AgustÃ-n F Fernandez

List of Publications by Year
in descending order

138	11,261	38742 50	30087 103
papers	citations	h-index	g-index

148	148	148	21269
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Epigenetic Profiling and Response to CD19 Chimeric Antigen Receptor T-Cell Therapy in B-Cell Malignancies. Journal of the National Cancer Institute, 2022, 114, 436-445.	6.3	29
2	Classification of follicular-patterned thyroid lesions using a minimal set of epigenetic biomarkers. European Journal of Endocrinology, 2022, 187, 335-347.	3.7	2
3	Epigenetic loss of m1A RNA demethylase ALKBH3 in Hodgkin lymphoma targets collagen, conferring poor clinical outcome. Blood, 2021, 137, 994-999.	1.4	30
4	Methylation of the Sclerostin (SOST) Gene in Serum Free DNA: A New Bone Biomarker?. Genetic Testing and Molecular Biomarkers, 2021, 25, 42-47.	0.7	0
5	Nicotinamide N-methyltransferase: At the crossroads between cellular metabolism and epigenetic regulation. Molecular Metabolism, 2021, 45, 101165.	6.5	56
6	Conservation of Aging and Cancer Epigenetic Signatures across Human and Mouse. Molecular Biology and Evolution, 2021, 38, 3415-3435.	8.9	5
7	Integrative methylome-transcriptome analysis unravels cancer cell vulnerabilities in infant MLL-rearranged B cell acute lymphoblastic leukemia. Journal of Clinical Investigation, 2021, 131, .	8.2	14
8	Epigenetic Deregulation of the Histone Methyltransferase KMT5B Contributes to Malignant Transformation in Glioblastoma. Frontiers in Cell and Developmental Biology, 2021, 9, 671838.	3.7	6
9	DNA Methylomes and Epigenetic Age Acceleration Associations with Poor Metabolic Control in T1D. Biomedicines, 2021, 9, 13.	3.2	1
10	Physical exercise shapes the mouse brain epigenome. Molecular Metabolism, 2021, 54, 101398.	6.5	12
11	Epigenetic downregulation of TET3 reduces genomeâ€wide 5hmC levels and promotes glioblastoma tumorigenesis. International Journal of Cancer, 2020, 146, 373-387.	5.1	45
12	No genome-wide DNA methylation changes found associated with medium-term reduced graphene oxide exposure in human lung epithelial cells. Epigenetics, 2020, 15, 283-293.	2.7	6
13	Global hyperactivation of enhancers stabilizes human and mouse naive pluripotency through inhibition of CDK8/19 Mediator kinases. Nature Cell Biology, 2020, 22, 1223-1238.	10.3	35
14	Epigenetic loss of RNA-methyltransferase NSUN5 in glioma targets ribosomes to drive a stress adaptive translational program. Acta Neuropathologica, 2019, 138, 1053-1074.	7.7	106
15	Natural history and cell of origin of TCF3-ZNF384 and PTPN11 mutations in monozygotic twins with concordant BCP-ALL. Blood, 2019, 134, 900-905.	1.4	25
16	Epigenetic Deregulation of Protocadherin PCDHGC3 in Pheochromocytomas/Paragangliomas Associated With SDHB Mutations. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 5673-5692.	3.6	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. Clinical Epigenetics, 2019, 11, 81.	4.1	147

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19	Chromatin regulation by Histone H4 acetylation at Lysine 16 during cell death and differentiation in the myeloid compartment. Nucleic Acids Research, 2019, 47, 5016-5037.	14.5	23
20	Downregulation of specific FBXW7 isoforms with differential effects in T-cell lymphoblastic lymphoma. Oncogene, 2019, 38, 4620-4636.	5.9	12
21	Longitudinal genome-wide DNA methylation analysis uncovers persistent early-life DNA methylation changes. Journal of Translational Medicine, 2019, 17, 15.	4.4	44
22	Impacto funcional de polimorfismos del gen de la esclerostina sobre la metilaciÃ³n de ADN y la expresiÃ³n gÃ©nica. Revista De Osteoporosis Y Metabolismo Mineral, 2019, 11, 98-104.	0.3	0
23	SDHC Promoter Methylation, a Novel Pathogenic Mechanism in Parasympathetic Paragangliomas. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 295-305.	3.6	12
24	Distinct chromatin signatures of DNA hypomethylation in aging and cancer. Aging Cell, 2018, 17, e12744.	6.7	72
25	Epigenome-wide analysis reveals specific DNA hypermethylation of T cells during human hematopoietic differentiation. Epigenomics, 2018, 10, 903-923.	2.1	11
26	Quantification of Global DNA Methylation Levels by Mass Spectrometry. Methods in Molecular Biology, 2018, 1708, 49-58.	0.9	18
27	Alzheimer's disease DNA methylome of pyramidal layers in frontal cortex: laser-assisted microdissection study. Epigenomics, 2018, 10, 1365-1382.	2.1	27
28	MiR-873-5p acts as an epigenetic regulator in early stages of liver fibrosis and cirrhosis. Cell Death and Disease, 2018, 9, 958.	6.3	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. Nanomaterials, 2018, 8, 227.	4.1	15
31	The Methylome Landscape of Infant B-Cell Precursor Acute Lymphoblastic Leukemia. Experimental Hematology, 2018, 64, S85-S86.	0.4	0
32	Epigenetic prediction of response to anti-PD-1 treatment in non-small-cell lung cancer: a multicentre, retrospective analysis. Lancet Respiratory Medicine,the, 2018, 6, 771-781.	10.7	167
33	Loss of 5hmC identifies a new type of aberrant DNA hypermethylation in glioma. Human Molecular Genetics, 2018, 27, 3046-3059.	2.9	26
34	Epigenetic dysregulation ofTET2in human glioblastoma. Oncotarget, 2018, 9, 25922-25934.	1.8	29
35	The role of 5-hydroxymethylcytosine in development, aging and age-related diseases. Ageing Research Reviews, 2017, 37, 28-38.	10.9	69
36	Generation and characterization of a human iPSC cell line expressing inducible Cas9 in the â€œsafe harborâ€•AAVS1 locus. Stem Cell Research, 2017, 21, 137-140.	0.7	26

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37	Phenotypic characteristics of aged CD4⁺ CD28^{null} T lymphocytes are determined by changes in the whole-genome DNA methylation pattern. Aging Cell, 2017, 16, 293-303.	6.7	39
38	Differential analysis of genome-wide methylation and gene expression in mesenchymal stem cells of patients with fractures and osteoarthritis. Epigenetics, 2017, 12, 113-122.	2.7	60
39	DNA methylation changes in human lung epithelia cells exposed to multi-walled carbon nanotubes. Nanotoxicology, 2017, 11, 857-870.	3.0	36
40	Multilayer OMIC Data in Medullary Thyroid Carcinoma Identifies the STAT3 Pathway as a Potential Therapeutic Target in RETM918T Tumors. Clinical Cancer Research, 2017, 23, 1334-1345.	7.0	34
41	The effect of exposure to nanoparticles and nanomaterials on the mammalian epigenome. International Journal of Nanomedicine, 2016, Volume 11, 6297-6306.	6.7	78
42	The Impact of External Factors on the Epigenome:In Uteroand over Lifetime. BioMed Research International, 2016, 2016, 1-17.	1.9	76
43	Longitudinal study of DNA methylation during the first 5Âyears of life. Journal of Translational Medicine, 2016, 14, 160.	4.4	29
44	Bioinformatics Tools in Epigenomics Studies. , 2016, , 73-107.		1
45	Age-associated hydroxymethylation in human bone-marrow mesenchymal stem cells. Journal of Translational Medicine, 2016, 14, 207.	4.4	33
46	Generation of a human iPSC line from a patient with a defect of intergenomic communication. Stem Cell Research, 2016, 16, 120-123.	0.7	5
47	Generation of a human control iPSC line with a European mitochondrial haplogroup U background. Stem Cell Research, 2016, 16, 88-91.	0.7	3
48	Developmental refractoriness of MLL-rearranged human acute B-cell leukemias. Experimental Hematology, 2016, 44, S40.	0.4	0
49	MIR-873 Promotes Liver De-Differentiation and Fibrosis Targeting Glycine-N-Methyl Transferase. Journal of Hepatology, 2016, 64, S203-S204.	3.7	0
50	Development Refractoriness of MLL-Rearranged Human B Cell Acute Leukemias to Reprogramming into Pluripotency. Stem Cell Reports, 2016, 7, 602-618.	4.8	38
51	Generation of a human iPSC line from a patient with a mitochondrial encephalopathy due to mutations in the GFM1 gene. Stem Cell Research, 2016, 16, 124-127.	0.7	8
52	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. Nature Biotechnology, 2016, 34, 726-737.	17.5	270
53	Generation of a human iPSC line from a patient with Leigh syndrome. Stem Cell Research, 2016, 16, 63-66.	0.7	19
54	Generation of a human iPSC line from a patient with an optic atrophy â€˜plusâ€™ phenotype due to a mutation in the OPA1 gene. Stem Cell Research, 2016, 16, 673-676.	0.7	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. Stem Cell Research, 2016, 16, 766-769.	0.7	12
56	Oncometabolic Nuclear Reprogramming of Cancer Stemness. Stem Cell Reports, 2016, 6, 273-283.	4.8	34
57	Allele-Specific Reprogramming of Cancer Metabolism by the Long Non-coding RNA CCAT2. Molecular Cell, 2016, 61, 520-534.	9.7	142
58	Autoregulatory loop of nuclear corepressor 1 expression controls invasion, tumor growth, and metastasis. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E328-37.	7.1	41
59	Liver X Receptor Agonist Modifies the DNA Methylation Profile of Synapse and Neurogenesis-Related Genes in the Triple Transgenic Mouse Model of Alzheimerâ€™s Disease. Journal of Molecular Neuroscience, 2016, 58, 243-253.	2.3	27
60	Reprogramming human B cells into induced pluripotent stem cells and its enhancement by C/EBPÎ±. Leukemia, 2016, 30, 674-682.	7.2	36
61	Contribution of JAK2 mutations to T-cell lymphoblastic lymphoma development. Leukemia, 2016, 30, 94-103.	7.2	27
62	Nuclear DICKKOPF-1 as a biomarker of chemoresistance and poor clinical outcome in colorectal cancer. Oncotarget, 2015, 6, 5903-5917.	1.8	35
63	Glypican-1 identifies cancer exosomes and detects early pancreatic cancer. Nature, 2015, 523, 177-182.	27.8	2,240
64	DNA methylation patterns in newborns exposed to tobacco in utero. Journal of Translational Medicine, 2015, 13, 25.	4.4	75
65	Aberrant DNA methylation patterns of spermatozoa in men with unexplained infertility. Human Reproduction, 2015, 30, 1014-1028.	0.9	144
66	DNA Methylation Profiling in Pheochromocytoma and Paraganglioma Reveals Diagnostic and Prognostic Markers. Clinical Cancer Research, 2015, 21, 3020-3030.	7.0	53
67	Methylation of NKG2D ligands contributes to immune system evasion in acute myeloid leukemia. Genes and Immunity, 2015, 16, 71-82.	4.1	82
68	H3K4me1 marks DNA regions hypomethylated during aging in human stem and differentiated cells. Genome Research, 2015, 25, 27-40.	5.5	119
69	EPB41L3, TSP-1 and RASSF2 as new clinically relevant prognostic biomarkers in diffuse gliomas. Oncotarget, 2015, 6, 368-380.	1.8	23
70	Epigenetics of Aging. Current Genomics, 2015, 16, 435-440.	1.6	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. Epigenetics, 2014, 9, 566-578.	2.7	16

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73	Epigenetic alterations in endocrine-related cancer. Endocrine-Related Cancer, 2014, 21, R319-R330.	3.1	24
74	Negative neuronal differentiation of human adipose-derived stem cell clones. Regenerative Medicine, 2014, 9, 279-293.	1.7	6
75	LINE-1 methylation in granulocyte DNA and trihalomethane exposure is associated with bladder cancer risk. Epigenetics, 2014, 9, 1532-1539.	2.7	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. Diabetologia, 2014, 57, 1154-1158.	6.3	67
78	Single cell-derived clones from human adipose stem cells present different immunomodulatory properties. Clinical and Experimental Immunology, 2014, 176, 255-265.	2.6	21
79	LINE-1 methylation in leukocyte DNA, interaction with phosphatidylethanolamine N-methyltransferase variants and bladder cancer risk. British Journal of Cancer, 2014, 110, 2123-2130.	6.4	17
80	Lineage-restricted function of the pluripotency factor NANOG in stratified epithelia. Nature Communications, 2014, 5, 4226.	12.8	45
81	S-adenosylmethionine Levels Regulate the Schwann Cell DNA Methylome. Neuron, 2014, 81, 1024-1039.	8.1	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. Advances in Experimental Medicine and Biology, 2014, 753, 97-117.	1.6	15
84	The B cell transcription program mediates hypomethylation and overexpression of key genes in Epstein-Barr virus-associated proliferative conversion. Genome Biology, 2013, 14, R3.	9.6	53
85	A DNA methylation signature associated with the epigenetic repression of glycine N-methyltransferase in human hepatocellular carcinoma. Journal of Molecular Medicine, 2013, 91, 939-950.	3.9	29
86	Role of Sirtuins in Stem Cell Differentiation. Genes and Cancer, 2013, 4, 105-111.	1.9	33
87	DNA methylation-mediated silencing of PU.1 in leukemia cells resistant to cell differentiation. SpringerPlus, 2013, 2, 392.	1.2	5
88	Immune-Dependent and Independent Antitumor Activity of GM-CSF Aberrantly Expressed by Mouse and Human Colorectal Tumors. Cancer Research, 2013, 73, 395-405.	0.9	69
89	Genomeâ€wide profiling of bone reveals differentially methylated regions in osteoporosis and osteoarthritis. Arthritis and Rheumatism, 2013, 65, 197-205.	6.7	133
90	Contribution of genetic and epigenetic mechanisms to Wnt pathway activity in prevalent skeletal disorders. Gene, 2013, 532, 165-172.	2.2	42

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91	Genetic and Non-genetic Predictors of LINE-1 Methylation in Leukocyte DNA. Environmental Health Perspectives, 2013, 121, 650-656.	6.0	75
92	The role of genetics in the establishment and maintenance of the epigenome. Cellular and Molecular Life Sciences, 2013, 70, 1543-1573.	5.4	53
93	Aging epigenetics: Causes and consequences. Molecular Aspects of Medicine, 2013, 34, 765-781.	6.4	83
94	DNA Methylation Signatures Identify Biologically Distinct Thyroid Cancer Subtypes. Journal of Clinical Endocrinology and Metabolism, 2013, 98, 2811-2821.	3.6	100
95	DNA Methylation Biomarkers for Noninvasive Diagnosis of Colorectal Cancer. Cancer Prevention Research, 2013, 6, 656-665.	1.5	107
96	DNA methylation map of mouse and human brain identifies target genes in Alzheimerâ€™s disease. Brain, 2013, 136, 3018-3027.	7.6	129
97	DNA Methylation Dynamics in Blood after Hematopoietic Cell Transplant. PLoS ONE, 2013, 8, e56931.	2.5	24
98	LINE-1 methylation, lifetime trihalomethane exposure from drinking water and bladder cancer risk. ISEE Conference Abstracts, 2013, 2013, 4189.	0.0	0
99	A promoter DNA demethylation landscape of human hematopoietic differentiation. Nucleic Acids Research, 2012, 40, 116-131.	14.5	97
100	Role of DNA methylation in the regulation of the RANKL-OPG system in human bone. Epigenetics, 2012, 7, 83-91.	2.7	99
101	Commentaries on Viewpoint: Epigenetic regulation of the ACE gene might be more relevant to endurance physiology than the I/D polymorphism. Journal of Applied Physiology, 2012, 112, 1084-1085.	2.5	1
102	Silencing of Kruppel-like factor 2 by the histone methyltransferase EZH2 in human cancer. Oncogene, 2012, 31, 1988-1994.	5.9	93
103	A DNA methylation fingerprint of 1628 human samples. Genome Research, 2012, 22, 407-419.	5.5	341
104	Genome-Wide Analysis of DNA Methylation Differences in Muscle and Fat from Monozygotic Twins Discordant for Type 2 Diabetes. PLoS ONE, 2012, 7, e51302.	2.5	171
105	De novo DNA methyltransferases: oncogenes, tumor suppressors, or both?. Trends in Genetics, 2012, 28, 474-479.	6.7	35
106	A human ESC model for MLL-AF4 leukemic fusion gene reveals an impaired early hematopoietic-endothelial specification. Cell Research, 2012, 22, 986-1002.	12.0	49
107	Maintenance of Human Embryonic Stem Cells in Mesenchymal Stem Cell-Conditioned Media Augments Hematopoietic Specification. Stem Cells and Development, 2012, 21, 1549-1558.	2.1	27
108	A DNA methylation signature associated with aberrant promoter DNA hypermethylation of DNMT3B in human colorectal cancer. European Journal of Cancer, 2012, 48, 2270-2281.	2.8	23

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109	Global DNA hypomethylation in cancer: review of validated methods and clinical significance. Clinical Chemistry and Laboratory Medicine, 2012, 50, 1733-42.	2.3	85
110	1157 Association of LINE-1 Methylation With Risk of Bladder Cancer in the Spanish Population. European Journal of Cancer, 2012, 48, S278.	2.8	0
111	Effects of short-term high-fat overfeeding on genome-wide DNA methylation in the skeletal muscle of healthy young men. Diabetologia, 2012, 55, 3341-3349.	6.3	179
112	DNA methylation contributes to the regulation of sclerostin expression in human osteocytes. Journal of Bone and Mineral Research, 2012, 27, 926-937.	2.8	116
113	Distinct DNA methylomes of newborns and centenarians. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10522-10527.	7.1	687
114	Aberrant epigenetic regulation of bromodomain Brd4 in human colon cancer. Journal of Molecular Medicine, 2012, 90, 587-595.	3.9	50
115	Techniques to Study DNA Methylation and Histone Modification. , 2011, , 21-39.		3
116	Arrayâ€based DNA methylation profiling in acute myeloid leukaemia. British Journal of Haematology, 2011, 155, 65-72.	2.5	21
117	The effects of the dietary polyphenol resveratrol on human healthy aging and lifespan. Epigenetics, 2011, 6, 870-874.	2.7	56
118	Aging genetics and aging. , 2011, 2, 186-95.		31
119	A Genetic Defect in Exportin-5 Traps Precursor MicroRNAs in the Nucleus of Cancer Cells. Cancer Cell, 2010, 18, 303-315.	16.8	299
120	Viral epigenomes in human tumorigenesis. Oncogene, 2010, 29, 1405-1420.	5.9	76
121	Disrupted microRNA expression caused by Mecp2 loss in a mouse model of Rett syndrome. Epigenetics, 2010, 5, 656-663.	2.7	125
122	Changes in the pattern of DNA methylation associate with twin discordance in systemic lupus erythematosus. Genome Research, 2010, 20, 170-179.	5.5	569
123	Epigenetic repression of ROR2 has a Wnt-mediated, pro-tumourigenic role in colon cancer. Molecular Cancer, 2010, 9, 170.	19.2	61
124	DNA methylation epigenotypes in breast cancer molecular subtypes. Breast Cancer Research, 2010, 12, R77.	5.0	159
125	Epigenetics and environment: a complex relationship. Journal of Applied Physiology, 2010, 109, 243-251.	2.5	191
126	DNA Methylation Profiles and Their Relationship with Cytogenetic Status in Adult Acute Myeloid Leukemia. PLoS ONE, 2010, 5, e12197.	2.5	73

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127	Epigenetic regulation of aging. Discovery Medicine, 2010, 10, 225-33.	0.5	48
128	The dynamic DNA methylomes of double-stranded DNA viruses associated with human cancer. Genome Research, 2009, 19, 438-451.	5.5	218
129	Epigenetic Inactivation of the Circadian Clock Gene BMAL1 in Hematologic Malignancies. Cancer Research, 2009, 69, 8447-8454.	0.9	161
130	A microarray-based DNA methylation study of glioblastoma multiforme. Epigenetics, 2009, 4, 255-264.	2.7	155
131	A TARBP2 mutation in human cancer impairs microRNA processing and DICER1 function. Nature Genetics, 2009, 41, 365-370.	21.4	355
132	9237 Array based CpG island methylation-profiling in acute myelogenous leukemia at diagnosis and relapse. European Journal of Cancer, Supplement, 2009, 7, 571.	2.2	0
133	Epigenomic Analysis of Acute Myeloid Leukemia Identifies Specific Patterns and Markes with Clinical and Biological Relevance.. Blood, 2009, 114, 2394-2394.	1.4	0
134	Epigenetic Inactivation of the Groucho Homologue Gene TLE1 in Hematologic Malignancies. Cancer Research, 2008, 68, 4116-4122.	0.9	50
135	Promoter DNA Hypermethylation and Gene Repression in Undifferentiated Arabidopsis Cells. PLoS ONE, 2008, 3, e3306.	2.5	99
136	Mecp2-Null Mice Provide New Neuronal Targets for Rett Syndrome. PLoS ONE, 2008, 3, e3669.	2.5	106
137	Cancer Genes Hypermethylated in Human Embryonic Stem Cells. PLoS ONE, 2008, 3, e3294.	2.5	75
138	An autoregulatory loop of nuclear corepressor 1 expression controls hepatocarcinoma invasion, growth and metastasis. Endocrine Abstracts, 0, , .	0.0	0