

Ahmet Rasim Barutcu

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

1,240
citations

430442

18
h-index

610482

24
g-index

24
all docs

24
docs citations

24
times ranked

2392
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic mapping of nuclear domain-associated transcripts reveals speckles and lamina as hubs of functionally distinct retained introns. <i>Molecular Cell</i> , 2022, 82, 1035-1052.e9.	4.5	31
2	Interchromosomal interactions: A genomic love story of kissing chromosomes. <i>Journal of Cell Biology</i> , 2019, 218, 27-38.	2.3	98
3	Differential contribution of steady-state <i>scRNA</i> and active transcription in chromatin organization. <i>EMBO Reports</i> , 2019, 20, e48068.	2.0	61
4	Inter-chromosomal Contact Properties in Live-Cell Imaging and in Hi-C. <i>Molecular Cell</i> , 2018, 69, 1039-1045.e3.	4.5	60
5	A TAD boundary is preserved upon deletion of the CTCF-rich Firre locus. <i>Nature Communications</i> , 2018, 9, 1444.	5.8	97
6	Spatiotemporal allele organization by allele-specific CRISPR live-cell imaging (SNP-CLING). <i>Nature Structural and Molecular Biology</i> , 2018, 25, 176-184.	3.6	75
7	Intranuclear and higher-order chromatin organization of the major histone gene cluster in breast cancer. <i>Journal of Cellular Physiology</i> , 2018, 233, 1278-1290.	2.0	40
8	Enhancers in the Peril lincRNA locus regulate distant but not local genes. <i>Genome Biology</i> , 2018, 19, 219.	3.8	20
9	Reorganization of <i>inter</i> chromosomal interactions in the 2q37 deletion syndrome. <i>EMBO Journal</i> , 2018, 37, .	3.5	13
10	The connection between BRG1, CTCF and topoisomerases at TAD boundaries. <i>Nucleus</i> , 2017, 8, 150-155.	0.6	24
11	Identifying Nuclear Matrix-Attached DNA Across the Genome. <i>Journal of Cellular Physiology</i> , 2017, 232, 1295-1305.	2.0	19
12	Chromosomes at Work: Organization of Chromosome Territories in the Interphase Nucleus. <i>Journal of Cellular Biochemistry</i> , 2016, 117, 9-19.	1.2	39
13	Catching the Genome: A Compendium of Chromosome Conformation Capture Methods to Study Higher-Order Chromatin Organization. <i>Journal of Cellular Physiology</i> , 2016, 231, 31-35.	2.0	50
14	RUNX1 contributes to higher-order chromatin organization and gene regulation in breast cancer cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 1389-1397.	0.9	60
15	In Vivo Characterization of Linc-p21 Reveals Functional cis-Regulatory DNA Elements. <i>Cell Reports</i> , 2016, 16, 2178-2186.	2.9	94
16	SMARCA4 regulates gene expression and higher-order chromatin structure in proliferating mammary epithelial cells. <i>Genome Research</i> , 2016, 26, 1188-1201.	2.4	90
17	Chromatin interaction analysis reveals changes in small chromosome and telomere clustering between epithelial and breast cancer cells. <i>Genome Biology</i> , 2015, 16, 214.	3.8	206
18	The bone-specific Runx2-P1 promoter displays conserved three-dimensional chromatin structure with the syntenic Supt3h promoter. <i>Nucleic Acids Research</i> , 2014, 42, 10360-10372.	6.5	28

#	ARTICLE	IF	CITATIONS
19	Epigenetic landscape during osteoblastogenesis defines a differentiation-dependent Runx2 promoter region. <i>Gene</i> , 2014, 550, 1-9.	1.0	28
20	The PPAR γ Locus Makes Long-Range Chromatin Interactions with Selected Tissue-Specific Gene Loci during Adipocyte Differentiation in a Protein Kinase A Dependent Manner. <i>PLoS ONE</i> , 2014, 9, e86140.	1.1	14
21	Cancer-testis gene expression is associated with the methylenetetrahydrofolate reductase 677 C>T polymorphism in non-small cell lung carcinoma. <i>BMC Medical Genetics</i> , 2013, 14, 97.	2.1	5
22	Epigenetic Control of Cell Cycle-Dependent Histone Gene Expression Is a Principal Component of the Abbreviated Pluripotent Cell Cycle. <i>Molecular and Cellular Biology</i> , 2012, 32, 3860-3871.	1.1	25
23	Yeast one-hybrid assays for gene-centered human gene regulatory network mapping. <i>Nature Methods</i> , 2011, 8, 1050-1052.	9.0	48