

# Alvaro Rada-Iglesias

## List of Publications by Year in descending order

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Version: 2024-02-01

56  
papers

10,140  
citations

185998

28  
h-index

168136

53  
g-index

68  
all docs

68  
docs citations

68  
times ranked

17140  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
2	A unique chromatin signature uncovers early developmental enhancers in humans. <i>Nature</i> , 2011, 470, 279-283.	13.7	1,949
3	CHD7 cooperates with PBAF to control multipotent neural crest formation. <i>Nature</i> , 2010, 463, 958-962.	13.7	527
4	Epigenomic Annotation of Enhancers Predicts Transcriptional Regulators of Human Neural Crest. <i>Cell Stem Cell</i> , 2012, 11, 633-648.	5.2	283
5	Nucleosomes are well positioned in exons and carry characteristic histone modifications. <i>Genome Research</i> , 2009, 19, 1732-1741.	2.4	274
6	Monte Carlo feature selection for supervised classification. <i>Bioinformatics</i> , 2008, 24, 110-117.	1.8	262
7	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.	5.2	198
8	Sequence-specific regulator Prdm14 safeguards mouse ESCs from entering extraembryonic endoderm fates. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 120-127.	3.6	178
9	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, 405-418.	2.0	144
10	Butyrate mediates decrease of histone acetylation centered on transcription start sites and down-regulation of associated genes. <i>Genome Research</i> , 2007, 17, 708-719.	2.4	130
11	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.	5.2	90
12	Histone Acetylation and Methylation at Sites Initiating Divergent Polycistronic Transcription in <i>Trypanosoma cruzi</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 15884-15892.	1.6	89
13	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, 380-392.	2.4	85
14	Imputation of Orofacial Clefting Data Identifies Novel Risk Loci and Sheds Light on the Genetic Background of Cleft Lip ± Cleft Palate and Cleft Palate Only.. <i>Human Molecular Genetics</i> , 2017, 26, ddx012.	1.4	84
15	Forces driving the three-dimensional folding of eukaryotic genomes. <i>Molecular Systems Biology</i> , 2018, 14, e8214.	3.2	75
16	Foxd3 Promotes Exit from Naive Pluripotency through Enhancer Decommissioning and Inhibits Germline Specification. <i>Cell Stem Cell</i> , 2016, 18, 118-133.	5.2	73
17	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, 3435-3447.	1.4	71
18	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, 3067-3072.	3.3	68

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19	Is H3K4me1 at enhancers correlative or causative?. <i>Nature Genetics</i> , 2018, 50, 4-5.	9.4	67
20	Dosage analysis of the 7q11.23 Williams region identifies <i>BAZ1B</i> as a major human gene patterning the modern human face and underlying self-domestication. <i>Science Advances</i> , 2019, 5, eaaw7908.	4.7	67
21	Orphan CpG islands amplify poised enhancer regulatory activity and determine target gene responsiveness. <i>Nature Genetics</i> , 2021, 53, 1036-1049.	9.4	56
22	Niche stiffening compromises hair follicle stem cell potential during ageing by reducing bivalent promoter accessibility. <i>Nature Cell Biology</i> , 2021, 23, 771-781.	4.6	51
23	The chromatin, topological and regulatory properties of pluripotency-associated poised enhancers are conserved in vivo. <i>Nature Communications</i> , 2021, 12, 4344.	5.8	50
24	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.	3.6	49
25	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.	5.2	44
26	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.	2.3	43
27	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-e85.	6.5	34
28	Integrative epigenomic and genomic analysis of malignant pheochromocytoma. <i>Experimental and Molecular Medicine</i> , 2010, 42, 484.	3.2	32
29	Epigenomics-Based Identification of Major Cell Identity Regulators within Heterogeneous Cell Populations. <i>Cell Reports</i> , 2016, 17, 3062-3076.	2.9	29
30	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.	1.1	28
31	Histone H3 lysine 27 trimethylation in adult differentiated colon associated to cancer DNA hypermethylation. <i>Epigenetics</i> , 2009, 4, 107-113.	1.3	25
32	Lineage specific transcription factors and epigenetic regulators mediate TGF $\beta$ 2-dependent enhancer activation. <i>Nucleic Acids Research</i> , 2018, 46, 3351-3365.	6.5	24
33	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.	1.4	21
34	Enhancer-associated H3K4 methylation safeguards in vitro germline competence. <i>Nature Communications</i> , 2021, 12, 5771.	5.8	20
35	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.	1.8	18
36	The ubiquitin-conjugating enzyme UBE2K determines neurogenic potential through histone H3 in human embryonic stem cells. <i>Communications Biology</i> , 2020, 3, 262.	2.0	18

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37	Polycomb proteins as organizers of 3D genome architecture in embryonic stem cells. <i>Briefings in Functional Genomics</i> , 2019, 18, 358-366.	1.3	16
38	Pathological ASXL1 Mutations and Protein Variants Impair Neural Crest Development. <i>Stem Cell Reports</i> , 2019, 12, 861-868.	2.3	16
39	Overarching control of autophagy and DNA damage response by CHD6 revealed by modeling a rare human pathology. <i>Nature Communications</i> , 2021, 12, 3014.	5.8	16
40	The formation of the thumb requires direct modulation of <i>Gli3</i> transcription by <i>Hoxa13</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1090-1096.	3.3	15
41	Enhancer-gene specificity in development and disease. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	15
42	Pioneering Barren Land: Mitotic Bookmarking by Transcription Factors. <i>Developmental Cell</i> , 2013, 24, 342-344.	3.1	12
43	Rare or Overlooked? Structural Disruption of Regulatory Domains in Human Neurocristopathies. <i>Frontiers in Genetics</i> , 2020, 11, 688.	1.1	12
44	Transcriptional and epigenetic control of germline competence and specification. <i>Current Opinion in Cell Biology</i> , 2019, 61, 1-8.	2.6	11
45	MAPRE2 mutations result in altered human cranial neural crest migration, underlying craniofacial malformations in CSC-KT syndrome. <i>Scientific Reports</i> , 2021, 11, 4976.	1.6	10
46	Two polypyrimidine tracts in the nitric oxide synthase 2 gene: similar regulatory sequences with different properties. <i>Molecular Biology Reports</i> , 2010, 37, 2021-2030.	1.0	9
47	Integrative approaches generate insights into the architecture of non-syndromic cleft lip $\hat{\pm}$ cleft palate. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100038.	1.0	8
48	Genetic variation within transcriptional regulatory elements and its implications for human disease. <i>Biological Chemistry</i> , 2014, 395, 1453-1460.	1.2	7
49	JMJD3 intrinsically disordered region links the 3D-genome structure to TGF $\beta$ 2-dependent transcription activation. <i>Nature Communications</i> , 2022, 13, .	5.8	6
50	Chromatin Immunoprecipitation (ChIP) Protocol for Low-abundance Embryonic Samples. <i>Journal of Visualized Experiments</i> , 2017, , .	0.2	4
51	Pioneering of Enhancer Landscapes during Pluripotent State Transitions. <i>Cell Stem Cell</i> , 2018, 23, 149-151.	5.2	2
52	GARLIC: a bioinformatic toolkit for aetiologically connecting diseases and cell type-specific regulatory maps. <i>Human Molecular Genetics</i> , 2016, 26, ddw423.	1.4	1
53	Disruption of the TFAP2A Regulatory Domain Causes Banchio-Oculo-Facial Syndrome (BOFS) and Illuminates Pathomechanisms for Other Human Neurocristopathies. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
54	Enhancer Remodeling During Early Mammalian Embryogenesis: Lessons for Somatic Reprogramming, Rejuvenation, and Aging. <i>Current Stem Cell Reports</i> , 2016, 2, 263-272.	0.7	0

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55	Ready, Set&#226; Poised!: Polycomb target&#228;genes are bound by poised <scp>RNA</scp> &#228;polymerase <scp>II</scp> throughout differentiation. <i>Molecular Systems Biology</i> , 2017, 13, 950.	3.2	0
56	Protocol to study sufficiency of cis-regulatory elements in mouse embryonic stem cells using a CRISPR-mediated knockin approach. <i>STAR Protocols</i> , 2022, 3, 101492.	0.5	0