Esteban Ballestar

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3065800/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	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.	7.1	3,169
2	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.	21.4	1,710
3	Autophagy maintains stemness by preventing senescence. Nature, 2016, 529, 37-42.	27.8	1,013
4	Genetic Unmasking of an Epigenetically Silenced microRNA in Human Cancer Cells. Cancer Research, 2007, 67, 1424-1429.	0.9	883
5	Geriatric muscle stem cells switch reversible quiescence into senescence. Nature, 2014, 506, 316-321.	27.8	785
6	Mi-2 complex couples DNA methylation to chromatin remodelling and histone deacetylation. Nature Genetics, 1999, 23, 62-66.	21.4	720
7	Snail Mediates E-Cadherin Repression by the Recruitment of the Sin3A/Histone Deacetylase 1 (HDAC1)/HDAC2 Complex. Molecular and Cellular Biology, 2004, 24, 306-319.	2.3	672
8	Changes in the pattern of DNA methylation associate with twin discordance in systemic lupus erythematosus. Genome Research, 2010, 20, 170-179.	5.5	569
9	Notch Signaling Is Essential for Ventricular Chamber Development. Developmental Cell, 2007, 12, 415-429.	7.0	422
10	A DNA methylation fingerprint of 1628 human samples. Genome Research, 2012, 22, 407-419.	5.5	341
11	Methylâ€CpCâ€binding proteins. FEBS Journal, 2001, 268, 1-6.	0.2	300
12	Data integration in the era of omics: current and future challenges. BMC Systems Biology, 2014, 8, 11.	3.0	300
13	Methyl-CpG binding proteins identify novel sites of epigenetic inactivation in human cancer. EMBO Journal, 2003, 22, 6335-6345.	7.8	294
14	Epigenetic control of myeloid cell differentiation, identity and function. Nature Reviews Immunology, 2015, 15, 7-17.	22.7	292
15	DNA Methylation Polymorphisms Precede Any Histological Sign of Atherosclerosis in Mice Lacking Apolipoprotein E. Journal of Biological Chemistry, 2004, 279, 29147-29154.	3.4	279
16	A truncating mutation of HDAC2 in human cancers confers resistance to histone deacetylase inhibition. Nature Genetics, 2006, 38, 566-569.	21.4	254
17	The dynamic DNA methylomes of double-stranded DNA viruses associated with human cancer. Genome Research, 2009, 19, 438-451.	5.5	218
18	Genetic analysis of p38 MAP kinases in myogenesis: fundamental role of p38α in abrogating myoblast proliferation. EMBO Journal, 2007, 26, 1245-1256.	7.8	217

#	Article	IF	CITATIONS
19	The Epigenetic Face of Systemic Lupus Erythematosus. Journal of Immunology, 2006, 176, 7143-7147.	0.8	203
20	The affinity of different MBD proteins for a specific methylated locus depends on their intrinsic binding properties. Nucleic Acids Research, 2003, 31, 1765-1774.	14.5	202
21	Immunomodulatory effect of 5-azacytidine (5-azaC): potential role in the transplantation setting. Blood, 2010, 115, 107-121.	1.4	201
22	Allele-specific histone lysine methylation marks regulatory regions at imprinted mouse genes. EMBO Journal, 2002, 21, 6560-6570.	7.8	198
23	A Mouse Skin Multistage Carcinogenesis Model Reflects the Aberrant DNA Methylation Patterns of Human Tumors. Cancer Research, 2004, 64, 5527-5534.	0.9	193
24	PU.1 target genes undergo Tet2-coupled demethylation and DNMT3b-mediated methylation in monocyte-to-osteoclast differentiation. Genome Biology, 2013, 14, R99.	9.6	177
25	Methyl-DNA immunoprecipitation (MeDIP): Hunting down the DNA methylome. BioTechniques, 2008, 44, 35-43.	1.8	175
26	Human DNA Methyltransferase 1 Is Required for Maintenance of the Histone H3 Modification Pattern. Journal of Biological Chemistry, 2004, 279, 37175-37184.	3.4	171
27	The Wnt antagonist DICKKOPF-1 gene is induced by 1Â,25-dihydroxyvitamin D3 associated to the differentiation of human colon cancer cells. Carcinogenesis, 2007, 28, 1877-1884.	2.8	166
28	E47 phosphorylation by p38 MAPK promotes MyoD/E47 association and muscle-specific gene transcription. EMBO Journal, 2005, 24, 974-984.	7.8	165
29	Epigenetic Inactivation of the Circadian Clock Gene <i>BMAL1</i> in Hematologic Malignancies. Cancer Research, 2009, 69, 8447-8454.	0.9	161
30	Epigenetic alterations in autoimmune rheumatic diseases. Nature Reviews Rheumatology, 2011, 7, 263-271.	8.0	152
31	Effects of Rett Syndrome Mutations of the Methyl-CpG Binding Domain of the Transcriptional Repressor MeCP2 on Selectivity for Association with Methylated DNA. Biochemistry, 2000, 39, 7100-7106.	2.5	148
32	CSL–MAML-dependent Notch1 signaling controls T lineage–specific IL-7Rα gene expression in early human thymopoiesis and leukemia. Journal of Experimental Medicine, 2009, 206, 779-791.	8.5	145
33	A Robust and Highly Efficient Immune Cell Reprogramming System. Cell Stem Cell, 2009, 5, 554-566.	11.1	145
34	Identification of novel markers in rheumatoid arthritis through integrated analysis of DNA methylation and microRNA expression. Journal of Autoimmunity, 2013, 41, 6-16.	6.5	144
35	New insights into the biology and origin of mature aggressive B-cell lymphomas by combined epigenomic, genomic, and transcriptional profiling. Blood, 2009, 113, 2488-2497.	1.4	133
36	Epigenetic disruption of ribosomal RNA genes and nucleolar architecture in DNA methyltransferase 1 (Dnmt1) deficient cells. Nucleic Acids Research, 2007, 35, 2191-2198.	14.5	128

#	Article	IF	CITATIONS
37	IL-4 orchestrates STAT6-mediated DNA demethylation leading to dendritic cell differentiation. Genome Biology, 2016, 17, 4.	8.8	122
38	A Profile of Methyl-CpG Binding Domain Protein Occupancy of Hypermethylated Promoter CpG Islands of Tumor Suppressor Genes in Human Cancer. Cancer Research, 2006, 66, 8342-8346.	0.9	116
39	Prostaglandin E2 Leads to the Acquisition of DNMT3A-Dependent Tolerogenic Functions in Human Myeloid-Derived Suppressor Cells. Cell Reports, 2017, 21, 154-167.	6.4	116
40	Tolerogenic Dendritic Cells in Autoimmunity and Inflammatory Diseases. Trends in Immunology, 2021, 42, 59-75.	6.8	112
41	Core Histones Are Glutaminyl Substrates for Tissue Transglutaminase. Journal of Biological Chemistry, 1996, 271, 18817-18824.	3.4	109
42	The impact of chromatin in human cancer: linking DNA methylation to gene silencing. Carcinogenesis, 2002, 23, 1103-1109.	2.8	109
43	Promoter DNA Hypermethylation and Gene Repression in Undifferentiated Arabidopsis Cells. PLoS ONE, 2008, 3, e3306.	2.5	99
44	Epigenetic Signatures Associated with Different Levels of Differentiation Potential in Human Stem Cells. PLoS ONE, 2009, 4, e7809.	2.5	96
45	Epigenetics Lessons from Twins: Prospects for Autoimmune Disease. Clinical Reviews in Allergy and Immunology, 2010, 39, 30-41.	6.5	94
46	Discovery of Epigenetically Silenced Genes by Methylated DNA Immunoprecipitation in Colon Cancer Cells. Cancer Research, 2007, 67, 11481-11486.	0.9	89
47	Chapter 9 Epigenetic Gene Regulation in Cancer. Advances in Genetics, 2008, 61, 247-267.	1.8	86
48	Tet2 Facilitates the Derepression of Myeloid Target Genes during CEBPα-Induced Transdifferentiation of Pre-B Cells. Molecular Cell, 2012, 48, 266-276.	9.7	85
49	Environmental triggers and epigenetic deregulation in autoimmune disease. Discovery Medicine, 2011, 12, 535-45.	0.5	85
50	Epigenetic regulation of myogenesis. Epigenetics, 2009, 4, 541-550.	2.7	82
51	Monozygotic twins discordant for common variable immunodeficiency reveal impaired DNA demethylation during naÃ ⁻ ve-to-memory B-cell transition. Nature Communications, 2015, 6, 7335.	12.8	81
52	Integrative Analysis Reveals a Molecular Stratification of Systemic Autoimmune Diseases. Arthritis and Rheumatology, 2021, 73, 1073-1085.	5.6	81
53	NF-κB-direct activation of microRNAs with repressive effects on monocyte-specific genes is critical for osteoclast differentiation. Genome Biology, 2015, 16, 2.	8.8	77
54	Dioxin receptor and SLUG transcription factors regulate the insulator activity of B1 SINE retrotransposons via an RNA polymerase switch. Genome Research, 2011, 21, 422-432.	5.5	76

#	Article	IF	CITATIONS
55	Transcriptional profiling of MCF7 breast cancer cells in response to 5-Fluorouracil: Relationship with cell cycle changes and apoptosis, and identification of novel targets of p53. International Journal of Cancer, 2006, 119, 1164-1175.	5.1	74
56	Inflammatory cytokines and organ dysfunction associate with the aberrant DNA methylome of monocytes in sepsis. Genome Medicine, 2019, 11, 66.	8.2	73
57	The Chromatin Remodeling Complex Chd4/NuRD Controls Striated Muscle Identity and Metabolic Homeostasis. Cell Metabolism, 2016, 23, 881-892.	16.2	68
58	miRNAs as Therapeutic Targets in Inflammatory Disease. Trends in Pharmacological Sciences, 2019, 40, 853-865.	8.7	67
59	The impact of MECP2 mutations in the expression patterns of Rett syndrome patients. Human Genetics, 2005, 116, 91-104.	3.8	66
60	Methyl-CpG-binding proteins in cancer: blaming the DNA methylation messenger. Biochemistry and Cell Biology, 2005, 83, 374-384.	2.0	65
61	Epigenetic interplay between immune, stromal and cancer cells in the tumor microenvironment. Clinical Immunology, 2018, 196, 64-71.	3.2	61
62	DNA demethylation of inflammasome-associated genes is enhanced in patients with cryopyrin-associated periodic syndromes. Journal of Allergy and Clinical Immunology, 2017, 139, 202-211.e6.	2.9	57
63	Transcriptional targets of the chromatin-remodelling factor SMARCA4/BRG1 in lung cancer cells. Human Molecular Genetics, 2005, 14, 973-982.	2.9	55
64	Sampling time-dependent artifacts in single-cell genomics studies. Genome Biology, 2020, 21, 112.	8.8	55
65	Unmasking of epigenetically silenced candidate tumor suppressor genes by removal of methyl-CpG-binding domain proteins. Oncogene, 2008, 27, 3556-3566.	5.9	54
66	Understanding the Relevance of DNA Methylation Changes in Immune Differentiation and Disease. Genes, 2020, 11, 110.	2.4	54
67	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
68	An Introduction to Epigenetics. Advances in Experimental Medicine and Biology, 2011, 711, 1-11.	1.6	52
69	Epigenetic Inactivation of the Groucho Homologue Gene TLE1 in Hematologic Malignancies. Cancer Research, 2008, 68, 4116-4122.	0.9	50
70	Clinical value of DNA methylation markers in autoimmune rheumatic diseases. Nature Reviews Rheumatology, 2020, 16, 514-524.	8.0	48
71	Long-Range Epigenetic Silencing Associates with Deregulation of Ikaros Targets in Colorectal Cancer Cells. Molecular Cancer Research, 2011, 9, 1139-1151.	3.4	47
72	Genetic and Epigenetic Determinants in Autoinflammatory Diseases. Frontiers in Immunology, 2017, 8, 318.	4.8	47

#	Article	IF	CITATIONS
73	Inflammatory cytokines shape a changing DNA methylome in monocytes mirroring disease activity in rheumatoid arthritis. Annals of the Rheumatic Diseases, 2019, 78, 1505-1516.	0.9	47
74	New insights into the epigenetics of inflammatory rheumatic diseases. Nature Reviews Rheumatology, 2017, 13, 593-605.	8.0	46
75	Combinatorial effects of splice variants modulate function of Aiolos. Journal of Cell Science, 2007, 120, 2619-2630.	2.0	45
76	Specific hypermethylation of LINE-1 elements during abnormal overgrowth and differentiation of human placenta. Oncogene, 2007, 26, 2518-2524.	5.9	40
77	The p38 SAPK Is Recruited to Chromatin via Its Interaction with Transcription Factors. Journal of Biological Chemistry, 2010, 285, 31819-31828.	3.4	39
78	In vivo conditional deletion of HDAC7 reveals its requirement to establish proper B lymphocyte identity and development. Journal of Experimental Medicine, 2016, 213, 2591-2601.	8.5	39
79	SIRT1/2 orchestrate acquisition of DNA methylation and loss of histone H3 activating marks to prevent premature activation of inflammatory genes in macrophages. Nucleic Acids Research, 2020, 48, 665-681.	14.5	39
80	A Drosophila MBD family member is a transcriptional corepressor associated with specific genes. FEBS Journal, 2001, 268, 5397-5406.	0.2	37
81	Pre-B cell to macrophage transdifferentiation without significant promoter DNA methylation changes. Nucleic Acids Research, 2012, 40, 1954-1968.	14.5	37
82	Recruitment of CREB1 and Histone Deacetylase 2 (HDAC2) to the Mouse Ltbp-1 Promoter Regulates its Constitutive Expression in a Dioxin Receptor-dependent Manner. Journal of Molecular Biology, 2008, 380, 1-16.	4.2	36
83	TET2- and TDG-mediated changes are required for the acquisition of distinct histone modifications in divergent terminal differentiation of myeloid cells. Nucleic Acids Research, 2017, 45, 10002-10017.	14.5	36
84	Release of Hypoacetylated and Trimethylated Histone H4 Is an Epigenetic Marker of Early Apoptosis. Journal of Biological Chemistry, 2006, 281, 13540-13547.	3.4	34
85	Epstein–Barr virus-mediated transformation of B cells induces global chromatin changes independent to the acquisition of proliferation. Nucleic Acids Research, 2014, 42, 249-263.	14.5	34
86	Conformational Changes in the Nucleosome Followed by the Selective Accessibility of Histone Glutamines in the Transglutaminase Reaction:  Effects of Ionic Strength. Biochemistry, 2001, 40, 1922-1929.	2.5	33
87	The Epigenetic Breakdown of Cancer Cells: From DNA Methylation to Histone Modifications. , 2005, 38, 169-181.		33
88	Transforming pathways unleashed by a HDAC2 mutation in human cancer. Oncogene, 2008, 27, 4008-4012.	5.9	33
89	<i>BCRâ€ABL1</i> â€induced expression of <i>HSPA8</i> promotes cell survival in chronic myeloid leukaemia. British Journal of Haematology, 2008, 142, 571-582. 	2.5	33
90	Chromatin Immunoprecipitation. Methods in Molecular Biology, 2014, 1094, 309-318.	0.9	32

#	Article	IF	CITATIONS
91	Impaired recruitment of the histone methyltransferase DOT1L contributes to the incomplete reactivation of tumor suppressor genes upon DNA demethylation. Oncogene, 2009, 28, 4212-4224.	5.9	29
92	Chromatin-wide and transcriptome profiling integration uncovers p38î± MAPK as a global regulator of skeletal muscle differentiation. Skeletal Muscle, 2016, 6, 9.	4.2	29
93	Targeting aberrant DNA methylation in mesenchymal stromal cells as a treatment for myeloma bone disease. Nature Communications, 2021, 12, 421.	12.8	29
94	Epigenomics and transcriptomics of systemic sclerosis CD4+ T cells reveal long-range dysregulation of key inflammatory pathways mediated by disease-associated susceptibility loci. Genome Medicine, 2020, 12, 81.	8.2	28
95	Vitamin D receptor, STAT3, and TET2 cooperate to establish tolerogenesis. Cell Reports, 2022, 38, 110244.	6.4	28
96	NF-κB directly mediates epigenetic deregulation of common microRNAs in Epstein-Barr virus-mediated transformation of B-cells and in lymphomas. Nucleic Acids Research, 2014, 42, 11025-11039.	14.5	27
97	Epigenetic connections between autoimmune disorders and haematological malignancies. Trends in Immunology, 2008, 29, 616-623.	6.8	26
98	C/EBPa-Mediated Activation of MicroRNAs 34a and 223 Inhibits Lef1 Expression To Achieve Efficient Reprogramming into Macrophages. Molecular and Cellular Biology, 2014, 34, 1145-1157.	2.3	26
99	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. Scientific Data, 2019, 6, 256.	5.3	26
100	Epigenome-Wide Comparative Study Reveals Key Differences Between Mixed Connective Tissue Disease and Related Systemic Autoimmune Diseases. Frontiers in Immunology, 2019, 10, 1880.	4.8	26
101	In vivo analysis of DNA methylation patterns recognized by specific proteins: coupling ChIP and bisulfite analysis. BioTechniques, 2004, 37, 666-673.	1.8	25
102	Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses. Nature Communications, 2022, 13, 1779.	12.8	25
103	Epigenomic deregulation in the immune system. Epigenomics, 2011, 3, 697-713.	2.1	24
104	Stage-specific chromosomal association of Drosophila dMBD2/3 during genome activation. Chromosoma, 2002, 111, 13-21.	2.2	23
105	Capillary electrophoresis-based method to quantitate DNA–protein interactions. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2003, 789, 431-435.	2.3	23
106	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
107	Use of the Transglutaminase Reaction To Study the Dissociation of Histone N-Terminal Tails from DNA in Nucleosome Core Particlesâ€. Biochemistry, 1997, 36, 5963-5969.	2.5	22
108	Identification of (1H)-pyrroles as histone deacetylase inhibitors with antitumoral activity. Oncogene, 2009, 28, 1477-1484.	5.9	22

#	Article	IF	CITATIONS
109	Microglial innate memory and epigenetic reprogramming in neurological disorders. Progress in Neurobiology, 2021, 200, 101971.	5.7	21
110	Methylome and transcriptome profiling of giant cell arteritis monocytes reveals novel pathways involved in disease pathogenesis and molecular response to glucocorticoids. Annals of the Rheumatic Diseases, 2022, 81, 1290-1300.	0.9	20
111	Impaired CpG Demethylation in Common Variable Immunodeficiency Associates With B Cell Phenotype and Proliferation Rate. Frontiers in Immunology, 2019, 10, 878.	4.8	19
112	shinyÉPICo: a graphical pipeline to analyze Illumina DNA methylation arrays. Bioinformatics, 2021, 37, 257-259.	4.1	19
113	DNA methylation signatures in Sjögren syndrome. Nature Reviews Rheumatology, 2016, 12, 565-566.	8.0	18
114	Coordinated glucocorticoid receptor and MAFB action induces tolerogenesis and epigenome remodeling in dendritic cells. Nucleic Acids Research, 2022, 50, 108-126.	14.5	17
115	Prediction of the Progression of Undifferentiated Arthritis to Rheumatoid Arthritis Using DNA Methylation Profiling. Arthritis and Rheumatology, 2021, 73, 2229-2239.	5.6	16
116	Integrative epigenomics in Sjögren´s syndrome reveals novel pathways and a strong interaction between the HLA, autoantibodies and the interferon signature. Scientific Reports, 2021, 11, 23292.	3.3	16
117	Epigenetic regulation of PRAME in acute myeloid leukemia is different compared to CD34+ cells from healthy donors: Effect of 5-AZA treatment. Leukemia Research, 2012, 36, 895-899.	0.8	14
118	JAK2-STAT Epigenetically Regulates Tolerized Genes in Monocytes in the First Encounter With Gram-Negative Bacterial Endotoxins in Sepsis. Frontiers in Immunology, 2021, 12, 734652.	4.8	13
119	Epilepsy progression is associated with cumulative DNA methylation changes in inflammatory genes. Progress in Neurobiology, 2022, 209, 102207.	5.7	13
120	Epigenetics of Dendritic Cells in Tumor Immunology. Cancers, 2022, 14, 1179.	3.7	13
121	Epigenetic mechanisms of myeloid differentiation in the tumor microenvironment. Current Opinion in Pharmacology, 2017, 35, 20-29.	3.5	12
122	SnapShot: The Human DNA Methylome in Health and Disease. Cell, 2008, 135, 1144-1144.e1.	28.9	11
123	The synovial and blood monocyte DNA methylomes mirror prognosis, evolution, and treatment in early arthritis. JCI Insight, 2022, 7, .	5.0	11
124	Dissecting Epigenetic Dysregulation of Primary Antibody Deficiencies. Journal of Clinical Immunology, 2016, 36, 48-56.	3.8	10
125	Activation-induced cytidine deaminase targets SUV4-20-mediated histone H4K20 trimethylation to class-switch recombination sites. Scientific Reports, 2017, 7, 7594.	3.3	10
126	Autophagy maintains stemness by preventing senescence. Nature, 2016, 534, S3-S4.	27.8	9

#	ARTICLE	IF	CITATIONS
127	A Role for Methyl-CpG Binding Domain Protein 2 in the Modulation of the Estrogen Response of pS2/TFF1 Gene. PLoS ONE, 2010, 5, e9665.	2.5	9
128	What can clinical immunology learn from inborn errors of epigenetic regulators?. Journal of Allergy and Clinical Immunology, 2021, 147, 1602-1618.	2.9	8
129	Gains of <scp>DNA</scp> methylation in myeloid terminal differentiation are dispensable for gene silencing but influence the differentiated phenotype. FEBS Journal, 2015, 282, 1815-1825.	4.7	5
130	Activation-induced deaminase is critical for the establishment of DNA methylation patterns prior to the germinal center reaction. Nucleic Acids Research, 2021, 49, 5057-5073.	14.5	5
131	What can we learn from DNA methylation studies in lupus?. Clinical Immunology, 2022, 234, 108920.	3.2	3
132	Epigenetic alterations in autoimmune disease. Journal of Translational Medicine, 2011, 9, .	4.4	1
133	Insights into RA pathogenesis from DNA methylome analysis. Nature Reviews Rheumatology, 2015, 11, 386-388.	8.0	1
134	Disruption of Epigenetic Mechanisms in Autoimmune Syndromes. , 2012, , 349-378.		1
135	Epigenetic Basis of Autoimmune Disorders in Humans. , 2012, , 205-223.		0
136	Epigenetic Deregulation in Autoimmune Disease. , 2016, , 235-254.		0
137	Epigenetics in Autoinflammation. , 2019, , 49-60.		0
138	Epigenetic deregulation of immune cells in autoimmune and autoinflammatory diseases. , 2020, , 253-267.		0
139	Vitamin D Receptor, STAT3 and TET2 Cooperate to Establish Tolerogenesis. SSRN Electronic Journal, 0, , \cdot	0.4	0
140	Qualitative Determination of 5-Methylcytosine and Other Components of the DNA Methylation Machinery. , 2004, , 121-136.		0
141	Examining DNA–Protein Interactions with Genome-Wide Chromatin Immunoprecipitation Analysis. , 2010, , 33-45.		0
142	Effect of Demethylating Agents (5-Azacytidine/5-AzaC) On the Immune Response. Blood, 2010, 116, 2771-2771.	1.4	0
143	Effect of 5-Azacytidine (5-AzaC) In the Expression of PRAME In Acute Myeloid Leukemia (AML). Blood, 2010, 116, 3615-3615.	1.4	0

A Changing Epigenome in Health and Disease. , 2009, , 369-384.

0