

Mario F Fraga

List of Publications by Year in descending order

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Version: 2024-02-01

260
papers

34,420
citations

4641

85
h-index

3714

179
g-index

269
all docs

269
docs citations

269
times ranked

45252
citing authors

#	ARTICLE	IF	CITATIONS
1	From The Cover: Epigenetic differences arise during the lifetime of monozygotic twins. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10604-10609.	3.3	3,169
2	Glypican-1 identifies cancer exosomes and detects early pancreatic cancer. Nature, 2015, 523, 177-182.	13.7	2,240
3	The Polycomb group protein EZH2 directly controls DNA methylation. Nature, 2006, 439, 871-874.	13.7	1,964
4	Loss of acetylation at Lys16 and trimethylation at Lys20 of histone H4 is a common hallmark of human cancer. Nature Genetics, 2005, 37, 391-400.	9.4	1,710
5	Epigenetics and the environment: emerging patterns and implications. Nature Reviews Genetics, 2012, 13, 97-109.	7.7	1,524
6	The transcription factor Slug represses E-cadherin expression and induces epithelial to mesenchymal transitions: a comparison with Snail and E47 repressors. Journal of Cell Science, 2003, 116, 499-511.	1.2	1,021
7	Genetic Unmasking of an Epigenetically Silenced microRNA in Human Cancer Cells. Cancer Research, 2007, 67, 1424-1429.	0.4	883
8	Distinct DNA methylomes of newborns and centenarians. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10522-10527.	3.3	687
9	Epigenetics and aging: the targets and the marks. Trends in Genetics, 2007, 23, 413-418.	2.9	611
10	Changes in the pattern of DNA methylation associate with twin discordance in systemic lupus erythematosus. Genome Research, 2010, 20, 170-179.	2.4	569
11	DNA methyltransferases control telomere length and telomere recombination in mammalian cells. Nature Cell Biology, 2006, 8, 416-424.	4.6	538
12	Child Health, Developmental Plasticity, and Epigenetic Programming. Endocrine Reviews, 2011, 32, 159-224.	8.9	533
13	DNA methylation patterns in hereditary human cancers mimic sporadic tumorigenesis. Human Molecular Genetics, 2001, 10, 3001-3007.	1.4	374
14	DNA Methylation: A Profile of Methods and Applications. BioTechniques, 2002, 33, 632-649.	0.8	359
15	A DNA methylation fingerprint of 1628 human samples. Genome Research, 2012, 22, 407-419.	2.4	341
16	A Role for RNAi in the Selective Correction of DNA Methylation Defects. Science, 2009, 323, 1600-1604.	6.0	338
17	Evolutionary routes and KRAS dosage define pancreatic cancer phenotypes. Nature, 2018, 554, 62-68.	13.7	328
18	Epigenetic inactivation of the Wnt antagonist DICKKOPF-1 (DKK-1) gene in human colorectal cancer. Oncogene, 2006, 25, 4116-4121.	2.6	320

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19	The role of epigenetics in aging and age-related diseases. <i>Ageing Research Reviews</i> , 2009, 8, 268-276.	5.0	319
20	Role of the RB1 family in stabilizing histone methylation at constitutive heterochromatin. <i>Nature Cell Biology</i> , 2005, 7, 420-428.	4.6	314
21	Methyl-CpG binding proteins identify novel sites of epigenetic inactivation in human cancer. <i>EMBO Journal</i> , 2003, 22, 6335-6345.	3.5	294
22	Chromosomal Instability Correlates with Genome-wide DNA Demethylation in Human Primary Colorectal Cancers. <i>Cancer Research</i> , 2006, 66, 8462-9468.	0.4	286
23	A systematic profile of DNA methylation in human cancer cell lines. <i>Cancer Research</i> , 2003, 63, 1114-21.	0.4	286
24	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
25	Epigenetic regulation of adaptive responses of forest tree species to the environment. <i>Ecology and Evolution</i> , 2013, 3, 399-415.	0.8	271
26	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737.	9.4	270
27	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
28	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
29	Salermide, a Sirtuin inhibitor with a strong cancer-specific proapoptotic effect. <i>Oncogene</i> , 2009, 28, 781-791.	2.6	244
30	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
31	Procaine is a DNA-demethylating agent with growth-inhibitory effects in human cancer cells. <i>Cancer Research</i> , 2003, 63, 4984-9.	0.4	236
32	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
33	The dynamic DNA methylomes of double-stranded DNA viruses associated with human cancer. <i>Genome Research</i> , 2009, 19, 438-451.	2.4	218
34	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
35	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
36	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

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37	Epigenetics and environment: a complex relationship. <i>Journal of Applied Physiology</i> , 2010, 109, 243-251.	1.2	191
38	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
39	Reconstructing the DNA Methylation Maps of the Neandertal and the Denisovan. <i>Science</i> , 2014, 344, 523-527.	6.0	188
40	The Epigenetic Basis of Twin Discordance in Age-Related Diseases. <i>Pediatric Research</i> , 2007, 61, 38R-42R.	1.1	183
41	A Genetic Progression Model of BrafV600E-Induced Intestinal Tumorigenesis Reveals Targets for Therapeutic Intervention. <i>Cancer Cell</i> , 2013, 24, 15-29.	7.7	183
42	Research Resource: Transcriptional Profiling Reveals Different Pseudohypoxic Signatures in SDHB and VHL-Related Pheochromocytomas. <i>Molecular Endocrinology</i> , 2010, 24, 2382-2391.	3.7	179
43	Effects of short-term high-fat overfeeding on genome-wide DNA methylation in the skeletal muscle of healthy young men. <i>Diabetologia</i> , 2012, 55, 3341-3349.	2.9	179
44	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
45	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
46	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
47	The Wnt antagonist DICKKOPF-1 gene is induced by 1 α ,25-dihydroxyvitamin D ₃ associated to the differentiation of human colon cancer cells. <i>Carcinogenesis</i> , 2007, 28, 1877-1884.	1.3	166
48	DNA methylation epigenotypes in breast cancer molecular subtypes. <i>Breast Cancer Research</i> , 2010, 12, R77.	2.2	159
49	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
50	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
51	Towards the Human Cancer Epigenome: A First Draft of Histone Modifications. <i>Cell Cycle</i> , 2005, 4, 1377-1381.	1.3	149
52	Epigenetics in cancer therapy and nanomedicine. <i>Clinical Epigenetics</i> , 2019, 11, 81.	1.8	147
53	Genome-wide DNA methylation changes with age in disease-free human skeletal muscle. <i>Aging Cell</i> , 2014, 13, 360-366.	3.0	145
54	Aberrant DNA methylation patterns of spermatozoa in men with unexplained infertility. <i>Human Reproduction</i> , 2015, 30, 1014-1028.	0.4	144

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55	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
56	Allele-Specific Reprogramming of Cancer Metabolism by the Long Non-coding RNA CCAT2. <i>Molecular Cell</i> , 2016, 61, 520-534.	4.5	142
57	Genome-Wide Analysis of Epigenetic Silencing Identifies BEX1 and BEX2 as Candidate Tumor Suppressor Genes in Malignant Glioma. <i>Cancer Research</i> , 2006, 66, 6665-6674.	0.4	135
58	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
59	Genome-wide profiling of bone reveals differentially methylated regions in osteoporosis and osteoarthritis. <i>Arthritis and Rheumatism</i> , 2013, 65, 197-205.	6.7	133
60	DNA methylation: a promising landscape for immune system-related diseases. <i>Trends in Genetics</i> , 2012, 28, 506-514.	2.9	131
61	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
62	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
63	Genomic DNA methylation-demethylation during aging and reinvigoration of <i>Pinus radiata</i> . <i>Tree Physiology</i> , 2002, 22, 813-816.	1.4	123
64	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
65	H3K4me1 marks DNA regions hypomethylated during aging in human stem and differentiated cells. <i>Genome Research</i> , 2015, 25, 27-40.	2.4	119
66	Cancer Epigenetics and Methylation. <i>Science</i> , 2002, 297, 1807d-1808.	6.0	116
67	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
68	DNA methylation contributes to the regulation of sclerostin expression in human osteocytes. <i>Journal of Bone and Mineral Research</i> , 2012, 27, 926-937.	3.1	116
69	Involvement of DNA methylation in tree development and micropropagation. <i>Plant Cell, Tissue and Organ Culture</i> , 2007, 91, 75-86.	1.2	113
70	Epigenetic regulation of telomeres in human cancer. <i>Oncogene</i> , 2008, 27, 6817-6833.	2.6	111
71	Rapid quantification of DNA methylation by high performance capillary electrophoresis. <i>Electrophoresis</i> , 2000, 21, 2990-2994.	1.3	108
72	Multiple markers for melanoma progression regulated by DNA methylation: insights from transcriptomic studies. <i>Carcinogenesis</i> , 2005, 26, 1856-1867.	1.3	108

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73	DNA Methylation Biomarkers for Noninvasive Diagnosis of Colorectal Cancer. <i>Cancer Prevention Research</i> , 2013, 6, 656-665.	0.7	107
74	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.	3.9	106
75	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, 170-177.	1.5	103
76	Genetic and epigenetic regulation of aging. <i>Current Opinion in Immunology</i> , 2009, 21, 446-453.	2.4	101
77	TERRA recruitment of polycomb to telomeres is essential for histone trimethylation marks at telomeric heterochromatin. <i>Nature Communications</i> , 2018, 9, 1548.	5.8	101
78	DNA Methylation Signatures Identify Biologically Distinct Thyroid Cancer Subtypes. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013, 98, 2811-2821.	1.8	100
79	Promoter DNA Hypermethylation and Gene Repression in Undifferentiated Arabidopsis Cells. <i>PLoS ONE</i> , 2008, 3, e3306.	1.1	99
80	Role of DNA methylation in the regulation of the RANKL-OPG system in human bone. <i>Epigenetics</i> , 2012, 7, 83-91.	1.3	99
81	The dioxin receptor is silenced by promoter hypermethylation in human acute lymphoblastic leukemia through inhibition of Sp1 binding. <i>Carcinogenesis</i> , 2006, 27, 1099-1104.	1.3	97
82	A promoter DNA demethylation landscape of human hematopoietic differentiation. <i>Nucleic Acids Research</i> , 2012, 40, 116-131.	6.5	97
83	DNMT1 Inhibition Reprograms Pancreatic Cancer Stem Cells via Upregulation of the miR-17-92 Cluster. <i>Cancer Research</i> , 2016, 76, 4546-4558.	0.4	94
84	Angiostatic activity of DNA methyltransferase inhibitors. <i>Molecular Cancer Therapeutics</i> , 2006, 5, 467-475.	1.9	93
85	Identification of a DNA methylation signature in blood cells from persons with Down Syndrome. <i>Aging</i> , 2014, 7, 82-96.	1.4	92
86	Epigenetic Mechanisms Regulate MHC and Antigen Processing Molecules in Human Embryonic and Induced Pluripotent Stem Cells. <i>PLoS ONE</i> , 2010, 5, e10192.	1.1	91
87	Epigenetic loss of the familial tumor-suppressor gene exostosin-1 (EXT1) disrupts heparan sulfate synthesis in cancer cells. <i>Human Molecular Genetics</i> , 2004, 13, 2753-2765.	1.4	86
88	Molecular Analysis of a Multistep Lung Cancer Model Induced by Chronic Inflammation Reveals Epigenetic Regulation of p16, Activation of the DNA Damage Response Pathway. <i>Neoplasia</i> , 2007, 9, 840-IN12.	2.3	86
89	Genetic variants in epigenetic genes and breast cancer risk. <i>Carcinogenesis</i> , 2006, 27, 1661-1669.	1.3	85
90	Global DNA hypomethylation in cancer: review of validated methods and clinical significance. <i>Clinical Chemistry and Laboratory Medicine</i> , 2012, 50, 1733-42.	1.4	85

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91	Phase-change related epigenetic and physiological changes in <i>Pinus radiata</i> D. Don. <i>Planta</i> , 2002, 215, 672-678.	1.6	84
92	Discovery of Salermide-Related Sirtuin Inhibitors: Binding Mode Studies and Antiproliferative Effects in Cancer Cells Including Cancer Stem Cells. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 10937-10947.	2.9	84
93	Aging epigenetics: Causes and consequences. <i>Molecular Aspects of Medicine</i> , 2013, 34, 765-781.	2.7	83
94	Methylation of NKG2D ligands contributes to immune system evasion in acute myeloid leukemia. <i>Genes and Immunity</i> , 2015, 16, 71-82.	2.2	82
95	Fatty liver and fibrosis in glycine N-methyltransferase knockout mice is prevented by nicotinamide. <i>Hepatology</i> , 2010, 52, 105-114.	3.6	81
96	The effect of exposure to nanoparticles and nanomaterials on the mammalian epigenome. <i>International Journal of Nanomedicine</i> , 2016, Volume 11, 6297-6306.	3.3	78
97	Novel epigenetically deregulated genes in testicular cancer include homeobox genes and SCGB3A1 (HIN-1). <i>Journal of Pathology</i> , 2006, 210, 441-449.	2.1	77
98	The <i>ADAMTS12</i> metalloprotease gene is epigenetically silenced in tumor cells and transcriptionally activated in the stroma during progression of colon cancer. <i>Journal of Cell Science</i> , 2009, 122, 2906-2913.	1.2	76
99	Genetic and Non-genetic Predictors of LINE-1 Methylation in Leukocyte DNA. <i>Environmental Health Perspectives</i> , 2013, 121, 650-656.	2.8	75
100	DNA methylation patterns in newborns exposed to tobacco in utero. <i>Journal of Translational Medicine</i> , 2015, 13, 25.	1.8	75
101	Cancer Genes Hypermethylated in Human Embryonic Stem Cells. <i>PLoS ONE</i> , 2008, 3, e3294.	1.1	75
102	The absence of p53 is critical for the induction of apoptosis by 5-aza-2'-deoxycytidine. <i>Oncogene</i> , 2004, 23, 735-743.	2.6	73
103	Distinct chromatin signatures of DNA hypomethylation in aging and cancer. <i>Aging Cell</i> , 2018, 17, e12744.	3.0	72
104	Immune-Dependent and Independent Antitumor Activity of GM-CSF Aberrantly Expressed by Mouse and Human Colorectal Tumors. <i>Cancer Research</i> , 2013, 73, 395-405.	0.4	69
105	The role of 5-hydroxymethylcytosine in development, aging and age-related diseases. <i>Ageing Research Reviews</i> , 2017, 37, 28-38.	5.0	69
106	Altered expression of adhesion molecules and epithelial-mesenchymal transition in silica-induced rat lung carcinogenesis. <i>Laboratory Investigation</i> , 2004, 84, 999-1012.	1.7	68
107	Young men with low birthweight exhibit decreased plasticity of genome-wide muscle DNA methylation by high-fat overfeeding. <i>Diabetologia</i> , 2014, 57, 1154-1158.	2.9	67
108	S-adenosylmethionine Levels Regulate the Schwann Cell DNA Methylome. <i>Neuron</i> , 2014, 81, 1024-1039.	3.8	67

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109	The impact of MECP2 mutations in the expression patterns of Rett syndrome patients. <i>Human Genetics</i> , 2005, 116, 91-104.	1.8	66
110	Variations in DNA Methylation Patterns During the Cell Cycle of HeLa Cells. <i>Epigenetics</i> , 2007, 2, 54-65.	1.3	66
111	Regulation of DNA Methylation Patterns by CK2-Mediated Phosphorylation of Dnmt3a. <i>Cell Reports</i> , 2014, 8, 743-753.	2.9	66
112	Vitamin C uncouples the Warburg metabolic switch in KRAS mutant colon cancer. <i>Oncotarget</i> , 2016, 7, 47954-47965.	0.8	66
113	iPSCs from cancer cells: challenges and opportunities. <i>Trends in Molecular Medicine</i> , 2012, 18, 245-247.	3.5	65
114	The novel DNA methylation inhibitor zebularine is effective against the development of murine T-cell lymphoma. <i>Blood</i> , 2006, 107, 1174-1177.	0.6	64
115	Abnormal PcG protein expression in Hodgkin's lymphoma. Relation with E2F6 and NF κ B transcription factors. <i>Journal of Pathology</i> , 2004, 204, 528-537.	2.1	63
116	Prelamin A causes progeria through cell-extrinsic mechanisms and prevents cancer invasion. <i>Nature Communications</i> , 2013, 4, 2268.	5.8	63
117	Epigenetic repression of ROR2 has a Wnt-mediated, pro-tumourigenic role in colon cancer. <i>Molecular Cancer</i> , 2010, 9, 170.	7.9	61
118	Differential analysis of genome-wide methylation and gene expression in mesenchymal stem cells of patients with fractures and osteoarthritis. <i>Epigenetics</i> , 2017, 12, 113-122.	1.3	60
119	Multi-omic rejuvenation of naturally aged tissues by a single cycle of transient reprogramming. <i>Aging Cell</i> , 2022, 21, e13578.	3.0	60
120	The RNA-binding protein HuR regulates DNA methylation through stabilization of DNMT3b mRNA. <i>Nucleic Acids Research</i> , 2009, 37, 2658-2671.	6.5	56
121	The effects of the dietary polyphenol resveratrol on human healthy aging and lifespan. <i>Epigenetics</i> , 2011, 6, 870-874.	1.3	56
122	Nicotinamide N-methyltransferase: At the crossroads between cellular metabolism and epigenetic regulation. <i>Molecular Metabolism</i> , 2021, 45, 101165.	3.0	56
123	CpG island promoter hypermethylation of the Ras-effector gene NORE1A occurs in the context of a wild-type K-ras in lung cancer. <i>Oncogene</i> , 2004, 23, 8695-8699.	2.6	55
124	Unmasking of epigenetically silenced candidate tumor suppressor genes by removal of methyl-CpG-binding domain proteins. <i>Oncogene</i> , 2008, 27, 3556-3566.	2.6	54
125	Epigenetic regulation of the immune system in health and disease. <i>Tissue Antigens</i> , 2010, 76, 431-439.	1.0	54
126	The B cell transcription program mediates hypomethylation and overexpression of key genes in Epstein-Barr virus-associated proliferative conversion. <i>Genome Biology</i> , 2013, 14, R3.	13.9	53

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127	The role of genetics in the establishment and maintenance of the epigenome. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 1543-1573.	2.4	53
128	DNA Methylation Profiling in Pheochromocytoma and Paraganglioma Reveals Diagnostic and Prognostic Markers. <i>Clinical Cancer Research</i> , 2015, 21, 3020-3030.	3.2	53
129	Epigenetic Inactivation of the Groucho Homologue Gene TLE1 in Hematologic Malignancies. <i>Cancer Research</i> , 2008, 68, 4116-4122.	0.4	50
130	Nuclear envelope alterations generate an aging-like epigenetic pattern in mice deficient in Zmpste24 metalloprotease. <i>Aging Cell</i> , 2010, 9, 947-957.	3.0	50
131	Aberrant epigenetic regulation of bromodomain Brd4 in human colon cancer. <i>Journal of Molecular Medicine</i> , 2012, 90, 587-595.	1.7	50
132	A human ESC model for MLL-AF4 leukemic fusion gene reveals an impaired early hematopoietic-endothelial specification. <i>Cell Research</i> , 2012, 22, 986-1002.	5.7	49
133	Combinatorial effects of splice variants modulate function of Aiolos. <i>Journal of Cell Science</i> , 2007, 120, 2619-2630.	1.2	45
134	Lineage-restricted function of the pluripotency factor NANOG in stratified epithelia. <i>Nature Communications</i> , 2014, 5, 4226.	5.8	45
135	Epigenetic downregulation of TET3 reduces genome-wide 5hmC levels and promotes glioblastoma tumorigenesis. <i>International Journal of Cancer</i> , 2020, 146, 373-387.	2.3	45
136	Metallothionein 1E is methylated in malignant melanoma and increases sensitivity to cisplatin-induced apoptosis. <i>Melanoma Research</i> , 2010, 20, 392-400.	0.6	44
137	Beckwith-Wiedemann syndrome and uniparental disomy 11p: fine mapping of the recombination breakpoints and evaluation of several techniques. <i>European Journal of Human Genetics</i> , 2011, 19, 416-421.	1.4	44
138	Longitudinal genome-wide DNA methylation analysis uncovers persistent early-life DNA methylation changes. <i>Journal of Translational Medicine</i> , 2019, 17, 15.	1.8	44
139	Frequent aberrant expression of the human ether Å go-go (hEAG1) potassium channel in head and neck cancer: pathobiological mechanisms and clinical implications. <i>Journal of Molecular Medicine</i> , 2012, 90, 1173-1184.	1.7	43
140	Genetic and epigenetic profile of sporadic pheochromocytomas. <i>Journal of Medical Genetics</i> , 2004, 41, 30e-30.	1.5	42
141	Checkpoint kinase 1 (CHK1) protein and mRNA expression is downregulated in aggressive variants of human lymphoid neoplasms. <i>Leukemia</i> , 2005, 19, 112-117.	3.3	42
142	Contribution of genetic and epigenetic mechanisms to Wnt pathway activity in prevalent skeletal disorders. <i>Gene</i> , 2013, 532, 165-172.	1.0	42
143	Autoregulatory loop of nuclear corepressor 1 expression controls invasion, tumor growth, and metastasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E328-37.	3.3	41
144	Epigenetic Alterations of the Wnt/Catenin Pathway in Human Disease. <i>Endocrine, Metabolic and Immune Disorders - Drug Targets</i> , 2007, 7, 13-21.	0.6	40

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145	Specific hypermethylation of LINE-1 elements during abnormal overgrowth and differentiation of human placenta. <i>Oncogene</i> , 2007, 26, 2518-2524.	2.6	40
146	Identification of Triâ€•and Tetracyclic Pyrimidinediones as Sirtuin Inhibitors. <i>ChemMedChem</i> , 2010, 5, 674-677.	1.6	40
147	Epigenetics of Aging. <i>Current Genomics</i> , 2015, 16, 435-440.	0.7	39
148	Development Refractoriness of MLL-Rearranged Human B Cell Acute Leukemias to Reprogramming into Pluripotency. <i>Stem Cell Reports</i> , 2016, 7, 602-618.	2.3	38
149	MiR-873-5p acts as an epigenetic regulator in early stages of liver fibrosis and cirrhosis. <i>Cell Death and Disease</i> , 2018, 9, 958.	2.7	38
150	Reprogramming human B cells into induced pluripotent stem cells and its enhancement by C/EBPÎ±. <i>Leukemia</i> , 2016, 30, 674-682.	3.3	36
151	DNA methylation changes in human lung epithelia cells exposed to multi-walled carbon nanotubes. <i>Nanotoxicology</i> , 2017, 11, 857-870.	1.6	36
152	Discovery of Reversible DNA Methyltransferase and Lysine Methyltransferase G9a Inhibitors with Antitumoral in Vivo Efficacy. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 6518-6545.	2.9	36
153	The growing role of gene methylation on endocrine function. <i>Journal of Molecular Endocrinology</i> , 2011, 47, R75-R89.	1.1	35
154	De novo DNA methyltransferases: oncogenes, tumor suppressors, or both?. <i>Trends in Genetics</i> , 2012, 28, 474-479.	2.9	35
155	Hypomethylation of LINE-1, and not centromeric SAT-Î±, is associated with centromeric instability in head and neck squamous cell carcinoma. <i>Cellular Oncology (Dordrecht)</i> , 2012, 35, 259-267.	2.1	35
156	Nuclear DICKKOPF-1 as a biomarker of chemoresistance and poor clinical outcome in colorectal cancer. <i>Oncotarget</i> , 2015, 6, 5903-5917.	0.8	35
157	Global hyperactivation of enhancers stabilizes human and mouse naive pluripotency through inhibition of CDK8/19 Mediator kinases. <i>Nature Cell Biology</i> , 2020, 22, 1223-1238.	4.6	35
158	Release of Hypoacetylated and Trimethylated Histone H4 Is an Epigenetic Marker of Early Apoptosis. <i>Journal of Biological Chemistry</i> , 2006, 281, 13540-13547.	1.6	34
159	Quantification of Global DNA Methylation by Capillary Electrophoresis and Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2009, 507, 23-34.	0.4	34
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