

# Esteban Ballestar

## List of Publications by Year in descending order

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144  
papers

19,672  
citations

23544

58  
h-index

12585

132  
g-index

161  
all docs

161  
docs citations

161  
times ranked

26842  
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	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
3	Autophagy maintains stemness by preventing senescence. Nature, 2016, 529, 37-42.	13.7	1,013
4	Genetic Unmasking of an Epigenetically Silenced microRNA in Human Cancer Cells. Cancer Research, 2007, 67, 1424-1429.	0.4	883
5	Geriatric muscle stem cells switch reversible quiescence into senescence. Nature, 2014, 506, 316-321.	13.7	785
6	Mi-2 complex couples DNA methylation to chromatin remodelling and histone deacetylation. Nature Genetics, 1999, 23, 62-66.	9.4	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.	1.1	672
8	Changes in the pattern of DNA methylation associate with twin discordance in systemic lupus erythematosus. Genome Research, 2010, 20, 170-179.	2.4	569
9	Notch Signaling Is Essential for Ventricular Chamber Development. Developmental Cell, 2007, 12, 415-429.	3.1	422
10	A DNA methylation fingerprint of 1628 human samples. Genome Research, 2012, 22, 407-419.	2.4	341
11	Methyl-CpG-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.	3.5	294
14	Epigenetic control of myeloid cell differentiation, identity and function. Nature Reviews Immunology, 2015, 15, 7-17.	10.6	292
15	DNA Methylation Polymorphisms Precede Any Histological Sign of Atherosclerosis in Mice Lacking Apolipoprotein E. Journal of Biological Chemistry, 2004, 279, 29147-29154.	1.6	279
16	A truncating mutation of HDAC2 in human cancers confers resistance to histone deacetylase inhibition. Nature Genetics, 2006, 38, 566-569.	9.4	254
17	The dynamic DNA methylomes of double-stranded DNA viruses associated with human cancer. Genome Research, 2009, 19, 438-451.	2.4	218
18	Genetic analysis of p38 MAP kinases in myogenesis: fundamental role of p38 $\alpha$ in abrogating myoblast proliferation. EMBO Journal, 2007, 26, 1245-1256.	3.5	217

#	ARTICLE	IF	CITATIONS
19	The Epigenetic Face of Systemic Lupus Erythematosus. <i>Journal of Immunology</i> , 2006, 176, 7143-7147.	0.4	203
20	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
21	Immunomodulatory effect of 5-azacytidine (5-azaC): potential role in the transplantation setting. <i>Blood</i> , 2010, 115, 107-121.	0.6	201
22	Allele-specific histone lysine methylation marks regulatory regions at imprinted mouse genes. <i>EMBO Journal</i> , 2002, 21, 6560-6570.	3.5	198
23	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
24	PU.1 target genes undergo Tet2-coupled demethylation and DNMT3b-mediated methylation in monocyte-to-osteoclast differentiation. <i>Genome Biology</i> , 2013, 14, R99.	13.9	177
25	Methyl-DNA immunoprecipitation (MeDIP): Hunting down the DNA methylome. <i>BioTechniques</i> , 2008, 44, 35-43.	0.8	175
26	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
27	The Wnt antagonist DICKKOPF-1 gene is induced by 1 $\alpha$ ,25-dihydroxyvitamin D3 associated to the differentiation of human colon cancer cells. <i>Carcinogenesis</i> , 2007, 28, 1877-1884.	1.3	166
28	E47 phosphorylation by p38 MAPK promotes MyoD/E47 association and muscle-specific gene transcription. <i>EMBO Journal</i> , 2005, 24, 974-984.	3.5	165
29	Epigenetic Inactivation of the Circadian Clock Gene <i>BMAL1</i> in Hematologic Malignancies. <i>Cancer Research</i> , 2009, 69, 8447-8454.	0.4	161
30	Epigenetic alterations in autoimmune rheumatic diseases. <i>Nature Reviews Rheumatology</i> , 2011, 7, 263-271.	3.5	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. <i>Biochemistry</i> , 2000, 39, 7100-7106.	1.2	148
32	CSL-dependent MAML-dependent Notch1 signaling controls T lineage-specific IL-7R $\alpha$ gene expression in early human thymopoiesis and leukemia. <i>Journal of Experimental Medicine</i> , 2009, 206, 779-791.	4.2	145
33	A Robust and Highly Efficient Immune Cell Reprogramming System. <i>Cell Stem Cell</i> , 2009, 5, 554-566.	5.2	145
34	Identification of novel markers in rheumatoid arthritis through integrated analysis of DNA methylation and microRNA expression. <i>Journal of Autoimmunity</i> , 2013, 41, 6-16.	3.0	144
35	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
36	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

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37	IL-4 orchestrates STAT6-mediated DNA demethylation leading to dendritic cell differentiation. <i>Genome Biology</i> , 2016, 17, 4.	3.8	122
38	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
39	Prostaglandin E2 Leads to the Acquisition of DNMT3A-Dependent Tolerogenic Functions in Human Myeloid-Derived Suppressor Cells. <i>Cell Reports</i> , 2017, 21, 154-167.	2.9	116
40	Tolerogenic Dendritic Cells in Autoimmunity and Inflammatory Diseases. <i>Trends in Immunology</i> , 2021, 42, 59-75.	2.9	112
41	Core Histones Are Glutaminy Substrates for Tissue Transglutaminase. <i>Journal of Biological Chemistry</i> , 1996, 271, 18817-18824.	1.6	109
42	The impact of chromatin in human cancer: linking DNA methylation to gene silencing. <i>Carcinogenesis</i> , 2002, 23, 1103-1109.	1.3	109
43	Promoter DNA Hypermethylation and Gene Repression in Undifferentiated Arabidopsis Cells. <i>PLoS ONE</i> , 2008, 3, e3306.	1.1	99
44	Epigenetic Signatures Associated with Different Levels of Differentiation Potential in Human Stem Cells. <i>PLoS ONE</i> , 2009, 4, e7809.	1.1	96
45	Epigenetics Lessons from Twins: Prospects for Autoimmune Disease. <i>Clinical Reviews in Allergy and Immunology</i> , 2010, 39, 30-41.	2.9	94
46	Discovery of Epigenetically Silenced Genes by Methylated DNA Immunoprecipitation in Colon Cancer Cells. <i>Cancer Research</i> , 2007, 67, 11481-11486.	0.4	89
47	Chapter 9 Epigenetic Gene Regulation in Cancer. <i>Advances in Genetics</i> , 2008, 61, 247-267.	0.8	86
48	Tet2 Facilitates the Derepression of Myeloid Target Genes during CEBP $\beta$ -Induced Transdifferentiation of Pre-B Cells. <i>Molecular Cell</i> , 2012, 48, 266-276.	4.5	85
49	Environmental triggers and epigenetic deregulation in autoimmune disease. <i>Discovery Medicine</i> , 2011, 12, 535-45.	0.5	85
50	Epigenetic regulation of myogenesis. <i>Epigenetics</i> , 2009, 4, 541-550.	1.3	82
51	Monozygotic twins discordant for common variable immunodeficiency reveal impaired DNA demethylation during na $\text{I}^{\text{ve}}$ -to-memory B-cell transition. <i>Nature Communications</i> , 2015, 6, 7335.	5.8	81
52	Integrative Analysis Reveals a Molecular Stratification of Systemic Autoimmune Diseases. <i>Arthritis and Rheumatology</i> , 2021, 73, 1073-1085.	2.9	81
53	NF- $\kappa$ B-direct activation of microRNAs with repressive effects on monocyte-specific genes is critical for osteoclast differentiation. <i>Genome Biology</i> , 2015, 16, 2.	3.8	77
54	Dioxin receptor and SLUG transcription factors regulate the insulator activity of B1 SINE retrotransposons via an RNA polymerase switch. <i>Genome Research</i> , 2011, 21, 422-432.	2.4	76

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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. <i>International Journal of Cancer</i> , 2006, 119, 1164-1175.	2.3	74
56	Inflammatory cytokines and organ dysfunction associate with the aberrant DNA methylome of monocytes in sepsis. <i>Genome Medicine</i> , 2019, 11, 66.	3.6	73
57	The Chromatin Remodeling Complex Chd4/NuRD Controls Striated Muscle Identity and Metabolic Homeostasis. <i>Cell Metabolism</i> , 2016, 23, 881-892.	7.2	68
58	miRNAs as Therapeutic Targets in Inflammatory Disease. <i>Trends in Pharmacological Sciences</i> , 2019, 40, 853-865.	4.0	67
59	The impact of MECP2 mutations in the expression patterns of Rett syndrome patients. <i>Human Genetics</i> , 2005, 116, 91-104.	1.8	66
60	Methyl-CpG-binding proteins in cancer: blaming the DNA methylation messenger. <i>Biochemistry and Cell Biology</i> , 2005, 83, 374-384.	0.9	65
61	Epigenetic interplay between immune, stromal and cancer cells in the tumor microenvironment. <i>Clinical Immunology</i> , 2018, 196, 64-71.	1.4	61
62	DNA demethylation of inflammasome-associated genes is enhanced in patients with cryopyrin-associated periodic syndromes. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 202-211.e6.	1.5	57
63	Transcriptional targets of the chromatin-remodelling factor SMARCA4/BRG1 in lung cancer cells. <i>Human Molecular Genetics</i> , 2005, 14, 973-982.	1.4	55
64	Sampling time-dependent artifacts in single-cell genomics studies. <i>Genome Biology</i> , 2020, 21, 112.	3.8	55
65	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
66	Understanding the Relevance of DNA Methylation Changes in Immune Differentiation and Disease. <i>Genes</i> , 2020, 11, 110.	1.0	54
67	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
68	An Introduction to Epigenetics. <i>Advances in Experimental Medicine and Biology</i> , 2011, 711, 1-11.	0.8	52
69	Epigenetic Inactivation of the Groucho Homologue Gene TLE1 in Hematologic Malignancies. <i>Cancer Research</i> , 2008, 68, 4116-4122.	0.4	50
70	Clinical value of DNA methylation markers in autoimmune rheumatic diseases. <i>Nature Reviews Rheumatology</i> , 2020, 16, 514-524.	3.5	48
71	Long-Range Epigenetic Silencing Associates with Deregulation of Ikaros Targets in Colorectal Cancer Cells. <i>Molecular Cancer Research</i> , 2011, 9, 1139-1151.	1.5	47
72	Genetic and Epigenetic Determinants in Autoinflammatory Diseases. <i>Frontiers in Immunology</i> , 2017, 8, 318.	2.2	47

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73	Inflammatory cytokines shape a changing DNA methylome in monocytes mirroring disease activity in rheumatoid arthritis. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 1505-1516.	0.5	47
74	New insights into the epigenetics of inflammatory rheumatic diseases. <i>Nature Reviews Rheumatology</i> , 2017, 13, 593-605.	3.5	46
75	Combinatorial effects of splice variants modulate function of Aiolos. <i>Journal of Cell Science</i> , 2007, 120, 2619-2630.	1.2	45
76	Specific hypermethylation of LINE-1 elements during abnormal overgrowth and differentiation of human placenta. <i>Oncogene</i> , 2007, 26, 2518-2524.	2.6	40
77	The p38 SAPK Is Recruited to Chromatin via Its Interaction with Transcription Factors. <i>Journal of Biological Chemistry</i> , 2010, 285, 31819-31828.	1.6	39
78	In vivo conditional deletion of HDAC7 reveals its requirement to establish proper B lymphocyte identity and development. <i>Journal of Experimental Medicine</i> , 2016, 213, 2591-2601.	4.2	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. <i>Nucleic Acids Research</i> , 2020, 48, 665-681.	6.5	39
80	A Drosophila MBD family member is a transcriptional corepressor associated with specific genes. <i>FEBS Journal</i> , 2001, 268, 5397-5406.	0.2	37
81	Pre-B cell to macrophage transdifferentiation without significant promoter DNA methylation changes. <i>Nucleic Acids Research</i> , 2012, 40, 1954-1968.	6.5	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. <i>Journal of Molecular Biology</i> , 2008, 380, 1-16.	2.0	36
83	TET2- and TDG-mediated changes are required for the acquisition of distinct histone modifications in divergent terminal differentiation of myeloid cells. <i>Nucleic Acids Research</i> , 2017, 45, 10002-10017.	6.5	36
84	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
85	Epstein-Barr virus-mediated transformation of B cells induces global chromatin changes independent to the acquisition of proliferation. <i>Nucleic Acids Research</i> , 2014, 42, 249-263.	6.5	34
86	Conformational Changes in the Nucleosome Followed by the Selective Accessibility of Histone Glutamines in the Transglutaminase Reaction: Effects of Ionic Strength. <i>Biochemistry</i> , 2001, 40, 1922-1929.	1.2	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. <i>Oncogene</i> , 2008, 27, 4008-4012.	2.6	33
89	<i>Bcr</i> -induced expression of <i>HSPA8</i> promotes cell survival in chronic myeloid leukaemia. <i>British Journal of Haematology</i> , 2008, 142, 571-582.	1.2	33
90	Chromatin Immunoprecipitation. <i>Methods in Molecular Biology</i> , 2014, 1094, 309-318.	0.4	32

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91	Impaired recruitment of the histone methyltransferase DOT1L contributes to the incomplete reactivation of tumor suppressor genes upon DNA demethylation. <i>Oncogene</i> , 2009, 28, 4212-4224.	2.6	29
92	Chromatin-wide and transcriptome profiling integration uncovers p38 $\beta$ MAPK as a global regulator of skeletal muscle differentiation. <i>Skeletal Muscle</i> , 2016, 6, 9.	1.9	29
93	Targeting aberrant DNA methylation in mesenchymal stromal cells as a treatment for myeloma bone disease. <i>Nature Communications</i> , 2021, 12, 421.	5.8	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. <i>Genome Medicine</i> , 2020, 12, 81.	3.6	28
95	Vitamin D receptor, STAT3, and TET2 cooperate to establish tolerogenesis. <i>Cell Reports</i> , 2022, 38, 110244.	2.9	28
96	NF- $\kappa$ B directly mediates epigenetic deregulation of common microRNAs in Epstein-Barr virus-mediated transformation of B-cells and in lymphomas. <i>Nucleic Acids Research</i> , 2014, 42, 11025-11039.	6.5	27
97	Epigenetic connections between autoimmune disorders and haematological malignancies. <i>Trends in Immunology</i> , 2008, 29, 616-623.	2.9	26
98	C/EBP $\alpha$ -Mediated Activation of MicroRNAs 34a and 223 Inhibits Lef1 Expression To Achieve Efficient Reprogramming into Macrophages. <i>Molecular and Cellular Biology</i> , 2014, 34, 1145-1157.	1.1	26
99	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. <i>Scientific Data</i> , 2019, 6, 256.	2.4	26
100	Epigenome-Wide Comparative Study Reveals Key Differences Between Mixed Connective Tissue Disease and Related Systemic Autoimmune Diseases. <i>Frontiers in Immunology</i> , 2019, 10, 1880.	2.2	26
101	In vivo analysis of DNA methylation patterns recognized by specific proteins: coupling ChIP and bisulfite analysis. <i>BioTechniques</i> , 2004, 37, 666-673.	0.8	25
102	Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses. <i>Nature Communications</i> , 2022, 13, 1779.	5.8	25
103	Epigenomic deregulation in the immune system. <i>Epigenomics</i> , 2011, 3, 697-713.	1.0	24
104	Stage-specific chromosomal association of Drosophila dMBD2/3 during genome activation. <i>Chromosoma</i> , 2002, 111, 13-21.	1.0	23
105	Capillary electrophoresis-based method to quantitate DNA-protein interactions. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2003, 789, 431-435.	1.2	23
106	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
107	Use of the Transglutaminase Reaction To Study the Dissociation of Histone N-Terminal Tails from DNA in Nucleosome Core Particles. <i>Biochemistry</i> , 1997, 36, 5963-5969.	1.2	22
108	Identification of (1H)-pyrroles as histone deacetylase inhibitors with antitumoral activity. <i>Oncogene</i> , 2009, 28, 1477-1484.	2.6	22

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109	Microglial innate memory and epigenetic reprogramming in neurological disorders. <i>Progress in Neurobiology</i> , 2021, 200, 101971.	2.8	21
110	Methylome and transcriptome profiling of giant cell arteritis monocytes reveals novel pathways involved in disease pathogenesis and molecular response to glucocorticoids. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, 1290-1300.	0.5	20
111	Impaired CpG Demethylation in Common Variable Immunodeficiency Associates With B Cell Phenotype and Proliferation Rate. <i>Frontiers in Immunology</i> , 2019, 10, 878.	2.2	19
112	shinyPICo: a graphical pipeline to analyze Illumina DNA methylation arrays. <i>Bioinformatics</i> , 2021, 37, 257-259.	1.8	19
113	DNA methylation signatures in Sjögren syndrome. <i>Nature Reviews Rheumatology</i> , 2016, 12, 565-566.	3.5	18
114	Coordinated glucocorticoid receptor and MAFB action induces tolerogenesis and epigenome remodeling in dendritic cells. <i>Nucleic Acids Research</i> , 2022, 50, 108-126.	6.5	17
115	Prediction of the Progression of Undifferentiated Arthritis to Rheumatoid Arthritis Using DNA Methylation Profiling. <i>Arthritis and Rheumatology</i> , 2021, 73, 2229-2239.	2.9	16
116	Integrative epigenomics in Sjögren's syndrome reveals novel pathways and a strong interaction between the HLA, autoantibodies and the interferon signature. <i>Scientific Reports</i> , 2021, 11, 23292.	1.6	16
117	Epigenetic regulation of PRAME in acute myeloid leukemia is different compared to CD34+ cells from healthy donors: Effect of 5-AZA treatment. <i>Leukemia Research</i> , 2012, 36, 895-899.	0.4	14
118	JAK2-STAT Epigenetically Regulates Tolerized Genes in Monocytes in the First Encounter With Gram-Negative Bacterial Endotoxins in Sepsis. <i>Frontiers in Immunology</i> , 2021, 12, 734652.	2.2	13
119	Epilepsy progression is associated with cumulative DNA methylation changes in inflammatory genes. <i>Progress in Neurobiology</i> , 2022, 209, 102207.	2.8	13
120	Epigenetics of Dendritic Cells in Tumor Immunology. <i>Cancers</i> , 2022, 14, 1179.	1.7	13
121	Epigenetic mechanisms of myeloid differentiation in the tumor microenvironment. <i>Current Opinion in Pharmacology</i> , 2017, 35, 20-29.	1.7	12
122	SnapShot: The Human DNA Methylome in Health and Disease. <i>Cell</i> , 2008, 135, 1144-1144.e1.	13.5	11
123	The synovial and blood monocyte DNA methylomes mirror prognosis, evolution, and treatment in early arthritis. <i>JCI Insight</i> , 2022, 7, .	2.3	11
124	Dissecting Epigenetic Dysregulation of Primary Antibody Deficiencies. <i>Journal of Clinical Immunology</i> , 2016, 36, 48-56.	2.0	10
125	Activation-induced cytidine deaminase targets SUV4-20-mediated histone H4K20 trimethylation to class-switch recombination sites. <i>Scientific Reports</i> , 2017, 7, 7594.	1.6	10
126	Autophagy maintains stemness by preventing senescence. <i>Nature</i> , 2016, 534, S3-S4.	13.7	9



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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.	1.1	9
128	What can clinical immunology learn from inborn errors of epigenetic regulators?. Journal of Allergy and Clinical Immunology, 2021, 147, 1602-1618.	1.5	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.	2.2	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.	6.5	5
131	What can we learn from DNA methylation studies in lupus?. Clinical Immunology, 2022, 234, 108920.	1.4	3
132	Epigenetic alterations in autoimmune disease. Journal of Translational Medicine, 2011, 9, .	1.8	1
133	Insights into RA pathogenesis from DNA methylome analysis. Nature Reviews Rheumatology, 2015, 11, 386-388.	3.5	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, , .	0.4	0
140	Qualitative Determination of 5-Methylcytosine and Other Components of the DNA Methylation Machinery. , 2004, , 121-136.		0
141	Examining DNAâ€™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.	0.6	0
143	Effect of 5-Azacytidine (5-AzaC) In the Expression of PRAME In Acute Myeloid Leukemia (AML). Blood, 2010, 116, 3615-3615.	0.6	0
144	A Changing Epigenome in Health and Disease. , 2009, , 369-384.		0