

# Juan M Vaquerizas

## List of Publications by Year in descending order

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Version: 2024-02-01

61  
papers

24,172  
citations

94433

37  
h-index

133252

59  
g-index

72  
all docs

72  
docs citations

72  
times ranked

43897  
citing authors

#	ARTICLE	IF	CITATIONS
1	Zebrafish transposable elements show extensive diversification in age, genomic distribution, and developmental expression. <i>Genome Research</i> , 2022, 32, 1408-1423.	5.5	29
2	Emerging mechanisms and dynamics of three-dimensional genome organisation at zygotic genome activation. <i>Current Opinion in Cell Biology</i> , 2022, 74, 37-46.	5.4	10
3	Lima1 mediates the pluripotency control of membrane dynamics and cellular metabolism. <i>Nature Communications</i> , 2022, 13, 610.	12.8	8
4	Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. <i>Nature Genetics</i> , 2022, 54, 1037-1050.	21.4	26
5	The Transition from Quiescent to Activated States in Human Hematopoietic Stem Cells Is Governed by Dynamic 3D Genome Reorganization. <i>Cell Stem Cell</i> , 2021, 28, 488-501.e10.	11.1	51
6	Germ cell differentiation requires Tdrd7-dependent chromatin and transcriptome reprogramming marked by germ plasm relocalization. <i>Developmental Cell</i> , 2021, 56, 641-656.e5.	7.0	18
7	Independence of chromatin conformation and gene regulation during <i>Drosophila</i> dorsoventral patterning. <i>Nature Genetics</i> , 2021, 53, 487-499.	21.4	108
8	One-step Reprogramming of Human Fibroblasts into Oligodendrocyte-like Cells by SOX10, OLIG2, and NKX6.2. <i>Stem Cell Reports</i> , 2021, 16, 771-783.	4.8	19
9	Repression of endogenous retroviruses prevents antiviral immune response and is required for mammary gland development. <i>Cell Stem Cell</i> , 2021, 28, 1790-1804.e8.	11.1	10
10	Chromatin architecture transitions from zebrafish sperm through early embryogenesis. <i>Genome Research</i> , 2021, 31, 981-994.	5.5	48
11	Ronin governs the metabolic capacity of the embryonic lineage for post-implantation development. <i>EMBO Reports</i> , 2021, 22, e53048.	4.5	4
12	CHESS enables quantitative comparison of chromatin contact data and automatic feature extraction. <i>Nature Genetics</i> , 2020, 52, 1247-1255.	21.4	32
13	FAN-C: a feature-rich framework for the analysis and visualisation of chromosome conformation capture data. <i>Genome Biology</i> , 2020, 21, 303.	8.8	100
14	Heterochromatin establishment during early mammalian development is regulated by pericentromeric RNA and characterized by non-repressive H3K9me3. <i>Nature Cell Biology</i> , 2020, 22, 767-778.	10.3	71
15	Cohesin Disrupts Polycomb-Dependent Chromosome Interactions in Embryonic Stem Cells. <i>Cell Reports</i> , 2020, 30, 820-835.e10.	6.4	129
16	Visualising three-dimensional genome organisation in two dimensions. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	10
17	Endothelial EphB4 maintains vascular integrity and transport function in adult heart. <i>ELife</i> , 2019, 8, .	6.0	38
18	A molecular roadmap for the emergence of early-embryonic-like cells in culture. <i>Nature Genetics</i> , 2018, 50, 106-119.	21.4	144

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19	Generation of Genome-wide Chromatin Conformation Capture Libraries from Tightly Staged Early <i>Drosophila</i> Embryos. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	2
20	Chromatin conformation analysis of primary patient tissue using a low input Hi-C method. <i>Nature Communications</i> , 2018, 9, 4938.	12.8	89
21	The Birth of the 3D Genome during Early Embryonic Development. <i>Trends in Genetics</i> , 2018, 34, 903-914.	6.7	65
22	<i>Xrp1</i> genetically interacts with the ALS-associated <i>FUS</i> orthologue <i>caz</i> and mediates its toxicity. <i>Journal of Cell Biology</i> , 2018, 217, 3947-3964.	5.2	23
23	Cellâ€‘matrix signals specify bone endothelial cells during developmental osteogenesis. <i>Nature Cell Biology</i> , 2017, 19, 189-201.	10.3	161
24	Chromatin Architecture Emerges during Zygotic Genome Activation Independent of Transcription. <i>Cell</i> , 2017, 169, 216-228.e19.	28.9	411
25	Transcriptional regulation of endothelial cell behavior during sprouting angiogenesis. <i>Nature Communications</i> , 2017, 8, 726.	12.8	71
26	Dual randomization of oligonucleotides to reduce the bias in ribosome-profiling libraries. <i>Methods</i> , 2016, 107, 89-97.	3.8	50
27	Panoramic views of the early epigenome. <i>Nature</i> , 2016, 537, 494-496.	27.8	9
28	TADtool: visual parameter identification for TAD-calling algorithms. <i>Bioinformatics</i> , 2016, 32, 3190-3192.	4.1	73
29	Early embryonic-like cells are induced by downregulating replication-dependent chromatin assembly. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 662-671.	8.2	274
30	DNA-Binding Specificities of Human Transcription Factors. <i>Cell</i> , 2013, 152, 327-339.	28.9	1,085
31	Response to Comments on â€œ <i>Drosophila</i> Dosage Compensation Involves Enhanced Pol II Recruitment to Male X-Linked Promotersâ€‘. <i>Science</i> , 2013, 340, 273-273.	12.6	15
32	The NSL Complex Regulates Housekeeping Genes in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2012, 8, e1002736.	3.5	80
33	m:Explorer: multinomial regression models reveal positive and negative regulators of longevity in yeast quiescence. <i>Genome Biology</i> , 2012, 13, R55.	9.6	7
34	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	27.8	15,516
35	The MOF Chromobarrel Domain Controls Genome-wide H4K16 Acetylation and Spreading of the MSL Complex. <i>Developmental Cell</i> , 2012, 22, 610-624.	7.0	63
36	<i>Drosophila</i> Dosage Compensation Involves Enhanced Pol II Recruitment to Male X-Linked Promoters. <i>Science</i> , 2012, 337, 742-746.	12.6	69

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37	How Do You Find Transcription Factors? Computational Approaches to Compile and Annotate Repertoires of Regulators for Any Genome. <i>Methods in Molecular Biology</i> , 2012, 786, 3-19.	0.9	11
38	Large-Scale Nuclear Architecture and Transcriptional Control. <i>Sub-Cellular Biochemistry</i> , 2011, 52, 279-295.	2.4	4
39	SpeCond: a method to detect condition-specific gene expression. <i>Genome Biology</i> , 2011, 12, 413.	9.6	0
40	SpeCond: a method to detect condition-specific gene expression. <i>Genome Biology</i> , 2011, 12, R101.	9.6	19
41	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	5.6	1,257
42	Comprehensive reanalysis of transcription factor knockout expression data in <i>Saccharomyces cerevisiae</i> reveals many new targets. <i>Nucleic Acids Research</i> , 2010, 38, 4768-4777.	14.5	102
43	Nuclear Pore Proteins Nup153 and Megator Define Transcriptionally Active Regions in the <i>Drosophila</i> Genome. <i>PLoS Genetics</i> , 2010, 6, e1000846.	3.5	218
44	The Nonspecific Lethal Complex Is a Transcriptional Regulator in <i>Drosophila</i> . <i>Molecular Cell</i> , 2010, 38, 827-841.	9.7	131
45	Multiplexed massively parallel SELEX for characterization of human transcription factor binding specificities. <i>Genome Research</i> , 2010, 20, 861-873.	5.5	382
46	A census of human transcription factors: function, expression and evolution. <i>Nature Reviews Genetics</i> , 2009, 10, 252-263.	16.3	1,357
47	Genome-wide Analysis Reveals MOF as a Key Regulator of Dosage Compensation and Gene Expression in <i>Drosophila</i> . <i>Cell</i> , 2008, 133, 813-828.	28.9	144
48	Identification of conserved domains in the promoter regions of nitric oxide synthase 2: implications for the species-specific transcription and evolutionary differences. <i>BMC Genomics</i> , 2007, 8, 271.	2.8	17
49	Exploring the reasons for the large density of triplex-forming oligonucleotide target sequences in the human regulatory regions. <i>BMC Genomics</i> , 2006, 7, 63.	2.8	46
50	Next station in microarray data analysis: GEPAS. <i>Nucleic Acids Research</i> , 2006, 34, W486-W491.	14.5	107
51	BABELOMICS: a systems biology perspective in the functional annotation of genome-scale experiments. <i>Nucleic Acids Research</i> , 2006, 34, W472-W476.	14.5	240
52	PupaSuite: finding functional single nucleotide polymorphisms for large-scale genotyping purposes. <i>Nucleic Acids Research</i> , 2006, 34, W621-W625.	14.5	194
53	Highly specific and accurate selection of siRNAs for high-throughput functional assays. <i>Bioinformatics</i> , 2005, 21, 1376-1382.	4.1	49
54	BABELOMICS: a suite of web tools for functional annotation and analysis of groups of genes in high-throughput experiments. <i>Nucleic Acids Research</i> , 2005, 33, W460-W464.	14.5	217

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55	PupasView: a visual tool for selecting suitable SNPs, with putative pathological effect in genes, for genotyping purposes. <i>Nucleic Acids Research</i> , 2005, 33, W501-W505.	14.5	253
56	GEPAS, an experiment-oriented pipeline for the analysis of microarray gene expression data. <i>Nucleic Acids Research</i> , 2005, 33, W616-W620.	14.5	86
57	Characterization of the Proteomic and Genomic Profiles of Chronic Lymphocytic Leukemia Patients with Distinct Clinical Prognosis According to the Mutational Status of the IgVH and BCL6 and Expression Level of CD38 and ZAP70.. <i>Blood</i> , 2005, 106, 3272-3272.	1.4	0
58	New challenges in gene expression data analysis and the extended GEPAS. <i>Nucleic Acids Research</i> , 2004, 32, W485-W491.	14.5	47
59	PupaSNP Finder: a web tool for finding SNPs with putative effect at transcriptional level. <i>Nucleic Acids Research</i> , 2004, 32, W242-W248.	14.5	86
60	DNMAD: web-based diagnosis and normalization for microarray data. <i>Bioinformatics</i> , 2004, 20, 3656-3658.	4.1	56
61	GEPAS: a web-based resource for microarray gene expression data analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3461-3467.	14.5	161