

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	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.	3.0	29
2	Multi-omic rejuvenation of naturally aged tissues by a single cycle of transient reprogramming. <i>Aging Cell</i> , 2022, 21, e13578.	3.0	60
3	Blood DNA Methylation Patterns in Older Adults With Evolving Dementia. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2022, 77, 1743-1749.	1.7	12
4	Pdx1 Is Transcriptionally Regulated by EGR-1 during Nitric Oxide-Induced Endoderm Differentiation of Mouse Embryonic Stem Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3920.	1.8	0
5	Enhanced Detection of Viral RNA Species Using FokI-Assisted Digestion of DNA Duplexes and DNA/RNA Hybrids. <i>Analytical Chemistry</i> , 2022, 94, 6760-6770.	3.2	2
6	Classification of follicular-patterned thyroid lesions using a minimal set of epigenetic biomarkers. <i>European Journal of Endocrinology</i> , 2022, 187, 335-347.	1.9	2
7	Epigenetic loss of m1A RNA demethylase ALKBH3 in Hodgkin lymphoma targets collagen, conferring poor clinical outcome. <i>Blood</i> , 2021, 137, 994-999.	0.6	30
8	Methylation of the Sclerostin (SOST) Gene in Serum Free DNA: A New Bone Biomarker?. <i>Genetic Testing and Molecular Biomarkers</i> , 2021, 25, 42-47.	0.3	0
9	Nicotinamide N-methyltransferase: At the crossroads between cellular metabolism and epigenetic regulation. <i>Molecular Metabolism</i> , 2021, 45, 101165.	3.0	56
10	Conservation of Aging and Cancer Epigenetic Signatures across Human and Mouse. <i>Molecular Biology and Evolution</i> , 2021, 38, 3415-3435.	3.5	5
11	Stability of Imprinting and Differentiation Capacity in Na ⁺ -ve Human Cells Induced by Chemical Inhibition of CDK8 and CDK19. <i>Cells</i> , 2021, 10, 876.	1.8	0
12	Integrative methylome-transcriptome analysis unravels cancer cell vulnerabilities in infant MLL-rearranged B cell acute lymphoblastic leukemia. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	14
13	Epigenetic Deregulation of the Histone Methyltransferase KMT5B Contributes to Malignant Transformation in Glioblastoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 671838.	1.8	6
14	DNA Methylomes and Epigenetic Age Acceleration Associations with Poor Metabolic Control in T1D. <i>Biomedicines</i> , 2021, 9, 13.	1.4	1
15	Physical exercise shapes the mouse brain epigenome. <i>Molecular Metabolism</i> , 2021, 54, 101398.	3.0	12
16	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
17	No genome-wide DNA methylation changes found associated with medium-term reduced graphene oxide exposure in human lung epithelial cells. <i>Epigenetics</i> , 2020, 15, 283-293.	1.3	6
18	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

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19	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
20	Epigenetics: At the Crossroads Between Genetic and Environmental Determinants of Disease. , 2019, , 105-128.		0
21	Natural history and cell of origin of TCF3-ZNF384 and PTPN11 mutations in monozygotic twins with concordant BCP-ALL. <i>Blood</i> , 2019, 134, 900-905.	0.6	25
22	Epigenetic Deregulation of Protocadherin PCDHGC3 in Pheochromocytomas/Paragangliomas Associated With SDHB Mutations. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 5673-5692.	1.8	7
23	Epigenetics and Lifestyle: The Impact of Stress, Diet, and Social Habits on Tissue Homeostasis. , 2019, , 461-489.		3
24	Epigenetics in cancer therapy and nanomedicine. <i>Clinical Epigenetics</i> , 2019, 11, 81.	1.8	147
25	Chromatin regulation by Histone H4 acetylation at Lysine 16 during cell death and differentiation in the myeloid compartment. <i>Nucleic Acids Research</i> , 2019, 47, 5016-5037.	6.5	23
26	Downregulation of specific FBXW7 isoforms with differential effects in T-cell lymphoblastic lymphoma. <i>Oncogene</i> , 2019, 38, 4620-4636.	2.6	12
27	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
28	Impacto funcional de polimorfismos del gen de la esclerostina sobre la metilaci3n de ADN y la expresi3n g4nica. <i>Revista De Osteoporosis Y Metabolismo Mineral</i> , 2019, 11, 98-104.	0.3	0
29	SDHC Promoter Methylation, a Novel Pathogenic Mechanism in Parasympathetic Paragangliomas. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 295-305.	1.8	12
30	Distinct chromatin signatures of DNA hypomethylation in aging and cancer. <i>Aging Cell</i> , 2018, 17, e12744.	3.0	72
31	TERRA recruitment of polycomb to telomeres is essential for histone trymethylation marks at telomeric heterochromatin. <i>Nature Communications</i> , 2018, 9, 1548.	5.8	101
32	Epigenome-wide analysis reveals specific DNA hypermethylation of T cells during human hematopoietic differentiation. <i>Epigenomics</i> , 2018, 10, 903-923.	1.0	11
33	Evolutionary routes and KRAS dosage define pancreatic cancer phenotypes. <i>Nature</i> , 2018, 554, 62-68.	13.7	328
34	Quantification of Global DNA Methylation Levels by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2018, 1708, 49-58.	0.4	18
35	DNA methylation reprogramming of human cancer cells by expression of a plant 5-methylcytosine DNA glycosylase. <i>Epigenetics</i> , 2018, 13, 95-107.	1.3	8
36	Deregulation of the imprinted DLK1-DIO3 locus ncRNAs is associated with replicative senescence of human adipose-derived stem cells. <i>PLoS ONE</i> , 2018, 13, e0206534.	1.1	9

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37	Alzheimer's disease DNA methylome of pyramidal layers in frontal cortex: laser-assisted microdissection study. <i>Epigenomics</i> , 2018, 10, 1365-1382.	1.0	27
38	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
39	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
40	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
41	Loss of 5hmC identifies a new type of aberrant DNA hypermethylation in glioma. <i>Human Molecular Genetics</i> , 2018, 27, 3046-3059.	1.4	26
42	Epigenetic dysregulation of <i>TET2</i> in human glioblastoma. <i>Oncotarget</i> , 2018, 9, 25922-25934.	0.8	29
43	The role of 5-hydroxymethylcytosine in development, aging and age-related diseases. <i>Ageing Research Reviews</i> , 2017, 37, 28-38.	5.0	69
44	Generation and characterization of a human iPSC cell line expressing inducible Cas9 in the "safe harbor" AAVS1 locus. <i>Stem Cell Research</i> , 2017, 21, 137-140.	0.3	26
45	Interindividual epigenetic variability: Sound or noise?. <i>BioEssays</i> , 2017, 39, 1700055.	1.2	17
46	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
47	DNA methylation changes in human lung epithelia cells exposed to multi-walled carbon nanotubes. <i>Nanotoxicology</i> , 2017, 11, 857-870.	1.6	36
48	Multilayer OMIC Data in Medullary Thyroid Carcinoma Identifies the STAT3 Pathway as a Potential Therapeutic Target in <i>RET</i> M918T Tumors. <i>Clinical Cancer Research</i> , 2017, 23, 1334-1345.	3.2	34
49	Altered intragenic DNA methylation of <i>HOOK2</i> gene in adipose tissue from individuals with obesity and type 2 diabetes. <i>PLoS ONE</i> , 2017, 12, e0189153.	1.1	20
50	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
51	Longitudinal study of DNA methylation during the first 5 years of life. <i>Journal of Translational Medicine</i> , 2016, 14, 160.	1.8	29
52	Bioinformatics Tools in Epigenomics Studies. , 2016, , 73-107.		1
53	Age-associated hydroxymethylation in human bone-marrow mesenchymal stem cells. <i>Journal of Translational Medicine</i> , 2016, 14, 207.	1.8	33
54	Differentiation of Mouse Embryonic Stem Cells toward Functional Pancreatic β -Cell Surrogates through Epigenetic Regulation of <i>Pdx1</i> by Nitric Oxide. <i>Cell Transplantation</i> , 2016, 25, 1879-1892.	1.2	15

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55	Generation of a human iPSC line from a patient with a defect of intergenomic communication. <i>Stem Cell Research</i> , 2016, 16, 120-123.	0.3	5
56	Generation of a human control iPSC line with a European mitochondrial haplogroup U background. <i>Stem Cell Research</i> , 2016, 16, 88-91.	0.3	3
57	Clinical and molecular analyses of Beckwith-Wiedemann syndrome: Comparison between spontaneous conception and assisted reproduction techniques. <i>American Journal of Medical Genetics, Part A</i> , 2016, 170, 2740-2749.	0.7	30
58	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
59	HERG1A potassium channel is the predominant isoform in head and neck squamous cell carcinomas: evidence for regulation by epigenetic mechanisms. <i>Scientific Reports</i> , 2016, 6, 19666.	1.6	10
60	Generation of a human iPSC line from a patient with a mitochondrial encephalopathy due to mutations in the GFM1 gene. <i>Stem Cell Research</i> , 2016, 16, 124-127.	0.3	8
61	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737.	9.4	270
62	Generation of a human iPSC line from a patient with Leigh syndrome. <i>Stem Cell Research</i> , 2016, 16, 63-66.	0.3	19
63	Generation of a human iPSC line from a patient with an optic atrophy $\hat{+}$ phenotype due to a mutation in the OPA1 gene. <i>Stem Cell Research</i> , 2016, 16, 673-676.	0.3	12
64	Generation of a human iPSC line from a patient with Leigh syndrome caused by a mutation in the MT-ATP6 gene. <i>Stem Cell Research</i> , 2016, 16, 766-769.	0.3	12
65	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
66	The transcription factor Slug represses <i>E-cadherin</i> expression and induces epithelial to mesenchymal transitions: a comparison with Snail and E47 repressors. <i>Journal of Cell Science</i> , 2016, 129, 1283-1283.	1.2	12
67	Oncometabolic Nuclear Reprogramming of Cancer Stemness. <i>Stem Cell Reports</i> , 2016, 6, 273-283.	2.3	34
68	Allele-Specific Reprogramming of Cancer Metabolism by the Long Non-coding RNA CCAT2. <i>Molecular Cell</i> , 2016, 61, 520-534.	4.5	142
69	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
70	Liver X Receptor Agonist Modifies the DNA Methylation Profile of Synapse and Neurogenesis-Related Genes in the Triple Transgenic Mouse Model of Alzheimer's Disease. <i>Journal of Molecular Neuroscience</i> , 2016, 58, 243-253.	1.1	27
71	Reprogramming human B cells into induced pluripotent stem cells and its enhancement by C/EBP $\hat{+}$. <i>Leukemia</i> , 2016, 30, 674-682.	3.3	36
72	Contribution of JAK2 mutations to T-cell lymphoblastic lymphoma development. <i>Leukemia</i> , 2016, 30, 94-103.	3.3	27

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73	Vitamin C uncouples the Warburg metabolic switch in KRAS mutant colon cancer. <i>Oncotarget</i> , 2016, 7, 47954-47965.	0.8	66
74	P0260 : Liver kinase B1 as an oncogenic driver in liver cancer. <i>Journal of Hepatology</i> , 2015, 62, S403.	1.8	0
75	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
76	Glypican-1 identifies cancer exosomes and detects early pancreatic cancer. <i>Nature</i> , 2015, 523, 177-182.	13.7	2,240
77	DNA methylation patterns in newborns exposed to tobacco in utero. <i>Journal of Translational Medicine</i> , 2015, 13, 25.	1.8	75
78	Aberrant DNA methylation patterns of spermatozoa in men with unexplained infertility. <i>Human Reproduction</i> , 2015, 30, 1014-1028.	0.4	144
79	DNA Methylation Profiling in Pheochromocytoma and Paraganglioma Reveals Diagnostic and Prognostic Markers. <i>Clinical Cancer Research</i> , 2015, 21, 3020-3030.	3.2	53
80	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
81	H3K4me1 marks DNA regions hypomethylated during aging in human stem and differentiated cells. <i>Genome Research</i> , 2015, 25, 27-40.	2.4	119
82	Epigenetics of Aging. <i>Current Genomics</i> , 2015, 16, 435-440.	0.7	39
83	Identification of a DNA methylation signature in blood cells from persons with Down Syndrome. <i>Aging</i> , 2014, 7, 82-96.	1.4	92
84	Role of BRD4 in hematopoietic differentiation of embryonic stem cells. <i>Epigenetics</i> , 2014, 9, 566-578.	1.3	16
85	Epigenetic alterations in endocrine-related cancer. <i>Endocrine-Related Cancer</i> , 2014, 21, R319-R330.	1.6	24
86	Negative neuronal differentiation of human adipose-derived stem cell clones. <i>Regenerative Medicine</i> , 2014, 9, 279-293.	0.8	6
87	Genome-wide DNA methylation changes with age in disease-free human skeletal muscle. <i>Aging Cell</i> , 2014, 13, 360-366.	3.0	145
88	LINE-1 methylation in granulocyte DNA and trihalomethane exposure is associated with bladder cancer risk. <i>Epigenetics</i> , 2014, 9, 1532-1539.	1.3	24
89	Epigenetics, Inflammation, and Aging. , 2014, , 85-101.		4
90	Reconstructing the DNA Methylation Maps of the Neandertal and the Denisovan. <i>Science</i> , 2014, 344, 523-527.	6.0	188

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91	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
92	Single cell-derived clones from human adipose stem cells present different immunomodulatory properties. <i>Clinical and Experimental Immunology</i> , 2014, 176, 255-265.	1.1	21
93	Regulation of DNA Methylation Patterns by CK2-Mediated Phosphorylation of Dnmt3a. <i>Cell Reports</i> , 2014, 8, 743-753.	2.9	66
94	LINE-1 methylation in leukocyte DNA, interaction with phosphatidylethanolamine N-methyltransferase variants and bladder cancer risk. <i>British Journal of Cancer</i> , 2014, 110, 2123-2130.	2.9	17
95	Lineage-restricted function of the pluripotency factor NANOG in stratified epithelia. <i>Nature Communications</i> , 2014, 5, 4226.	5.8	45
96	S-adenosylmethionine Levels Regulate the Schwann Cell DNA Methylome. <i>Neuron</i> , 2014, 81, 1024-1039.	3.8	67
97	Role of Epigenetics in Neural Differentiation: Implications for Health and Disease. , 2014, , 63-79.		2
98	The Epigenetic Basis of Adaptation and Responses to Environmental Change: Perspective on Human Reproduction. <i>Advances in Experimental Medicine and Biology</i> , 2014, 753, 97-117.	0.8	15
99	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
100	A DNA methylation signature associated with the epigenetic repression of glycine N-methyltransferase in human hepatocellular carcinoma. <i>Journal of Molecular Medicine</i> , 2013, 91, 939-950.	1.7	29
101	Epigenetic regulation of adaptive responses of forest tree species to the environment. <i>Ecology and Evolution</i> , 2013, 3, 399-415.	0.8	271
102	Role of Sirtuins in Stem Cell Differentiation. <i>Genes and Cancer</i> , 2013, 4, 105-111.	0.6	33
103	DNA methylation-mediated silencing of PU.1 in leukemia cells resistant to cell differentiation. <i>SpringerPlus</i> , 2013, 2, 392.	1.2	5
104	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
105	Prelamin A causes progeria through cell-extrinsic mechanisms and prevents cancer invasion. <i>Nature Communications</i> , 2013, 4, 2268.	5.8	63
106	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
107	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
108	Contribution of genetic and epigenetic mechanisms to Wnt pathway activity in prevalent skeletal disorders. <i>Gene</i> , 2013, 532, 165-172.	1.0	42

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109	Genetic and Non-genetic Predictors of LINE-1 Methylation in Leukocyte DNA. <i>Environmental Health Perspectives</i> , 2013, 121, 650-656.	2.8	75
110	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
111	Aging epigenetics: Causes and consequences. <i>Molecular Aspects of Medicine</i> , 2013, 34, 765-781.	2.7	83
112	DNA Methylation Signatures Identify Biologically Distinct Thyroid Cancer Subtypes. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013, 98, 2811-2821.	1.8	100
113	DNA Methylation Biomarkers for Noninvasive Diagnosis of Colorectal Cancer. <i>Cancer Prevention Research</i> , 2013, 6, 656-665.	0.7	107
114	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
115	Zebularine regulates early stages of mESC differentiation: effect on cardiac commitment. <i>Cell Death and Disease</i> , 2013, 4, e570-e570.	2.7	21
116	DNA Methylation Dynamics in Blood after Hematopoietic Cell Transplant. <i>PLoS ONE</i> , 2013, 8, e56931.	1.1	24
117	A promoter DNA demethylation landscape of human hematopoietic differentiation. <i>Nucleic Acids Research</i> , 2012, 40, 116-131.	6.5	97
118	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
119	Commentaries on Viewpoint: Epigenetic regulation of the ACE gene might be more relevant to endurance physiology than the I/D polymorphism. <i>Journal of Applied Physiology</i> , 2012, 112, 1084-1085.	1.2	1
120	A DNA methylation fingerprint of 1628 human samples. <i>Genome Research</i> , 2012, 22, 407-419.	2.4	341
121	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
122	De novo DNA methyltransferases: oncogenes, tumor suppressors, or both?. <i>Trends in Genetics</i> , 2012, 28, 474-479.	2.9	35
123	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
124	801 Frequent Aberrant Expression of the Human Ether a Go-go (hEAG1) Potassium Channel in Head and Neck Cancer – Pathobiological Mechanisms and Clinical Implications. <i>European Journal of Cancer</i> , 2012, 48, S191.	1.3	0
125	Frequent aberrant expression of the human ether A 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
126	Hypomethylation of LINE-1, and not centromeric SAT- β , is associated with centromeric instability in head and neck squamous cell carcinoma. <i>Cellular Oncology (Dordrecht)</i> , 2012, 35, 259-267.	2.1	35

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127	Maintenance of Human Embryonic Stem Cells in Mesenchymal Stem Cell-Conditioned Media Augments Hematopoietic Specification. <i>Stem Cells and Development</i> , 2012, 21, 1549-1558.	1.1	27
128	iPSCs from cancer cells: challenges and opportunities. <i>Trends in Molecular Medicine</i> , 2012, 18, 245-247.	3.5	65
129	A DNA methylation signature associated with aberrant promoter DNA hypermethylation of DNMT3B in human colorectal cancer. <i>European Journal of Cancer</i> , 2012, 48, 2270-2281.	1.3	23
130	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
131	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
132	DNA methylation: a promising landscape for immune system-related diseases. <i>Trends in Genetics</i> , 2012, 28, 506-514.	2.9	131
133	1157 Association of LINE-1 Methylation With Risk of Bladder Cancer in the Spanish Population. <i>European Journal of Cancer</i> , 2012, 48, S278.	1.3	0
134	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
135	Epigenetics of Embryonic Stem Cells. <i>Advances in Experimental Medicine and Biology</i> , 2012, 741, 231-253.	0.8	9
136	Epigenetics, the Role of DNA Methylation in Tree Development. <i>Methods in Molecular Biology</i> , 2012, 877, 277-301.	0.4	6
137	Basic Procedures for Epigenetic Analysis in Plant Cell and Tissue Culture. <i>Methods in Molecular Biology</i> , 2012, 877, 325-341.	0.4	4
138	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
139	Distinct DNA methylomes of newborns and centenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10522-10527.	3.3	687
140	Aberrant epigenetic regulation of bromodomain Brd4 in human colon cancer. <i>Journal of Molecular Medicine</i> , 2012, 90, 587-595.	1.7	50
141	Epigenetics and the environment: emerging patterns and implications. <i>Nature Reviews Genetics</i> , 2012, 13, 97-109.	7.7	1,524
142	Epigenetic Code and Self-Identity. <i>Advances in Experimental Medicine and Biology</i> , 2012, 738, 236-255.	0.8	13
143	Techniques to Study DNA Methylation and Histone Modification. , 2011, , 21-39.		3
144	Child Health, Developmental Plasticity, and Epigenetic Programming. <i>Endocrine Reviews</i> , 2011, 32, 159-224.	8.9	533

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145	Beckwith's 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
146	The effects of the dietary polyphenol resveratrol on human healthy aging and lifespan. <i>Epigenetics</i> , 2011, 6, 870-874.	1.3	56
147	Constitutional mosaic genome-wide uniparental disomy due to diploidisation: an unusual cancer-predisposing mechanism. <i>Journal of Medical Genetics</i> , 2011, 48, 212-216.	1.5	32
148	The growing role of gene methylation on endocrine function. <i>Journal of Molecular Endocrinology</i> , 2011, 47, R75-R89.	1.1	35
149	Sirt1 brings stemness closer to cancer and aging. <i>Aging</i> , 2011, 3, 162-167.	1.4	31
150	Aging genetics and aging. , 2011, 2, 186-95.		31
151	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
152	A Possible Role for Epigenetics in Age-Dependent Bone Diseases. <i>Clinical Reviews in Bone and Mineral Metabolism</i> , 2010, 8, 95-99.	1.3	1
153	Identification of Tri- and Tetracyclic Pyrimidinediones as Sirtuin Inhibitors. <i>ChemMedChem</i> , 2010, 5, 674-677.	1.6	40
154	Fatty liver and fibrosis in glycine N-methyltransferase knockout mice is prevented by nicotinamide. <i>Hepatology</i> , 2010, 52, 105-114.	3.6	81
155	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
156	Epigenetic regulation of the immune system in health and disease. <i>Tissue Antigens</i> , 2010, 76, 431-439.	1.0	54
157	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
158	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
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