

Javier RodrÃ-guez-Ubreva

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

3,327
citations

471371

17
h-index

610775

24
g-index

26
all docs

26
docs citations

26
times ranked

6358
citing authors

#	ARTICLE	IF	CITATIONS
1	The synovial and blood monocyte DNA methylomes mirror prognosis, evolution, and treatment in early arthritis. <i>JCI Insight</i> , 2022, 7, .	2.3	11
2	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
3	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
4	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
5	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
6	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. <i>Scientific Data</i> , 2019, 6, 256.	2.4	26
7	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
8	Epigenetic interplay between immune, stromal and cancer cells in the tumor microenvironment. <i>Clinical Immunology</i> , 2018, 196, 64-71.	1.4	61
9	Epigenetic mechanisms of myeloid differentiation in the tumor microenvironment. <i>Current Opinion in Pharmacology</i> , 2017, 35, 20-29.	1.7	12
10	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
11	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
12	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
13	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
14	Dissecting Epigenetic Dysregulation of Primary Antibody Deficiencies. <i>Journal of Clinical Immunology</i> , 2016, 36, 48-56.	2.0	10
15	IL-4 orchestrates STAT6-mediated DNA demethylation leading to dendritic cell differentiation. <i>Genome Biology</i> , 2016, 17, 4.	3.8	122
16	Autophagy maintains stemness by preventing senescence. <i>Nature</i> , 2016, 529, 37-42.	18.7	1,013
17	Monozygotic twins discordant for common variable immunodeficiency reveal impaired DNA demethylation during naïve-to-memory B-cell transition. <i>Nature Communications</i> , 2015, 6, 7335.	5.8	81
18	NF- κ 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

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19	Geriatric muscle stem cells switch reversible quiescence into senescence. <i>Nature</i> , 2014, 506, 316-321.	13.7	785
20	Chromatin Immunoprecipitation. <i>Methods in Molecular Biology</i> , 2014, 1094, 309-318.	0.4	32
21	C/EBPa-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
22	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
23	Pre-B cell to macrophage transdifferentiation without significant promoter DNA methylation changes. <i>Nucleic Acids Research</i> , 2012, 40, 1954-1968.	6.5	37
24	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