Altuna Akalin

List of Publications by Year
in descending order

64 papers	7,937 citations	101535 36 h-index	128286 60 g-index
89 all docs	89 docs citations	89 times ranked	15124 citing authors

#	Article	IF	Citations
1	methylKit: a comprehensive R package for the analysis of genome-wide DNA methylation profiles. Genome Biology, 2012, 13, R87.	9.6	1,541
2	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 140, 744-752.	28.9	667
3	Genomic profiling of DNA methyltransferases reveals a role for DNMT3B in genic methylation. Nature, 2015, 520, 243-247.	27.8	566
4	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	21.4	408
5	Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E944-53.	7.1	332
6	Genomic regulatory blocks encompass multiple neighboring genes and maintain conserved synteny in vertebrates. Genome Research, 2007, 17, 545-555.	5.5	312
7	Complex Loci in Human and Mouse Genomes. PLoS Genetics, 2006, 2, e47.	3.5	290
8	Base-Pair Resolution DNA Methylation Sequencing Reveals Profoundly Divergent Epigenetic Landscapes in Acute Myeloid Leukemia. PLoS Genetics, 2012, 8, e1002781.	3.5	263
9	genomation: a toolkit to summarize, annotate and visualize genomic intervals. Bioinformatics, 2015, 31, 1127-1129.	4.1	263
10	Transcriptomic profiling of SARS-CoV-2 infected human cell lines identifies HSP90 as target for COVID-19 therapy. IScience, 2021, 24, 102151.	4.1	202
11	Two independent transcription initiation codes overlap on vertebrate core promoters. Nature, 2014, 507, 381-385.	27.8	182
12	RNA localization is a key determinant of neurite-enriched proteome. Nature Communications, 2017, 8, 583.	12.8	176
13	Zebrafish enhancer detection (ZED) vector: A new tool to facilitate transgenesis and the functional analysis of <i>cis</i>â€‐regulatory regions in zebrafish. Developmental Dynamics, 2009, 238, 2409-2417.	1.8	153
14	DoRiNA 2.0â€"upgrading the doRiNA database of RNA interactions in post-transcriptional regulation. Nucleic Acids Research, 2015, 43, D160-D167.	14.5	136
15	Induction of sarcomas by mutant IDH2. Genes and Development, 2013, 27, 1986-1998.	5.9	135
16	Single-nucleus transcriptomics reveals functional compartmentalization in syncytial skeletal muscle cells. Nature Communications, 2020, 11, 6375.	12.8	122
17	Dynamic regulation of the transcription initiation landscape at single nucleotide resolution during vertebrate embryogenesis. Genome Research, 2013, 23, 1938-1950.	5.5	119
18	Strategies for analyzing bisulfite sequencing data. Journal of Biotechnology, 2017, 261, 105-115.	3.8	113

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19	Cell-type specialization is encoded by specific chromatin topologies. Nature, 2021, 599, 684-691.	27.8	112
20	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	5.5	109
21	An optimized algorithm for detecting and annotating regional differential methylation. BMC Bioinformatics, 2013, 14, S10.	2.6	105
22	Mutations in Disordered Regions Can Cause Disease by Creating Dileucine Motifs. Cell, 2018, 175, 239-253.e17.	28.9	97
23	Single-cell RNA-sequencing of herpes simplex virus 1-infected cells connects NRF2 activation to an antiviral program. Nature Communications, 2019, 10, 4878.	12.8	96
24	Transcriptional features of genomic regulatory blocks. Genome Biology, 2009, 10, R38.	9.6	90
25	FACT Sets a Barrier for Cell Fate Reprogramming in Caenorhabditis elegans and Human Cells. Developmental Cell, 2018, 46, 611-626.e12.	7.0	89
26	Alternative 3â€² UTRs direct localization of functionally diverse protein isoforms in neuronal compartments. Nucleic Acids Research, 2019, 47, 2560-2573.	14.5	86
27	Single-cell analyses of aging, inflammation and senescence. Ageing Research Reviews, 2020, 64, 101156.	10.9	85
28	Differential Evolution of the 13 Atlantic Salmon Hox Clusters. Molecular Biology and Evolution, 2008, 25, 1333-1343.	8.9	66
29	PiGx: reproducible genomics analysis pipelines with GNU Guix. GigaScience, 2018, 7, .	6.4	66
30	Evaluation of colorectal cancer subtypes and cell lines using deep learning. Life Science Alliance, 2019, 2, e201900517.	2.8	65
31	The SIB Swiss Institute of Bioinformaticsâ€™ resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	14.5	64
32	netSmooth: Network-smoothing based imputation for single cell RNA-seq. F1000Research, 2018, 7, 8.	1.6	56
33	Deciphering human ribonucleoprotein regulatory networks. Nucleic Acids Research, 2019, 47, 570-581.	14.5	54
34	Promoter architecture of mouse olfactory receptor genes. Genome Research, 2012, 22, 486-497.	5.5	52
35	Widespread activation of antisense transcription of the host genome during herpes simplex virus 1 infection. Genome Biology, 2017, 18, 209.	8.8	49
36	Deep learning for genomics using Janggu. Nature Communications, 2020, 11, 3488.	12.8	47

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37	RNA polymerase II primes Polycomb‐repressed developmental genes throughout terminal neuronal differentiation. Molecular Systems Biology, 2017, 13, 946.	7.2	44
38	HOT or not: examining the basis of high-occupancy target regions. Nucleic Acids Research, 2019, 47, 5735-5745.	14.5	41
39	The RNA workbench: best practices for RNA and high-throughput sequencing bioinformatics in Galaxy. Nucleic Acids Research, 2017, 45, W560-W566.	14.5	38
40	Long non-coding RNAs defining major subtypes of B cell precursor acute lymphoblastic leukemia. Journal of Hematology and Oncology, 2019, 12, 8.	17.0	38
41	Global identification of functional microRNA-mRNA interactions in Drosophila. Nature Communications, 2019, 10, 1626.	12.8	35
42	Transcriptional repression of *NFKBIA* triggers constitutive IKK‐and proteasome‐independent p65/RelA activation in senescence. EMBO Journal, 2021, 40, e104296.	7.8	34
43	netSmooth: Network-smoothing based imputation for single cell RNA-seq. F1000Research, 2018, 7, 8.	1.6	34
44	RCAS: an RNA centric annotation system for transcriptome-wide regions of interest. Nucleic Acids Research, 2017, 45, e91-e91.	14.5	23
45	Nuclear Organization in the Spinal Cord Depends on Motor Neuron Lamination Orchestrated by Catenin and Afadin Function. Cell Reports, 2018, 22, 1681-1694.	6.4	21
46	The IκB kinase complex is a regulator of mRNA stability. EMBO Journal, 2018, 37, .	7.8	21
47	PHF3 regulates neuronal gene expression through the Pol II CTD reader domain SPOC. Nature Communications, 2021, 12, 6078.	12.8	21
48	Autocrine LTA signaling drives NF-κB and JAK-STAT activity and myeloid gene expression in Hodgkin lymphoma. Blood, 2019, 133, 1489-1494.	1.4	20
49	Identifying tumor cells at the single-cell level using machine learning. Genome Biology, 2022, 23, .	8.8	19
50	Cis-regulatory characterization of sequence conservation surrounding the Hox4 genes. Developmental Biology, 2010, 340, 269-282.	2.0	17
51	Functional interplay of Epstein-Barr virus oncoproteins in a mouse model of B cell lymphomagenesis. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14421-14432.	7.1	17
52	Simultaneous dimensionality reduction and integration for single-cell ATAC-seq data using deep learning. Nature Machine Intelligence, 2022, 4, 162-168.	16.0	15
53	Dissecting the Transcriptional Regulatory Properties of Human Chromosome 16 Highly Conserved Non-Coding Regions. PLoS ONE, 2011, 6, e24824.	2.5	13
54	The conserved histone chaperone LIN‐53 is required for normal lifespan and maintenance of muscle integrity in *Caenorhabditis elegans*. Aging Cell, 2019, 18, e13012.	6.7	13

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55	NanoCAGE analysis of the mouse olfactory epithelium identifies the expression of vomeronasal receptors and of proximal LINE elements. Frontiers in Cellular Neuroscience, 2014, 8, 41.	3.7	11
56	Parallel genetics of regulatory sequences using scalable genome editing inÂvivo. Cell Reports, 2021, 35, 108988.	6.4	9
57	Single-cell-resolved dynamics of chromatin architecture delineate cell and regulatory states in zebrafish embryos. Cell Genomics, 2022, 2, 100083.	6.5	8
58	PDGFA-associated protein 1 protects mature B lymphocytes from stress-induced cell death and promotes antibody gene diversification. Journal of Experimental Medicine, 2020, 217, .	8.5	7
59	Genome-Wide Analysis of DNA Methylation Patterns by High-Throughput Sequencing. , 2016, , 197-221.		5
60	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 141, 369.	28.9	4
61	netSmooth: Network-smoothing based imputation for single cell RNA-seq. F1000Research, 0, 7, 8.	1.6	3
62	Rapid Inflammasome Activation Is Attenuated in Post-Myocardial Infarction Monocytes. Frontiers in Immunology, 2022, 13, 857455.	4.8	3
63	PREDICTING THE BINDING AFFINITY OF MHC CLASS II PEPTIDES. , 2006, , .		2
64	Translog, a web browser for studying the expression divergence of homologous genes. BMC Bioinformatics, 2010, 11, S59.	2.6	0