

Aditi Kanhere

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

1,991
citations

516710

16
h-index

526287

27
g-index

30
all docs

30
docs citations

30
times ranked

4012
citing authors

#	ARTICLE	IF	CITATIONS
1	Combined transcriptomic and phosphoproteomic analysis of BMP4 signaling in human embryonic stem cells. <i>Stem Cell Research</i> , 2021, 50, 102133.	0.7	3
2	Antisense RNAs during early vertebrate development are divided in groups with distinct features. <i>Genome Research</i> , 2021, 31, 995-1010.	5.5	7
3	A long intergenic non-coding RNA regulates nuclear localization of DNA methyl transferase-1. <i>IScience</i> , 2021, 24, 102273.	4.1	7
4	The Missing Link Between Cancer-Associated Variants and LncRNAs. <i>Trends in Genetics</i> , 2021, 37, 410-413.	6.7	4
5	8q24.21 Locus: A Paradigm to Link Non-Coding RNAs, Genome Polymorphisms and Cancer. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1094.	4.1	15
6	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	5.5	109
7	Autoregulation of JARID2 through PRC2 interaction with its antisense ncRNA. <i>BMC Research Notes</i> , 2020, 13, 501.	1.4	0
8	A novel form of JARID2 is required for differentiation in lineage-committed cells. <i>EMBO Journal</i> , 2019, 38, .	7.8	19
9	Regulation of Leukocytes by TspanC8 Tetraspanins and the "Molecular Scissor" ADAM10. <i>Frontiers in Immunology</i> , 2018, 9, 1451.	4.8	24
10	Exercise and high-fat feeding remodel transcript-metabolite interactive networks in mouse skeletal muscle. <i>Scientific Reports</i> , 2017, 7, 13485.	3.3	16
11	Identification of RNA-Protein Interactions Through In Vitro RNA Pull-Down Assays. <i>Methods in Molecular Biology</i> , 2016, 1480, 99-113.	0.9	21
12	Exon junction complex proteins bind nascent transcripts independently of pre-mRNA splicing in <i>Drosophila melanogaster</i> . <i>ELife</i> , 2016, 5, .	6.0	19
13	Genome-Wide Regulatory Analysis Reveals That T-bet Controls Th17 Lineage Differentiation through Direct Suppression of IRF4. <i>Journal of Immunology</i> , 2013, 191, 5925-5932.	0.8	39
14	Modulation of Enhancer Looping and Differential Gene Targeting by Epstein-Barr Virus Transcription Factors Directs Cellular Reprogramming. <i>PLoS Pathogens</i> , 2013, 9, e1003636.	4.7	85
15	Genome-Wide Analyses of Zta Binding to the Epstein-Barr Virus Genome Reveals Interactions in both Early and Late Lytic Cycles and an Epigenetic Switch Leading to an Altered Binding Profile. <i>Journal of Virology</i> , 2012, 86, 12494-12502.	3.4	33
16	Downregulation of Integrin Receptor-Signaling Genes by Epstein-Barr Virus EBNA 3C via Promoter-Proximal and -Distal Binding Elements. <i>Journal of Virology</i> , 2012, 86, 5165-5178.	3.4	40
17	T-bet and GATA3 orchestrate Th1 and Th2 differentiation through lineage-specific targeting of distal regulatory elements. <i>Nature Communications</i> , 2012, 3, 1268.	12.8	292
18	Noncoding RNA localisation mechanisms in chromatin regulation. <i>Silence: A Journal of RNA Regulation</i> , 2012, 3, 2.	8.1	7

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19	IL-2 Regulates Expression of <i>C-MAF</i> in Human CD4 T Cells. <i>Journal of Immunology</i> , 2011, 187, 3721-3729.	0.8	29
20	Short RNAs Are Transcribed from Repressed Polycomb Target Genes and Interact with Polycomb Repressive Complex-2. <i>Molecular Cell</i> , 2010, 38, 675-688.	9.7	338
21	Horizontal Gene Transfers in prokaryotes show differential preferences for metabolic and translational genes. <i>BMC Evolutionary Biology</i> , 2009, 9, 9.	3.2	44
22	CpG-depleted promoters harbor tissue-specific transcription factor binding signals—implications for motif overrepresentation analyses. <i>Nucleic Acids Research</i> , 2009, 37, 6305-6315.	14.5	44
23	Predicting transcription factor affinities to DNA from a biophysical model. <i>Bioinformatics</i> , 2007, 23, 134-141.	4.1	184
24	A novel method for prokaryotic promoter prediction based on DNA stability. <i>BMC Bioinformatics</i> , 2005, 6, 1.	2.6	462
25	Structural properties of promoters: similarities and differences between prokaryotes and eukaryotes. <i>Nucleic Acids Research</i> , 2005, 33, 3165-3175.	14.5	117
26	Identification of the domains for DNA binding and transactivation function of C protein from bacteriophage Mu. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 272-282.	2.6	6
27	An assessment of three dinucleotide parameters to predict DNA curvature by quantitative comparison with experimental data. <i>Nucleic Acids Research</i> , 2003, 31, 2647-2658.	14.5	22