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List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

8,332
citations

109321

35
h-index

189892

50
g-index

56
all docs

56
docs citations

56
times ranked

11649
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromosome Conformation Capture Carbon Copy (5C): A massively parallel solution for mapping interactions between genomic elements. <i>Genome Research</i> , 2006, 16, 1299-1309.	5.5	1,026
2	miRNPs: a novel class of ribonucleoproteins containing numerous microRNAs. <i>Genes and Development</i> , 2002, 16, 720-728.	5.9	926
3	Complex multi-enhancer contacts captured by genome architecture mapping. <i>Nature</i> , 2017, 543, 519-524.	27.8	562
4	Complexity of chromatin folding is captured by the strings and binders switch model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16173-16178.	7.1	493
5	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. <i>Nature</i> , 2015, 526, 112-117.	27.8	483
6	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
7	Gene expression during acute and prolonged hypoxia is regulated by distinct mechanisms of translational control. <i>EMBO Journal</i> , 2006, 25, 1114-1125.	7.8	328
8	Numerous microRNPs in neuronal cells containing novel microRNAs. <i>Rna</i> , 2003, 9, 180-186.	3.5	321
9	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. <i>Molecular Systems Biology</i> , 2015, 11, 852.	7.2	305
10	Spatial genome organization: contrasting views from chromosome conformation capture and fluorescence in situ hybridization. <i>Genes and Development</i> , 2014, 28, 2778-2791.	5.9	230
11	eIF4A3 is a novel component of the exon junction complex. <i>Rna</i> , 2004, 10, 200-209.	3.5	215
12	A role for the eIF4E-binding protein 4E-T in P-body formation and mRNA decay. <i>Journal of Cell Biology</i> , 2005, 170, 913-924.	5.2	210
13	Pharmacological inhibition of DNA-PK stimulates Cas9-mediated genome editing. <i>Genome Medicine</i> , 2015, 7, 93.	8.2	199
14	Suppression of cap-dependent translation in mitosis. <i>Genes and Development</i> , 2001, 15, 2083-2093.	5.9	192
15	Translation Is Required to Remove Y14 from mRNAs in the Cytoplasm. <i>Current Biology</i> , 2002, 12, 1060-1067.	3.9	191
16	An Overview of Genome Organization and How We Got There: from FISH to Hi-C. <i>Microbiology and Molecular Biology Reviews</i> , 2015, 79, 347-372.	6.6	190
17	Mapping networks of physical interactions between genomic elements using 5C technology. <i>Nature Protocols</i> , 2007, 2, 988-1002.	12.0	180
18	Clustering of Tissue-Specific Sub-TADs Accompanies the Regulation of HoxA Genes in Developing Limbs. <i>PLoS Genetics</i> , 2013, 9, e1004018.	3.5	164

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19	Three-dimensional modeling of chromatin structure from interaction frequency data using Markov chain Monte Carlo sampling. <i>BMC Bioinformatics</i> , 2011, 12, 414.	2.6	151
20	The three-dimensional architecture of Hox cluster silencing. <i>Nucleic Acids Research</i> , 2010, 38, 7472-7484.	14.5	126
21	SMARCA4 loss is synthetic lethal with CDK4/6 inhibition in non-small cell lung cancer. <i>Nature Communications</i> , 2019, 10, 557.	12.8	125
22	Nuclear Eukaryotic Initiation Factor 4e (Eif4e) Colocalizes with Splicing Factors in Speckles. <i>Journal of Cell Biology</i> , 2000, 148, 239-246.	5.2	119
23	Repurposing CRISPR/Cas9 for in situ functional assays. <i>Genes and Development</i> , 2013, 27, 2602-2614.	5.9	110
24	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	5.5	109
25	Chromatin conformation signatures of cellular differentiation. <i>Genome Biology</i> , 2009, 10, R37.	9.6	108
26	Protospacer Adjacent Motif (PAM)-Distal Sequences Engage CRISPR Cas9 DNA Target Cleavage. <i>PLoS ONE</i> , 2014, 9, e109213.	2.5	94
27	Disease-Causing 7.4 kb Cis-Regulatory Deletion Disrupting Conserved Non-Coding Sequences and Their Interaction with the FOXL2 Promotor: Implications for Mutation Screening. <i>PLoS Genetics</i> , 2009, 5, e1000522.	3.5	83
28	CDK4/6 inhibitors target SMARCA4-determined cyclin D1 deficiency in hypercalcemic small cell carcinoma of the ovary. <i>Nature Communications</i> , 2019, 10, 558.	12.8	76
29	Reciprocal regulation of chromatin state and architecture by HOTAIRM1 contributes to temporal collinear HOXA gene activation. <i>Nucleic Acids Research</i> , 2016, 45, gkw966.	14.5	56
30	Chromosome organization in the nucleus â€” charting new territory across the Hi-Cs. <i>Current Opinion in Genetics and Development</i> , 2012, 22, 125-131.	3.3	52
31	PAM multiplicity marks genomic target sites as inhibitory to CRISPR-Cas9 editing. <i>Nature Communications</i> , 2015, 6, 10124.	12.8	52
32	Shaping the Genome with Non-Coding RNAs. <i>Current Genomics</i> , 2011, 12, 307-321.	1.6	45
33	Hox in motion: tracking HoxA cluster conformation during differentiation. <i>Nucleic Acids Research</i> , 2014, 42, 1524-1540.	14.5	45
34	From cells to chromatin: Capturing snapshots of genome organization with 5C technology. <i>Methods</i> , 2012, 58, 255-267.	3.8	42
35	Chromosome Conformation Capture Carbon Copy Technology. <i>Current Protocols in Molecular Biology</i> , 2007, 80, Unit 21.14.	2.9	39
36	Chromatin conformation signatures: ideal human disease biomarkers?. <i>Biomarkers in Medicine</i> , 2010, 4, 611-629.	1.4	39

#	ARTICLE	IF	CITATIONS
37	Discovering genome regulation with 3C and 3C-related technologies. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 401-410.	1.9	34
38	Classifying leukemia types with chromatin conformation data. <i>Genome Biology</i> , 2014, 15, R60.	9.6	32
39	PRC2-Associated Chromatin Contacts in the Developing Limb Reveal a Possible Mechanism for the Atypical Role of PRC2 in HoxA Gene Expression. <i>Developmental Cell</i> , 2019, 50, 184-196.e4.	7.0	30
40	Computing Chromosome Conformation. <i>Methods in Molecular Biology</i> , 2010, 674, 251-268.	0.9	24
41	HiFi: estimating DNA-DNA interaction frequency from Hi-C data at restriction-fragment resolution. <i>Genome Biology</i> , 2020, 21, 11.	8.8	24
42	A Torrent of Data: Mapping Chromatin Organization Using 5C and High-Throughput Sequencing. <i>Methods in Enzymology</i> , 2012, 513, 113-141.	1.0	23
43	Analysis of long-range interactions in primary human cells identifies cooperative <i>CFTR</i> regulatory elements. <i>Nucleic Acids Research</i> , 2016, 44, 2564-2576.	14.5	19
44	Double-Stranded Biotinylated Donor Enhances Homology-Directed Repair in Combination with Cas9 Monoavidin in Mammalian Cells. <i>CRISPR Journal</i> , 2018, 1, 414-430.	2.9	12
45	Chromosome folding and its regulation in health and disease. <i>Current Opinion in Genetics and Development</i> , 2017, 43, 23-30.	3.3	9
46	Spatial Organization of Epigenomes. <i>Current Molecular Biology Reports</i> , 2016, 2, 1-9.	1.6	4
47	2C-ChIP: measuring chromatin immunoprecipitation signal from defined genomic regions with deep sequencing. <i>BMC Genomics</i> , 2019, 20, 162.	2.8	4
48	Novel long-range regulatory mechanisms controlling PKD2 gene expression. <i>BMC Genomics</i> , 2018, 19, 515.	2.8	3
49	LAMPS: an analysis pipeline for sequence-specific ligation-mediated amplification reads. <i>BMC Research Notes</i> , 2020, 13, 273.	1.4	3
50	3D genome mapping and analysis methods. <i>Methods</i> , 2018, 142, 1-2.	3.8	2
51	Mapping and Visualizing Spatial Genome Organization. , 2016, , 359-383.		0
52	PRC2-Dependent Tissue-Specific 3D Architecture in the Developing Limb Reveals a Possible Mechanism for the Atypical Role of PRC2 in Gene Activation. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
53	Profiling Chromatin Landscape at High Resolution and Throughput with 2C-ChIP. <i>Methods in Molecular Biology</i> , 2021, 2157, 127-157.	0.9	0