

Enrique Blanco

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

5,292
citations

257450

24
h-index

233421

45
g-index

52
all docs

52
docs citations

52
times ranked

9606
citing authors

#	ARTICLE	IF	CITATIONS
1	In vivo temporal resolution of acute promyelocytic leukemia progression reveals a role of <i>Klf4</i> in suppressing early leukemic transformation. <i>Genes and Development</i> , 2022, 36, 451-467.	5.9	1
2	Polycomb Factor PHF19 Controls Cell Growth and Differentiation Toward Erythroid Pathway in Chronic Myeloid Leukemia Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 655201.	3.7	7
3	SpikChIP: a novel computational methodology to compare multiple ChIP-seq using spike-in chromatin. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab064.	3.2	5
4	Differential contribution to gene expression prediction of histone modifications at enhancers or promoters. <i>PLoS Computational Biology</i> , 2021, 17, e1009368.	3.2	9
5	Productive visualization of high-throughput sequencing data using the SeqCode open portable platform. <i>Scientific Reports</i> , 2021, 11, 19545.	3.3	9
6	Neuron type-specific increase in lamin B1 contributes to nuclear dysfunction in Huntington's disease. <i>EMBO Molecular Medicine</i> , 2021, 13, e12105.	6.9	28
7	The Bivalent Genome: Characterization, Structure, and Regulation. <i>Trends in Genetics</i> , 2020, 36, 118-131.	6.7	112
8	The Polycomb-associated factor PHF19 controls hematopoietic stem cell state and differentiation. <i>Science Advances</i> , 2020, 6, eabb2745.	10.3	20
9	RING1B recruits EWSR1-FLI1 and cooperates in the remodeling of chromatin necessary for Ewing sarcoma tumorigenesis. <i>Science Advances</i> , 2020, 6, .	10.3	24
10	Transgenerational epigenetic regulation associated with the amelioration of Duchenne Muscular Dystrophy. <i>EMBO Molecular Medicine</i> , 2020, 12, e12063.	6.9	11
11	PHF19 mediated regulation of proliferation and invasiveness in prostate cancer cells. <i>ELife</i> , 2020, 9, .	6.0	23
12	GATA2 Promotes Hematopoietic Development and Represses Cardiac Differentiation of Human Mesoderm. <i>Stem Cell Reports</i> , 2019, 13, 515-529.	4.8	27
13	Chromatin capture links the metabolic enzyme AHCY to stem cell proliferation. <i>Science Advances</i> , 2019, 5, eaav2448.	10.3	38
14	Using geneid to Identify Genes. <i>Current Protocols in Bioinformatics</i> , 2018, 64, e56.	25.8	112
15	Promoter bivalency favors an open chromatin architecture in embryonic stem cells. <i>Nature Genetics</i> , 2018, 50, 1452-1462.	21.4	113
16	Lamin B1 mapping reveals the existence of dynamic and functional euchromatin lamin B1 domains. <i>Nature Communications</i> , 2018, 9, 3420.	12.8	66
17	3D structures of individual mammalian genomes studied by single-cell Hi-C. <i>Nature</i> , 2017, 544, 59-64.	27.8	691
18	The Polycomb group protein CBX6 is an essential regulator of embryonic stem cell identity. <i>Nature Communications</i> , 2017, 8, 1235.	12.8	26

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19	Dnmt3a and Dnmt3b Associate with Enhancers to Regulate Human Epidermal Stem Cell Homeostasis. <i>Cell Stem Cell</i> , 2016, 19, 491-501.	11.1	170
20	EPOP Functionally Links Elongin and Polycomb in Pluripotent Stem Cells. <i>Molecular Cell</i> , 2016, 64, 645-658.	9.7	117
21	Cabut/ <scp>dTIEG</scp> associates with the transcription factor Yorkie for growth control. <i>EMBO Reports</i> , 2015, 16, 362-369.	4.5	12
22	Identification and Functional Analysis of Healing Regulators in Drosophila. <i>PLoS Genetics</i> , 2015, 11, e1004965.	3.5	8
23	Absence of canonical marks of active chromatin in developmentally regulated genes. <i>Nature Genetics</i> , 2015, 47, 1158-1167.	21.4	75
24	Polycomb Regulates Mesoderm Cell Fate-Specification in Embryonic Stem Cells through Activation and Repression Mechanisms. <i>Cell Stem Cell</i> , 2015, 17, 300-315.	11.1	124
25	Brk regulates wing disc growth in part via repression of Myc expression. <i>EMBO Reports</i> , 2013, 14, 261-268.	4.5	33
26	The BTB-zinc Finger Transcription Factor Abrupt Acts as an Epithelial Oncogene in Drosophila melanogaster through Maintaining a Progenitor-like Cell State. <i>PLoS Genetics</i> , 2013, 9, e1003627.	3.5	31
27	ReLA, a local alignment search tool for the identification of distal and proximal gene regulatory regions and their conserved transcription factor binding sites. <i>Bioinformatics</i> , 2012, 28, 763-770.	4.1	11
28	Use of ChIP-Seq data for the design of a multiple promoter-alignment method. <i>Nucleic Acids Research</i> , 2012, 40, e52-e52.	14.5	23
29	CBS: an open platform that integrates predictive methods and epigenetics information to characterize conserved regulatory features in multiple Drosophila genomes. <i>BMC Genomics</i> , 2012, 13, 688.	2.8	1
30	Active and passive MDMA (â€ˆecstasyâ€™™) intake induces differential transcriptional changes in the mouse brain. <i>Genes, Brain and Behavior</i> , 2012, 11, 38-51.	2.2	20
31	Genome-wide chromatin occupancy analysis reveals a role for ASH2 in transcriptional pausing. <i>Nucleic Acids Research</i> , 2011, 39, 4628-4639.	14.5	34
32	Gene expression following induction of regeneration in Drosophila wing imaginal discs. Expression profile of regenerating wing discs. <i>BMC Developmental Biology</i> , 2010, 10, 94.	2.1	56
33	Hnf1 β (MODY3) Controls Tissue-Specific Transcriptional Programs and Exerts Opposed Effects on Cell Growth in Pancreatic Islets and Liver. <i>Molecular and Cellular Biology</i> , 2009, 29, 2945-2959.	2.3	122
34	Computational Gene Annotation in New Genome Assemblies Using GeneID. <i>Methods in Molecular Biology</i> , 2009, 537, 243-261.	0.9	28
35	Coordinate control of synaptic-layer specificity and rhodopsins in photoreceptor neurons. <i>Nature</i> , 2008, 456, 795-799.	27.8	77
36	Conserved chromosomal clustering of genes governed by chromatin regulators in Drosophila. <i>Genome Biology</i> , 2008, 9, R134.	9.6	16

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37	ORegAnno: an open-access community-driven resource for regulatory annotation. <i>Nucleic Acids Research</i> , 2007, 36, D107-D113.	14.5	227
38	Using geneid to Identify Genes. , 2007, Chapter 4, Unit 4.3.		281
39	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
40	Multiple non-collinear TF-map alignments of promoter regions. <i>BMC Bioinformatics</i> , 2007, 8, 138.	2.6	10
41	ABS: a database of Annotated regulatory Binding Sites from orthologous promoters. <i>Nucleic Acids Research</i> , 2006, 34, D63-D67.	14.5	56
42	Transcription Factor Map Alignment of Promoter Regions. <i>PLoS Computational Biology</i> , 2006, 2, e49.	3.2	50
43	Reconsidering the evolution of eukaryotic selenoproteins: a novel nonmammalian family with scattered phylogenetic distribution. <i>EMBO Reports</i> , 2004, 5, 71-77.	4.5	99
44	Transcriptional network controlled by the trithorax-group gene <i>ash2</i> in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3293-3298.	7.1	21
45	Using geneid to Identify Genes. <i>Current Protocols in Bioinformatics</i> , 2003, 00, 4.3.1.	25.8	37
46	GeneID in <i>Drosophila</i> . <i>Genome Research</i> , 2000, 10, 511-515.	5.5	331