinomas. <i>Oncogene</i> , 1998 , 17, 2413-7	9.2	392
526	lncRNAs and microRNAs with a role in cancer development. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016 , 1859, 169-76	6	390

525	Identification of an Immune-specific Class of Hepatocellular Carcinoma, Based on Molecular Features. <i>Gastroenterology</i> , 2017 , 153, 812-826	13.3	371
524	Notch signaling is essential for ventricular chamber development. <i>Developmental Cell</i> , 2007 , 12, 415-29	10.2	370
523	Cancer epigenomics: beyond genomics. <i>Current Opinion in Genetics and Development</i> , 2012 , 22, 50-5	4.9	369
522	Validation of a DNA methylation microarray for 850,000 CpG sites of the human genome enriched in enhancer sequences. <i>Epigenomics</i> , 2016 , 8, 389-99	4.4	352
521	A TARBP2 mutation in human cancer impairs microRNA processing and DICER1 function. <i>Nature Genetics</i> , 2009 , 41, 365-70	36.3	317
520	DNA methylation: a profile of methods and applications. <i>BioTechniques</i> , 2002 , 33, 632, 634, 636-49	2.5	312
519	A role for RNAi in the selective correction of DNA methylation defects. <i>Science</i> , 2009 , 323, 1600-4	33.3	302
518	Role of the RB1 family in stabilizing histone methylation at constitutive heterochromatin. <i>Nature Cell Biology</i> , 2005 , 7, 420-8	23.4	279
517	A DNA methylation fingerprint of 1628 human samples. <i>Genome Research</i> , 2012 , 22, 407-19	9.7	273
516	DNA methylation contributes to natural human variation. <i>Genome Research</i> , 2013 , 23, 1363-72	9.7	272
515	Cis-acting noncoding RNAs: friends and foes. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 1068-75	17.6	270
514	Generating mutations but providing chemosensitivity: the role of O6-methylguanine DNA methyltransferase in human cancer. <i>Oncogene</i> , 2004 , 23, 1-8	9.2	262
513	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012 , 30, 224-6	44.5	261
512	A genetic defect in exportin-5 traps precursor microRNAs in the nucleus of cancer cells. <i>Cancer Cell</i> , 2010 , 18, 303-15	24.3	261
511	SOCS-1, a negative regulator of cytokine signaling, is frequently silenced by methylation in multiple myeloma. <i>Blood</i> , 2003 , 101, 2784-8	2.2	260
510	hMLH1 promoter hypermethylation is an early event in human endometrial tumorigenesis. <i>American Journal of Pathology</i> , 1999 , 155, 1767-72	5.8	260
509	Methyl-CpG binding proteins identify novel sites of epigenetic inactivation in human cancer. <i>EMBO Journal</i> , 2003 , 22, 6335-45	13	255
508	Epigenetic profiling to classify cancer of unknown primary: a multicentre, retrospective analysis. <i>Lancet Oncology</i> , 2016 , 17, 1386-1395	21.7	251

507	Relevance of DNA methylation in the management of cancer. <i>Lancet Oncology, The</i> , 2003 , 4, 351-8	21.7	251
506	DNA methylomes, histone codes and miRNAs: tying it all together. <i>International Journal of Biochemistry and Cell Biology</i> , 2009 , 41, 87-95	5.6	250
505	Chromosomal instability correlates with genome-wide DNA demethylation in human primary colorectal cancers. <i>Cancer Research</i> , 2006 , 66, 8462-9468	10.1	250
504	DNA methylation-based prognosis and epidrivers in hepatocellular carcinoma. <i>Hepatology</i> , 2015 , 61, 1945-56	11.2	237
503	Dysregulation of microRNAs in cancer: playing with fire. <i>FEBS Letters</i> , 2011 , 585, 2087-99	3.8	234
502	DNA methylation polymorphisms precede any histological sign of atherosclerosis in mice lacking apolipoprotein E. <i>Journal of Biological Chemistry</i> , 2004 , 279, 29147-54	5.4	233
501	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232
500	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, 554-69	9.7	232
499	A truncating mutation of HDAC2 in human cancers confers resistance to histone deacetylase inhibition. <i>Nature Genetics</i> , 2006 , 38, 566-9	36.3	228
498	Abnormalities of the APC/beta-catenin pathway in endometrial cancer. <i>Oncogene</i> , 2002 , 21, 7981-90	9.2	228
497	Histone deacetylase inhibitors: understanding a new wave of anticancer agents. <i>International Journal of Cancer</i> , 2004 , 112, 171-8	7.5	226
496	Tumor cell-specific BRCA1 and RASSF1A hypermethylation in serum, plasma, and peritoneal fluid from ovarian cancer patients. <i>Cancer Research</i> , 2004 , 64, 6476-81	10.1	225
495	Clinical epigenetics: seizing opportunities for translation. <i>Nature Reviews Genetics</i> , 2019 , 20, 109-127	30.1	222
494	Loss of the glycine N-methyltransferase gene leads to steatosis and hepatocellular carcinoma in mice. <i>Hepatology</i> , 2008 , 47, 1191-9	11.2	220
493	Hypermethylation of the DNA repair gene O(6)-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	9.7	219
492	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, 8429-39	4.8	218
491	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, 8822-7	11.5	213
490	A prognostic DNA methylation signature for stage I non-small-cell lung cancer. <i>Journal of Clinical Oncology</i> , 2013 , 31, 4140-7	2.2	210

489	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016 , 34, 726-37	44.5	204
488	The dynamic DNA methylomes of double-stranded DNA viruses associated with human cancer. <i>Genome Research</i> , 2009 , 19, 438-51	9.7	201
487	Genetic analysis of p38 MAP kinases in myogenesis: fundamental role of p38alpha in abrogating myoblast proliferation. <i>EMBO Journal</i> , 2007 , 26, 1245-56	13	194
486	Genomic DNA hypomethylation as a biomarker for bladder cancer susceptibility in the Spanish Bladder Cancer Study: a case-control study. <i>Lancet Oncology, The</i> , 2008 , 9, 359-66	21.7	193
485	Cross-talk between aging and cancer: the epigenetic language. <i>Annals of the New York Academy of Sciences</i> , 2007 , 1100, 60-74	6.5	189
484	The affinity of different MBD proteins for a specific methylated locus depends on their intrinsic binding properties. <i>Nucleic Acids Research</i> , 2003 , 31, 1765-74	20.1	184
483	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, 4394-9	11.5	183
482	Heterozygous disruption of Hic1 predisposes mice to a gender-dependent spectrum of malignant tumors. <i>Nature Genetics</i> , 2003 , 33, 197-202	36.3	182
481	A mouse skin multistage carcinogenesis model reflects the aberrant DNA methylation patterns of human tumors. <i>Cancer Research</i> , 2004 , 64, 5527-34	10.1	180
480	Epigenetic biomarkers for human cancer: the time is now. <i>Critical Reviews in Oncology/Hematology</i> , 2008 , 68, 1-11	7	177
479	The epigenetic face of systemic lupus erythematosus. <i>Journal of Immunology</i> , 2006 , 176, 7143-7	5.3	177
478	Allele-specific histone lysine methylation marks regulatory regions at imprinted mouse genes. <i>EMBO Journal</i> , 2002 , 21, 6560-70	13	177
477	Bromodomain inhibitors and cancer therapy: From structures to applications. <i>Epigenetics</i> , 2017 , 12, 323-339	3.7	171
476	RNA-RNA interactions in gene regulation: the coding and noncoding players. <i>Trends in Biochemical Sciences</i> , 2015 , 40, 248-56	10.3	166
475	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, 21830-5	11.5	162
474	DNA methylation map of human atherosclerosis. <i>Circulation: Cardiovascular Genetics</i> , 2014 , 7, 692-700		157
473	The epigenetic basis of twin discordance in age-related diseases. <i>Pediatric Research</i> , 2007 , 61, 38R-42R	3.2	155
472	Tumor-Related Molecular Mechanisms of Oxaliplatin Resistance. <i>Molecular Cancer Therapeutics</i> , 2015 , 14, 1767-76	6.1	154

471	Point mutation and homozygous deletion of PTEN/MMAC1 in primary bladder cancers. <i>Oncogene</i> , 1998 , 16, 3215-8	9.2	149
470	Methyl-DNA immunoprecipitation (MeDIP): hunting down the DNA methylome. <i>BioTechniques</i> , 2008 , 44, 35, 37, 39 passim	2.5	149
469	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, 208-15	7.5	149
468	Epigenetic inactivation of LKB1 in primary tumors associated with the Peutz-Jeghers syndrome. <i>Oncogene</i> , 2000 , 19, 164-8	9.2	149
467	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	3.7	148
466	Human DNA methyltransferase 1 is required for maintenance of the histone H3 modification pattern. <i>Journal of Biological Chemistry</i> , 2004 , 279, 37175-84	5.4	148
465	E47 phosphorylation by p38 MAPK promotes MyoD/E47 association and muscle-specific gene transcription. <i>EMBO Journal</i> , 2005 , 24, 974-84	13	147
464	A microarray-based DNA methylation study of glioblastoma multiforme. <i>Epigenetics</i> , 2009 , 4, 255-64	5.7	146
463	DNA methylation and cancer therapy: new developments and expectations. <i>Current Opinion in Oncology</i> , 2005 , 17, 55-60	4.2	146
462	The Wnt antagonist DICKKOPF-1 gene is induced by 1alpha,25-dihydroxyvitamin D3 associated to the differentiation of human colon cancer cells. <i>Carcinogenesis</i> , 2007 , 28, 1877-84	4.6	145
461	Breast cancer epigenetics: from DNA methylation to microRNAs. <i>Journal of Mammary Gland Biology and Neoplasia</i> , 2010 , 15, 5-17	2.4	144
460	Lung cancer epigenetics: From knowledge to applications. <i>Seminars in Cancer Biology</i> , 2018 , 51, 116-128	12.7	142
459	Epigenetic alterations involved in cancer stem cell reprogramming. <i>Molecular Oncology</i> , 2012 , 6, 620-36	7.9	142
458	Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. <i>Genome Biology</i> , 2016 , 17, 11	18.3	141
457	Towards the human cancer epigenome: a first draft of histone modifications. <i>Cell Cycle</i> , 2005 , 4, 1377-81	14.7	139
456	Intronic RNAs mediate EZH2 regulation of epigenetic targets. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 664-70	17.6	135
455	The necessity of a human epigenome project. <i>Carcinogenesis</i> , 2006 , 27, 1121-5	4.6	135
454	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, 13736-41	11.5	134

453	High-performance capillary electrophoretic method for the quantification of 5-methyl 2Pdeoxycytidine in genomic DNA: application to plant, animal and human cancer tissues. <i>Electrophoresis</i> , 2002 , 23, 1677-81	3.6	134
452	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, 5785-90	11.5	131
451	Epigenetic inactivation of the circadian clock gene BMAL1 in hematologic malignancies. <i>Cancer Research</i> , 2009 , 69, 8447-54	10.1	131
450	Genome-wide profiling of p53-regulated enhancer RNAs uncovers a subset of enhancers controlled by a lncRNA. <i>Nature Communications</i> , 2015 , 6, 6520	17.4	129
449	BRCA1 CpG island hypermethylation predicts sensitivity to poly(adenosine diphosphate)-ribose polymerase inhibitors. <i>Journal of Clinical Oncology</i> , 2010 , 28, e563-4; author reply e565-6	2.2	129
448	Differential DNA hypermethylation and hypomethylation signatures in colorectal cancer. <i>Human Molecular Genetics</i> , 2005 , 14, 319-26	5.6	127
447	How epigenetics can explain human metastasis: a new role for microRNAs. <i>Cell Cycle</i> , 2009 , 8, 377-82	4.7	124
446	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, 2565-71	10.1	124
445	MGMT hypermethylation: a prognostic foe, a predictive friend. <i>DNA Repair</i> , 2007 , 6, 1155-60	4.3	122
444	A CpG island hypermethylation profile of primary colorectal carcinomas and colon cancer cell lines. <i>Molecular Cancer</i> , 2004 , 3, 28	42.1	122
443	Genetic syndromes caused by mutations in epigenetic genes. <i>Human Genetics</i> , 2013 , 132, 359-83	6.3	121
442	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, 2488-97	2.2	121
441	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
440	An Adenine Code for DNA: A Second Life for N6-Methyladenine. <i>Cell</i> , 2015 , 161, 710-3	56.2	117
439	A DNA methylation-based definition of biologically distinct breast cancer subtypes. <i>Molecular Oncology</i> , 2015 , 9, 555-68	7.9	117
438	DNA methylation profiling in breast cancer discordant identical twins identifies DOK7 as novel epigenetic biomarker. <i>Carcinogenesis</i> , 2013 , 34, 102-8	4.6	117
437	CSL-MAML-dependent Notch1 signaling controls T lineage-specific IL-7R{alpha} gene expression in early human thymopoiesis and leukemia. <i>Journal of Experimental Medicine</i> , 2009 , 206, 779-91	16.6	117
436	Profiling aberrant DNA methylation in hematologic neoplasms: a view from the tip of the iceberg. <i>Clinical Immunology</i> , 2003 , 109, 80-8	9	116

435	Putative cis-regulatory drivers in colorectal cancer. <i>Nature</i> , 2014 , 512, 87-90	50.4	115
434	Whole-exome sequencing identifies MDH2 as a new familial paraganglioma gene. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	114
433	Epigenetic disruption of ribosomal RNA genes and nucleolar architecture in DNA methyltransferase 1 (Dnmt1) deficient cells. <i>Nucleic Acids Research</i> , 2007 , 35, 2191-8	20.1	113
432	Regulation of pri-miRNA processing by a long noncoding RNA transcribed from an ultraconserved region. <i>Molecular Cell</i> , 2014 , 55, 138-47	17.6	111
431	Mutator pathways unleashed by epigenetic silencing in human cancer. <i>Mutagenesis</i> , 2007 , 22, 247-53	2.8	110
430	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, 3940-7	2.2	110
429	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
428	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, 3214-22	2.2	109
427	Clustering of gene hypermethylation associated with clinical risk groups in neuroblastoma. <i>Journal of the National Cancer Institute</i> , 2004 , 96, 1208-19	9.7	109
426	Disrupted microRNA expression caused by Mecp2 loss in a mouse model of Rett syndrome. <i>Epigenetics</i> , 2010 , 5, 656-63	5.7	108
425	Mechanisms of Therapy Resistance in Patient-Derived Xenograft Models of BRCA1-Deficient Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	108
424	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
423	Abnormalities of E- and P-cadherin and catenin (beta-, gamma-catenin, and p120ctn) expression in endometrial cancer and endometrial atypical hyperplasia. <i>Journal of Pathology</i> , 2003 , 199, 471-8	9.4	107
422	Cancer epigenetics and methylation. <i>Science</i> , 2002 , 297, 1807-8; discussion 1807-8	33.3	107
421	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	11.5	106
420	MicroRNAs and cancer epigenetics: a macroevolution. <i>Current Opinion in Oncology</i> , 2010 , 22, 35-45	4.2	105
419	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, 8342-6	10.1	105
418	The Epitranscriptome of Noncoding RNAs in Cancer. <i>Cancer Discovery</i> , 2017 , 7, 359-368	24.4	104

417	DNA methylation map of mouse and human brain identifies target genes in Alzheimer's disease. <i>Brain</i> , 2013 , 136, 3018-27	11.2	104
416	Genetic unmasking of epigenetically silenced tumor suppressor genes in colon cancer cells deficient in DNA methyltransferases. <i>Human Molecular Genetics</i> , 2003 , 12, 2209-19	5.6	104
415	Human DNA methylomes of neurodegenerative diseases show common epigenomic patterns. <i>Translational Psychiatry</i> , 2016 , 6, e718	8.6	101
414	Hypermethylation of the hMLH1 gene promoter is associated with microsatellite instability in early human gastric neoplasia. <i>Oncogene</i> , 2001 , 20, 329-35	9.2	101
413	Multiple markers for melanoma progression regulated by DNA methylation: insights from transcriptomic studies. <i>Carcinogenesis</i> , 2005 , 26, 1856-67	4.6	96
412	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, 466-71	2.6	95
411	DNA methylation biomarkers for noninvasive diagnosis of colorectal cancer. <i>Cancer Prevention Research</i> , 2013 , 6, 656-65	3.2	95
410	BRCA1 epigenetic inactivation predicts sensitivity to platinum-based chemotherapy in breast and ovarian cancer. <i>Epigenetics</i> , 2012 , 7, 1225-9	5.7	95
409	CpG island promoter hypermethylation of the pro-apoptotic gene caspase-8 is a common hallmark of relapsed glioblastoma multiforme. <i>Carcinogenesis</i> , 2007 , 28, 1264-8	4.6	94
408	The impact of chromatin in human cancer: linking DNA methylation to gene silencing. <i>Carcinogenesis</i> , 2002 , 23, 1103-9	4.6	94
407	Cancer epigenetics: DNA methylation and chromatin alterations in human cancer. <i>Advances in Experimental Medicine and Biology</i> , 2003 , 532, 39-49	3.6	94
406	Digital PCR quantification of MGMT methylation refines prediction of clinical benefit from alkylating agents in glioblastoma and metastatic colorectal cancer. <i>Annals of Oncology</i> , 2015 , 26, 1994-1999	10.3	93
405	Dynamics of DNA methylation in recent human and great ape evolution. <i>PLoS Genetics</i> , 2013 , 9, e1003763	6.3	92
404	Promoter DNA hypermethylation and gene repression in undifferentiated Arabidopsis cells. <i>PLoS ONE</i> , 2008 , 3, e3306	3.7	92
403	Genetic and epigenetic screening for gene alterations of the chromatin-remodeling factor, SMARCA4/BRG1, in lung tumors. <i>Genes Chromosomes and Cancer</i> , 2004 , 41, 170-7	5	92
402	H3K4me1 marks DNA regions hypomethylated during aging in human stem and differentiated cells. <i>Genome Research</i> , 2015 , 25, 27-40	9.7	89
401	Mecp2-null mice provide new neuronal targets for Rett syndrome. <i>PLoS ONE</i> , 2008 , 3, e3669	3.7	89
400	Identification of inflammatory mediators in patients with Crohn's disease unresponsive to anti-TNF therapy. <i>Gut</i> , 2015 , 64, 233-42	19.2	88

399	Epigenetic inactivation of the putative DNA/RNA helicase SLFN11 in human cancer confers resistance to platinum drugs. <i>Oncotarget</i> , 2016 , 7, 3084-97	3.3	88
398	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	17.4	86
397	Loss of heterozygosity analysis at the BRCA loci in tumor samples from patients with familial breast cancer. <i>International Journal of Cancer</i> , 2002 , 99, 305-9	7.5	86
396	An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. <i>Nature Communications</i> , 2014 , 5, 5719	17.4	85
395	Promoter CpG island hypermethylation of the DNA repair enzyme MGMT predicts clinical response to dacarbazine in a phase II study for metastatic colorectal cancer. <i>Clinical Cancer Research</i> , 2013 , 19, 2265-72	12.9	85
394	Epigenetic signatures associated with different levels of differentiation potential in human stem cells. <i>PLoS ONE</i> , 2009 , 4, e7809	3.7	85
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