

Alvaro Rada-Iglesias

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

58

papers

8,113

citations

25

h-index

68

g-index

68

ext. papers

9,376

ext. citations

12.7

avg, IF

5.34

L-index

#	Paper	IF	Citations
58	JMJD3 intrinsically disordered region links the 3D-genome structure to TGFβ-dependent transcription activation. <i>Nature Communications</i> , 2022 , 13,	17.4	1
57	MAPRE2 mutations result in altered human cranial neural crest migration, underlying craniofacial malformations in CSC-KT syndrome. <i>Scientific Reports</i> , 2021 , 11, 4976	4.9	2
56	Overarching control of autophagy and DNA damage response by CHD6 revealed by modeling a rare human pathology. <i>Nature Communications</i> , 2021 , 12, 3014	17.4	1
55	Integrative approaches generate insights into the architecture of non-syndromic cleft lip with or without cleft palate.. <i>Human Genetics and Genomics Advances</i> , 2021 , 2, 100038	0.8	1
54	Orphan CpG islands amplify poised enhancer regulatory activity and determine target gene responsiveness. <i>Nature Genetics</i> , 2021 , 53, 1036-1049	36.3	10
53	Niche stiffening compromises hair follicle stem cell potential during ageing by reducing bivalent promoter accessibility. <i>Nature Cell Biology</i> , 2021 , 23, 771-781	23.4	6
52	The chromatin, topological and regulatory properties of pluripotency-associated poised enhancers are conserved in vivo. <i>Nature Communications</i> , 2021 , 12, 4344	17.4	6
51	Enhancer-associated H3K4 methylation safeguards in vitro germline competence. <i>Nature Communications</i> , 2021 , 12, 5771	17.4	5
50	The ubiquitin-conjugating enzyme UBE2K determines neurogenic potential through histone H3 in human embryonic stem cells. <i>Communications Biology</i> , 2020 , 3, 262	6.7	10
49	Epigenomic and Transcriptomic Changes During Human RPE EMT in a Stem Cell Model of Epiretinal Membrane Pathogenesis and Prevention by Nicotinamide. <i>Stem Cell Reports</i> , 2020 , 14, 631-647	8	19
48	The formation of the thumb requires direct modulation of transcription by Hoxa13. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 1090-1096	11.5	8
47	Rare or Overlooked? Structural Disruption of Regulatory Domains in Human Neurocristopathies. <i>Frontiers in Genetics</i> , 2020 , 11, 688	4.5	5
46	Transcriptional and epigenetic control of germline competence and specification. <i>Current Opinion in Cell Biology</i> , 2019 , 61, 1-8	9	7
45	Pathological ASXL1 Mutations and Protein Variants Impair Neural Crest Development. <i>Stem Cell Reports</i> , 2019 , 12, 861-868	8	8
44	Modeling the Pathological Long-Range Regulatory Effects of Human Structural Variation with Patient-Specific hiPSCs. <i>Cell Stem Cell</i> , 2019 , 24, 736-752.e12	18	43
43	Polycomb proteins as organizers of 3D genome architecture in embryonic stem cells. <i>Briefings in Functional Genomics</i> , 2019 , 18, 358-366	4.9	13
42	Dosage analysis of the 7q11.23 Williams region identifies as a major human gene patterning the modern human face and underlying self-domestication. <i>Science Advances</i> , 2019 , 5, eaaw7908	14.3	31

41	yyIncT Defines a Class of Divergently Transcribed lncRNAs and Safeguards the T-mediated Mesodermal Commitment of Human PSCs. <i>Cell Stem Cell</i> , 2019 , 24, 318-327.e8	18	27
40	Lineage specific transcription factors and epigenetic regulators mediate TGF β dependent enhancer activation. <i>Nucleic Acids Research</i> , 2018 , 46, 3351-3365	20.1	16
39	Is H3K4me1 at enhancers correlative or causative?. <i>Nature Genetics</i> , 2018 , 50, 4-5	36.3	32
38	Pioneering of Enhancer Landscapes during Pluripotent State Transitions. <i>Cell Stem Cell</i> , 2018 , 23, 149-151.e8	18	1
37	Mechanism suppressing H3K9 trimethylation in pluripotent stem cells and its demise by polyQ-expanded huntingtin mutations. <i>Human Molecular Genetics</i> , 2018 , 27, 4117-4134	5.6	17
36	Forces driving the three-dimensional folding of eukaryotic genomes. <i>Molecular Systems Biology</i> , 2018 , 14, e8214	12.2	55
35	Imputation of orofacial clefting data identifies novel risk loci and sheds light on the genetic background of cleft lip \square cleft palate and cleft palate only. <i>Human Molecular Genetics</i> , 2017 , 26, 829-842	5.6	55
34	PRC2 Facilitates the Regulatory Topology Required for Poised Enhancer Function during Pluripotent Stem Cell Differentiation. <i>Cell Stem Cell</i> , 2017 , 20, 689-705.e9	18	122
33	Chromatin Immunoprecipitation (ChIP) Protocol for Low-abundance Embryonic Samples. <i>Journal of Visualized Experiments</i> , 2017 ,	1.6	4
32	Ready, Set Poised!: Polycomb target genes are bound by poised RNA polymerase II throughout differentiation. <i>Molecular Systems Biology</i> , 2017 , 13, 950	12.2	
31	GARLIC: a bioinformatic toolkit for aetiologically connecting diseases and cell type-specific regulatory maps. <i>Human Molecular Genetics</i> , 2017 , 26, 742-752	5.6	1
30	Enhancer Remodeling During Early Mammalian Embryogenesis: Lessons for Somatic Reprogramming, Rejuvenation, and Aging. <i>Current Stem Cell Reports</i> , 2016 , 2, 263-272	1.8	
29	Foxd3 Promotes Exit from Naive Pluripotency through Enhancer Decommissioning and Inhibits Germline Specification. <i>Cell Stem Cell</i> , 2016 , 18, 118-33	18	56
28	Epigenomics-Based Identification of Major Cell Identity Regulators within Heterogeneous Cell Populations. <i>Cell Reports</i> , 2016 , 17, 3062-3076	10.6	18
27	Genetic variation within transcriptional regulatory elements and its implications for human disease. <i>Biological Chemistry</i> , 2014 , 395, 1453-60	4.5	4
26	Pioneering barren land: mitotic bookmarking by transcription factors. <i>Developmental Cell</i> , 2013 , 24, 342-40.2	40.2	10
25	Human genetic variation within neural crest enhancers: molecular and phenotypic implications. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20120360	5.8	13
24	The homeodomain-leucine zipper (HD-Zip) class I transcription factors ATHB7 and ATHB12 modulate abscisic acid signalling by regulating protein phosphatase 2C and abscisic acid receptor gene activities. <i>Plant Molecular Biology</i> , 2012 , 80, 405-18	4.6	106

23	Epigenomic annotation of enhancers predicts transcriptional regulators of human neural crest. <i>Cell Stem Cell</i> , 2012 , 11, 633-48	18	207
22	Sequence-specific regulator Prdm14 safeguards mouse ESCs from entering extraembryonic endoderm fates. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 120-7	17.6	156
21	A unique chromatin signature uncovers early developmental enhancers in humans. <i>Nature</i> , 2011 , 470, 279-83	50.4	1545
20	Epigenomics of human embryonic stem cells and induced pluripotent stem cells: insights into pluripotency and implications for disease. <i>Genome Medicine</i> , 2011 , 3, 36	14.4	39
19	CHD7 cooperates with PBAF to control multipotent neural crest formation. <i>Nature</i> , 2010 , 463, 958-62	50.4	431
18	Integrative epigenomic and genomic analysis of malignant pheochromocytoma. <i>Experimental and Molecular Medicine</i> , 2010 , 42, 484-502	12.8	29
17	Two polypyrimidine tracts in the nitric oxide synthase 2 gene: similar regulatory sequences with different properties. <i>Molecular Biology Reports</i> , 2010 , 37, 2021-30	2.8	9
16	Identification of candidate regulatory SNPs by combination of transcription-factor-binding site prediction, SNP genotyping and haploChIP. <i>Nucleic Acids Research</i> , 2009 , 37, e85	20.1	29
15	Histone H3 lysine 27 trimethylation in adult differentiated colon associated to cancer DNA hypermethylation. <i>Epigenetics</i> , 2009 , 4, 107-13	5.7	24
14	Nucleosomes are well positioned in exons and carry characteristic histone modifications. <i>Genome Research</i> , 2009 , 19, 1732-41	9.7	242
13	Histone acetylation and methylation at sites initiating divergent polycistronic transcription in <i>Trypanosoma cruzi</i> . <i>Journal of Biological Chemistry</i> , 2008 , 283, 15884-92	5.4	69
12	Monte Carlo feature selection for supervised classification. <i>Bioinformatics</i> , 2008 , 24, 110-7	7.2	155
11	Whole-genome maps of USF1 and USF2 binding and histone H3 acetylation reveal new aspects of promoter structure and candidate genes for common human disorders. <i>Genome Research</i> , 2008 , 18, 380-92	9.7	72
10	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
9	Butyrate mediates decrease of histone acetylation centered on transcription start sites and down-regulation of associated genes. <i>Genome Research</i> , 2007 , 17, 708-19	9.7	106
8	In vitro analysis of DNA-protein interactions by proximity ligation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 3067-72	11.5	63
7	Binding sites for metabolic disease related transcription factors inferred at base pair resolution by chromatin immunoprecipitation and genomic microarrays. <i>Human Molecular Genetics</i> , 2005 , 14, 3435-47	5.6	66
6	The promoter of inducible nitric oxide synthase implicated in glaucoma based on genetic analysis and nuclear factor binding. <i>Molecular Vision</i> , 2005 , 11, 950-7	2.3	25

5	Sp8 regulatory function in the limb bud ectoderm		1
4	Disruption of the TFAP2A Regulatory Domain Causes Banchio-Oculo-Facial Syndrome (BOFS) and Illuminates Pathomechanisms for Other Human Neurocristopathies. <i>SSRN Electronic Journal</i> ,	1	1
3	Enhancer-associated H3K4 methylation safeguards in vitro germline competence		4
2	Orphan CpG islands boost the regulatory activity of poised enhancers and dictate the responsiveness of their target genes		4
1	The chromatin, topological and regulatory properties of pluripotency-associated poised enhancers are conserved in vivo		1