

# 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	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	27.8	15,516
2	A census of human transcription factors: function, expression and evolution. <i>Nature Reviews Genetics</i> , 2009, 10, 252-263.	16.3	1,357
3	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	5.6	1,257
4	DNA-Binding Specificities of Human Transcription Factors. <i>Cell</i> , 2013, 152, 327-339.	28.9	1,085
5	Chromatin Architecture Emerges during Zygotic Genome Activation Independent of Transcription. <i>Cell</i> , 2017, 169, 216-228.e19.	28.9	411
6	Multiplexed massively parallel SELEX for characterization of human transcription factor binding specificities. <i>Genome Research</i> , 2010, 20, 861-873.	5.5	382
7	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
8	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
9	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
10	Nuclear Pore Proteins Nup153 and Megator Define Transcriptionally Active Regions in the Drosophila Genome. <i>PLoS Genetics</i> , 2010, 6, e1000846.	3.5	218
11	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
12	PupaSuite: finding functional single nucleotide polymorphisms for large-scale genotyping purposes. <i>Nucleic Acids Research</i> , 2006, 34, W621-W625.	14.5	194
13	GEPAS: a web-based resource for microarray gene expression data analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3461-3467.	14.5	161
14	Cellâ€™matrix signals specify bone endothelial cells during developmental osteogenesis. <i>Nature Cell Biology</i> , 2017, 19, 189-201.	10.3	161
15	Genome-wide Analysis Reveals MOF as a Key Regulator of Dosage Compensation and Gene Expression in Drosophila. <i>Cell</i> , 2008, 133, 813-828.	28.9	144
16	A molecular roadmap for the emergence of early-embryonic-like cells in culture. <i>Nature Genetics</i> , 2018, 50, 106-119.	21.4	144
17	The Nonspecific Lethal Complex Is a Transcriptional Regulator in Drosophila. <i>Molecular Cell</i> , 2010, 38, 827-841.	9.7	131
18	Cohesin Disrupts Polycomb-Dependent Chromosome Interactions in Embryonic Stem Cells. <i>Cell Reports</i> , 2020, 30, 820-835.e10.	6.4	129

#	ARTICLE	IF	CITATIONS
19	Independence of chromatin conformation and gene regulation during <i>Drosophila</i> dorsoventral patterning. <i>Nature Genetics</i> , 2021, 53, 487-499.	21.4	108
20	Next station in microarray data analysis: GEPAS. <i>Nucleic Acids Research</i> , 2006, 34, W486-W491.	14.5	107
21	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
22	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
23	Chromatin conformation analysis of primary patient tissue using a low input Hi-C method. <i>Nature Communications</i> , 2018, 9, 4938.	12.8	89
24	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
25	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
26	The NSL Complex Regulates Housekeeping Genes in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2012, 8, e1002736.	3.5	80
27	TADtool: visual parameter identification for TAD-calling algorithms. <i>Bioinformatics</i> , 2016, 32, 3190-3192.	4.1	73
28	Transcriptional regulation of endothelial cell behavior during sprouting angiogenesis. <i>Nature Communications</i> , 2017, 8, 726.	12.8	71
29	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
30	<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
31	The Birth of the 3D Genome during Early Embryonic Development. <i>Trends in Genetics</i> , 2018, 34, 903-914.	6.7	65
32	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
33	DNMAD: web-based diagnosis and normalization for microarray data. <i>Bioinformatics</i> , 2004, 20, 3656-3658.	4.1	56
34	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
35	Dual randomization of oligonucleotides to reduce the bias in ribosome-profiling libraries. <i>Methods</i> , 2016, 107, 89-97.	3.8	50
36	Highly specific and accurate selection of siRNAs for high-throughput functional assays. <i>Bioinformatics</i> , 2005, 21, 1376-1382.	4.1	49

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37	Chromatin architecture transitions from zebrafish sperm through early embryogenesis. <i>Genome Research</i> , 2021, 31, 981-994.	5.5	48
38	New challenges in gene expression data analysis and the extended GEPAS. <i>Nucleic Acids Research</i> , 2004, 32, W485-W491.	14.5	47
39	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
40	Endothelial EphB4 maintains vascular integrity and transport function in adult heart. <i>ELife</i> , 2019, 8, .	6.0	38
41	CHESSE enables quantitative comparison of chromatin contact data and automatic feature extraction. <i>Nature Genetics</i> , 2020, 52, 1247-1255.	21.4	32
42	Zebrafish transposable elements show extensive diversification in age, genomic distribution, and developmental expression. <i>Genome Research</i> , 2022, 32, 1408-1423.	5.5	29
43	Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. <i>Nature Genetics</i> , 2022, 54, 1037-1050.	21.4	26
44	<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
45	SpeCond: a method to detect condition-specific gene expression. <i>Genome Biology</i> , 2011, 12, R101.	9.6	19
46	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
47	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
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	Response to Comments on "Drosophila Dosage Compensation Involves Enhanced Pol II Recruitment to Male X-Linked Promoters". <i>Science</i> , 2013, 340, 273-273.	12.6	15
50	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
51	Visualising three-dimensional genome organisation in two dimensions. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	10
52	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
53	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
54	Panoramic views of the early epigenome. <i>Nature</i> , 2016, 537, 494-496.	27.8	9

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55	Lima1 mediates the pluripotency control of membrane dynamics and cellular metabolism. Nature Communications, 2022, 13, 610.	12.8	8
56	m:Explorer: multinomial regression models reveal positive and negative regulators of longevity in yeast quiescence. Genome Biology, 2012, 13, R55.	9.6	7
57	Large-Scale Nuclear Architecture and Transcriptional Control. Sub-Cellular Biochemistry, 2011, 52, 279-295.	2.4	4
58	Ronin governs the metabolic capacity of the embryonic lineage for postâ€mplantation development. EMBO Reports, 2021, 22, e53048.	4.5	4
59	Generation of Genome-wide Chromatin Conformation Capture Libraries from Tightly Staged Early <em>Drosophila</em> Embryos. Journal of Visualized Experiments, 2018, , .	0.3	2
60	SpeCond: a method to detect condition-specific gene expression. Genome Biology, 2011, 12, 413.	9.6	0
61	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.. Blood, 2005, 106, 3272-3272.	1.4	0