

Biola Maria Javierre

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

5,210
citations

218381

26
h-index

360668

35
g-index

48
all docs

48
docs citations

48
times ranked

10319
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. <i>Nature Communications</i> , 2021, 12, 2298.	5.8	32
2	MAX mutant small-cell lung cancers exhibit impaired activities of MGA-dependent noncanonical polycomb repressive complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2024824118.	3.3	9
3	B-cell leukemia transdifferentiation to macrophage involves reconfiguration of DNA methylation for long-range regulation. <i>Leukemia</i> , 2020, 34, 1158-1162.	3.3	13
4	From Loops to Looks: Transcription Factors and Chromatin Organization Shaping Terminal B Cell Differentiation. <i>Trends in Immunology</i> , 2020, 41, 46-60.	2.9	21
5	Highly interconnected enhancer communities control lineage-determining genes in human mesenchymal stem cells. <i>Nature Genetics</i> , 2020, 52, 1227-1238.	9.4	57
6	The Genome in a Three-Dimensional Context: Deciphering the Contribution of Noncoding Mutations at Enhancers to Blood Cancer. <i>Frontiers in Immunology</i> , 2020, 11, 592087.	2.2	4
7	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
8	Human pancreatic islet three-dimensional chromatin architecture provides insights into the genetics of type 2 diabetes. <i>Nature Genetics</i> , 2019, 51, 1137-1148.	9.4	208
9	Long-Range Enhancer Interactions Are Prevalent in Mouse Embryonic Stem Cells and Are Reorganized upon Pluripotent State Transition. <i>Cell Reports</i> , 2018, 22, 2615-2627.	2.9	99
10	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. <i>Nature Medicine</i> , 2018, 24, 868-880.	15.2	157
11	Promoter Capture Hi-C: High-resolution, Genome-wide Profiling of Promoter Interactions. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	66
12	Promoter interactome of human embryonic stem cell-derived cardiomyocytes connects GWAS regions to cardiac gene networks. <i>Nature Communications</i> , 2018, 9, 2526.	5.8	48
13	Induced Transdifferentiation of Leukemia B-Cells to Macrophages Involves Reconfiguration of the DNA Methylome. <i>Blood</i> , 2018, 132, 5115-5115.	0.6	0
14	Genome-wide mapping of long-range contacts unveils clustering of DNA double-strand breaks at damaged active genes. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 353-361.	3.6	221
15	Dynamic Rewiring of Promoter-Anchored Chromatin Loops during Adipocyte Differentiation. <i>Molecular Cell</i> , 2017, 66, 420-435.e5.	4.5	188
16	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. <i>Nature Communications</i> , 2017, 8, 16058.	5.8	50
17	Chromosome contacts in activated T cells identify autoimmune disease candidate genes. <i>Genome Biology</i> , 2017, 18, 165.	3.8	68
18	Integrating epigenomic data and 3D genomic structure with a new measure of chromatin assortativity. <i>Genome Biology</i> , 2016, 17, 152.	3.8	46

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19	CHiCAGO: robust detection of DNA looping interactions in Capture Hi-C data. <i>Genome Biology</i> , 2016, 17, 127.	3.8	344
20	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. <i>Cell</i> , 2016, 167, 1369-1384.e19.	13.5	863
21	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
22	IL-4 orchestrates STAT6-mediated DNA demethylation leading to dendritic cell differentiation. <i>Genome Biology</i> , 2016, 17, 4.	3.8	122
23	The pluripotent regulatory circuitry connecting promoters to their long-range interacting elements. <i>Genome Research</i> , 2015, 25, 582-597.	2.4	402
24	Comparison of Hi-C results using in-solution versus in-nucleus ligation. <i>Genome Biology</i> , 2015, 16, 175.	3.8	157
25	Polycomb repressive complex PRC1 spatially constrains the mouse embryonic stem cell genome. <i>Nature Genetics</i> , 2015, 47, 1179-1186.	9.4	330
26	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
27	Epigenetic Basis of Autoimmune Disorders in Humans. , 2012, , 205-223.		0
28	A New Epigenetic Challenge: Systemic Lupus Erythematosus. <i>Advances in Experimental Medicine and Biology</i> , 2011, 711, 117-136.	0.8	43
29	Leptin and TNF-alpha promoter methylation levels measured by MSP could predict the response to a low-calorie diet. <i>Journal of Physiology and Biochemistry</i> , 2011, 67, 463-470.	1.3	149
30	Epigenetic alterations in autoimmune disease. <i>Journal of Translational Medicine</i> , 2011, 9, .	1.8	1
31	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
32	Environmental triggers and epigenetic deregulation in autoimmune disease. <i>Discovery Medicine</i> , 2011, 12, 535-45.	0.5	85
33	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
34	The dynamic DNA methylomes of double-stranded DNA viruses associated with human cancer. <i>Genome Research</i> , 2009, 19, 438-451.	2.4	218
35	Epigenetic connections between autoimmune disorders and haematological malignancies. <i>Trends in Immunology</i> , 2008, 29, 616-623.	2.9	26
36	Increased expression of VEGF121/VEGF165-189 ratio results in a significant enhancement of human prostate tumor angiogenesis. <i>International Journal of Cancer</i> , 2007, 120, 2096-2109.	2.3	47