

# AgustÃ-n F Fernandez

## List of Publications by Year in descending order

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Version: 2024-02-01

138  
papers

11,261  
citations

38660

50  
h-index

30848

102  
g-index

148  
all docs

148  
docs citations

148  
times ranked

21269  
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	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
3	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
4	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
5	Nicotinamide N-methyltransferase: At the crossroads between cellular metabolism and epigenetic regulation. <i>Molecular Metabolism</i> , 2021, 45, 101165.	3.0	56
6	Conservation of Aging and Cancer Epigenetic Signatures across Human and Mouse. <i>Molecular Biology and Evolution</i> , 2021, 38, 3415-3435.	3.5	5
7	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
8	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
9	DNA Methylomes and Epigenetic Age Acceleration Associations with Poor Metabolic Control in T1D. <i>Biomedicines</i> , 2021, 9, 13.	1.4	1
10	Physical exercise shapes the mouse brain epigenome. <i>Molecular Metabolism</i> , 2021, 54, 101398.	3.0	12
11	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
12	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
13	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
14	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
15	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
16	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
17	Epigenetics and Lifestyle: The Impact of Stress, Diet, and Social Habits on Tissue Homeostasis. , 2019, , 461-489.		3
18	Epigenetics in cancer therapy and nanomedicine. <i>Clinical Epigenetics</i> , 2019, 11, 81.	1.8	147

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19	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
20	Downregulation of specific FBXW7 isoforms with differential effects in T-cell lymphoblastic lymphoma. <i>Oncogene</i> , 2019, 38, 4620-4636.	2.6	12
21	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
22	Impacto funcional de polimorfismos del gen de la esclerostina sobre la metilación de ADN y la expresión génica. <i>Revista De Osteoporosis Y Metabolismo Mineral</i> , 2019, 11, 98-104.	0.3	0
23	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
24	Distinct chromatin signatures of DNA hypomethylation in aging and cancer. <i>Aging Cell</i> , 2018, 17, e12744.	3.0	72
25	Epigenome-wide analysis reveals specific DNA hypermethylation of T cells during human hematopoietic differentiation. <i>Epigenomics</i> , 2018, 10, 903-923.	1.0	11
26	Quantification of Global DNA Methylation Levels by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2018, 1708, 49-58.	0.4	18
27	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
28	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
29	Changes in DNA Methylation Related to Male Infertility. , 2018, , 189-207.		0
30	Tailoring of Perpendicular Magnetic Anisotropy in Dy13Fe87 Thin Films with Hexagonal Antidot Lattice Nanostructure. <i>Nanomaterials</i> , 2018, 8, 227.	1.9	15
31	The Methylome Landscape of Infant B-Cell Precursor Acute Lymphoblastic Leukemia. <i>Experimental Hematology</i> , 2018, 64, S85-S86.	0.2	0
32	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
33	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
34	Epigenetic dysregulation of TET2 in human glioblastoma. <i>Oncotarget</i> , 2018, 9, 25922-25934.	0.8	29
35	The role of 5-hydroxymethylcytosine in development, aging and age-related diseases. <i>Ageing Research Reviews</i> , 2017, 37, 28-38.	5.0	69
36	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

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37	Phenotypic characteristics of aged CD4 <sup>+</sup> CD28 <sup>null</sup> T lymphocytes are determined by changes in the whole-genome DNA methylation pattern. <i>Aging Cell</i> , 2017, 16, 293-303.	3.0	39
38	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
39	DNA methylation changes in human lung epithelia cells exposed to multi-walled carbon nanotubes. <i>Nanotoxicology</i> , 2017, 11, 857-870.	1.6	36
40	Multilayer OMIC Data in Medullary Thyroid Carcinoma Identifies the STAT3 Pathway as a Potential Therapeutic Target in RET/M918T Tumors. <i>Clinical Cancer Research</i> , 2017, 23, 1334-1345.	3.2	34
41	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
42	The Impact of External Factors on the Epigenome: In Utero and over Lifetime. <i>BioMed Research International</i> , 2016, 2016, 1-17.	0.9	76
43	Longitudinal study of DNA methylation during the first 5 years of life. <i>Journal of Translational Medicine</i> , 2016, 14, 160.	1.8	29
44	Bioinformatics Tools in Epigenomics Studies. , 2016, , 73-107.		1
45	Age-associated hydroxymethylation in human bone-marrow mesenchymal stem cells. <i>Journal of Translational Medicine</i> , 2016, 14, 207.	1.8	33
46	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
47	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
48	Developmental refractoriness of MLL-rearranged human acute B-cell leukemias. <i>Experimental Hematology</i> , 2016, 44, S40.	0.2	0
49	MIR-873 Promotes Liver De-Differentiation and Fibrosis Targeting Glycine-N-Methyl Transferase. <i>Journal of Hepatology</i> , 2016, 64, S203-S204.	1.8	0
50	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
51	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
52	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737.	9.4	270
53	Generation of a human iPSC line from a patient with Leigh syndrome. <i>Stem Cell Research</i> , 2016, 16, 63-66.	0.3	19
54	Generation of a human iPSC line from a patient with an optic atrophy $\hat{\epsilon}$ plus $\hat{\epsilon}$ ™ phenotype due to a mutation in the OPA1 gene. <i>Stem Cell Research</i> , 2016, 16, 673-676.	0.3	12

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55	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
56	Oncometabolic Nuclear Reprogramming of Cancer Stemness. <i>Stem Cell Reports</i> , 2016, 6, 273-283.	2.3	34
57	Allele-Specific Reprogramming of Cancer Metabolism by the Long Non-coding RNA CCAT2. <i>Molecular Cell</i> , 2016, 61, 520-534.	4.5	142
58	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
59	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
60	Reprogramming human B cells into induced pluripotent stem cells and its enhancement by C/EBP $\beta$ . <i>Leukemia</i> , 2016, 30, 674-682.	3.3	36
61	Contribution of JAK2 mutations to T-cell lymphoblastic lymphoma development. <i>Leukemia</i> , 2016, 30, 94-103.	3.3	27
62	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
63	Glypican-1 identifies cancer exosomes and detects early pancreatic cancer. <i>Nature</i> , 2015, 523, 177-182.	13.7	2,240
64	DNA methylation patterns in newborns exposed to tobacco in utero. <i>Journal of Translational Medicine</i> , 2015, 13, 25.	1.8	75
65	Aberrant DNA methylation patterns of spermatozoa in men with unexplained infertility. <i>Human Reproduction</i> , 2015, 30, 1014-1028.	0.4	144
66	DNA Methylation Profiling in Pheochromocytoma and Paraganglioma Reveals Diagnostic and Prognostic Markers. <i>Clinical Cancer Research</i> , 2015, 21, 3020-3030.	3.2	53
67	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
68	H3K4me1 marks DNA regions hypomethylated during aging in human stem and differentiated cells. <i>Genome Research</i> , 2015, 25, 27-40.	2.4	119
69	EPB41L3, TSP-1 and RASSF2 as new clinically relevant prognostic biomarkers in diffuse gliomas. <i>Oncotarget</i> , 2015, 6, 368-380.	0.8	23
70	Epigenetics of Aging. <i>Current Genomics</i> , 2015, 16, 435-440.	0.7	39
71	Clinical Epigenetics in Cancer: Applications in Diagnosis, Prognosis and Therapy. , 2015, , 285-296.		0
72	Role of BRD4 in hematopoietic differentiation of embryonic stem cells. <i>Epigenetics</i> , 2014, 9, 566-578.	1.3	16

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73	Epigenetic alterations in endocrine-related cancer. <i>Endocrine-Related Cancer</i> , 2014, 21, R319-R330.	1.6	24
74	Negative neuronal differentiation of human adipose-derived stem cell clones. <i>Regenerative Medicine</i> , 2014, 9, 279-293.	0.8	6
75	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
76	Epigenetics, Inflammation, and Aging. , 2014, , 85-101.		4
77	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
78	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
79	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
80	Lineage-restricted function of the pluripotency factor NANOG in stratified epithelia. <i>Nature Communications</i> , 2014, 5, 4226.	5.8	45
81	S-adenosylmethionine Levels Regulate the Schwann Cell DNA Methylome. <i>Neuron</i> , 2014, 81, 1024-1039.	3.8	67
82	Role of Epigenetics in Neural Differentiation: Implications for Health and Disease. , 2014, , 63-79.		2
83	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
84	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
85	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
86	Role of Sirtuins in Stem Cell Differentiation. <i>Genes and Cancer</i> , 2013, 4, 105-111.	0.6	33
87	DNA methylation-mediated silencing of PU.1 in leukemia cells resistant to cell differentiation. <i>SpringerPlus</i> , 2013, 2, 392.	1.2	5
88	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
89	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
90	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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91	Genetic and Non-genetic Predictors of LINE-1 Methylation in Leukocyte DNA. <i>Environmental Health Perspectives</i> , 2013, 121, 650-656.	2.8	75
92	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
93	Aging epigenetics: Causes and consequences. <i>Molecular Aspects of Medicine</i> , 2013, 34, 765-781.	2.7	83
94	DNA Methylation Signatures Identify Biologically Distinct Thyroid Cancer Subtypes. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013, 98, 2811-2821.	1.8	100
95	DNA Methylation Biomarkers for Noninvasive Diagnosis of Colorectal Cancer. <i>Cancer Prevention Research</i> , 2013, 6, 656-665.	0.7	107
96	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
97	DNA Methylation Dynamics in Blood after Hematopoietic Cell Transplant. <i>PLoS ONE</i> , 2013, 8, e56931.	1.1	24
98	LINE-1 methylation, lifetime trihalomethane exposure from drinking water and bladder cancer risk. <i>ISEE Conference Abstracts</i> , 2013, 2013, 4189.	0.0	0
99	A promoter DNA demethylation landscape of human hematopoietic differentiation. <i>Nucleic Acids Research</i> , 2012, 40, 116-131.	6.5	97
100	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
101	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
102	Silencing of Kruppel-like factor 2 by the histone methyltransferase EZH2 in human cancer. <i>Oncogene</i> , 2012, 31, 1988-1994.	2.6	93
103	A DNA methylation fingerprint of 1628 human samples. <i>Genome Research</i> , 2012, 22, 407-419.	2.4	341
104	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
105	De novo DNA methyltransferases: oncogenes, tumor suppressors, or both?. <i>Trends in Genetics</i> , 2012, 28, 474-479.	2.9	35
106	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
107	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
108	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

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109	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
110	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
111	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
112	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
113	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
114	Aberrant epigenetic regulation of bromodomain Brd4 in human colon cancer. <i>Journal of Molecular Medicine</i> , 2012, 90, 587-595.	1.7	50
115	Techniques to Study DNA Methylation and Histone Modification. , 2011, , 21-39.		3
116	Array-based DNA methylation profiling in acute myeloid leukaemia. <i>British Journal of Haematology</i> , 2011, 155, 65-72.	1.2	21
117	The effects of the dietary polyphenol resveratrol on human healthy aging and lifespan. <i>Epigenetics</i> , 2011, 6, 870-874.	1.3	56
118	Ageing genetics and aging. , 2011, 2, 186-95.		31
119	A Genetic Defect in Exportin-5 Traps Precursor MicroRNAs in the Nucleus of Cancer Cells. <i>Cancer Cell</i> , 2010, 18, 303-315.	7.7	299
120	Viral epigenomes in human tumorigenesis. <i>Oncogene</i> , 2010, 29, 1405-1420.	2.6	76
121	Disrupted microRNA expression caused by Mecp2 loss in a mouse model of Rett syndrome. <i>Epigenetics</i> , 2010, 5, 656-663.	1.3	125
122	Changes in the pattern of DNA methylation associate with twin discordance in systemic lupus erythematosus. <i>Genome Research</i> , 2010, 20, 170-179.	2.4	569
123	Epigenetic repression of ROR2 has a Wnt-mediated, pro-tumourigenic role in colon cancer. <i>Molecular Cancer</i> , 2010, 9, 170.	7.9	61
124	DNA methylation epigenotypes in breast cancer molecular subtypes. <i>Breast Cancer Research</i> , 2010, 12, R77.	2.2	159
125	Epigenetics and environment: a complex relationship. <i>Journal of Applied Physiology</i> , 2010, 109, 243-251.	1.2	191
126	DNA Methylation Profiles and Their Relationship with Cytogenetic Status in Adult Acute Myeloid Leukemia. <i>PLoS ONE</i> , 2010, 5, e12197.	1.1	73



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127	Epigenetic regulation of aging. <i>Discovery Medicine</i> , 2010, 10, 225-33.	0.5	48
128	The dynamic DNA methylomes of double-stranded DNA viruses associated with human cancer. <i>Genome Research</i> , 2009, 19, 438-451.	2.4	218
129	Epigenetic Inactivation of the Circadian Clock Gene <i>BMAL1</i> in Hematologic Malignancies. <i>Cancer Research</i> , 2009, 69, 8447-8454.	0.4	161
130	A microarray-based DNA methylation study of glioblastoma multiforme. <i>Epigenetics</i> , 2009, 4, 255-264.	1.3	155
131	A TARBP2 mutation in human cancer impairs microRNA processing and DICER1 function. <i>Nature Genetics</i> , 2009, 41, 365-370.	9.4	355
132	9237 Array based CpG island methylation-profiling in acute myelogenous leukemia at diagnosis and relapse. <i>European Journal of Cancer, Supplement</i> , 2009, 7, 571.	2.2	0
133	Epigenomic Analysis of Acute Myeloid Leukemia Identifies Specific Patterns and Markers with Clinical and Biological Relevance.. <i>Blood</i> , 2009, 114, 2394-2394.	0.6	0
134	Epigenetic Inactivation of the Groucho Homologue Gene TLE1 in Hematologic Malignancies. <i>Cancer Research</i> , 2008, 68, 4116-4122.	0.4	50
135	Promoter DNA Hypermethylation and Gene Repression in Undifferentiated Arabidopsis Cells. <i>PLoS ONE</i> , 2008, 3, e3306.	1.1	99
136	Mecp2-Null Mice Provide New Neuronal Targets for Rett Syndrome. <i>PLoS ONE</i> , 2008, 3, e3669.	1.1	106
137	Cancer Genes Hypermethylated in Human Embryonic Stem Cells. <i>PLoS ONE</i> , 2008, 3, e3294.	1.1	75
138	An autoregulatory loop of nuclear corepressor 1 expression controls hepatocarcinoma invasion, growth and metastasis. <i>Endocrine Abstracts</i> , 0, , .	0.0	0