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List of Publications by Year
in descending order

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25 papers	8,051 citations	393982 19 h-index	580395 25 g-index
25 all docs	25 docs citations	25 times ranked	13935 citing authors

#	Article	IF	Citations
1	High-Resolution Profiling of Histone Methylations in the Human Genome. Cell, 2007, 129, 823-837.	13.5	6,036
2	Intragenic DNA methylation modulates alternative splicing by recruiting MeCP2 to promote exon recognition. Cell Research, 2013, 23, 1256-1269.	5.7	489
3	Characterization of genome-wide enhancer-promoter interactions reveals co-expression of interacting genes and modes of higher order chromatin organization. Cell Research, 2012, 22, 490-503.	5.7	238
4	Epigenome Mapping in Normal and Disease States. Circulation Research, 2010, 107, 327-339.	2.0	164
5	Pol II and its associated epigenetic marks are present at Pol IIIâ€“transcribed noncoding RNA genes. Nature Structural and Molecular Biology, 2010, 17, 629-634.	3.6	161
6	Detection of single nucleotide variations in expressed exons of the human genome using RNA-Seq. Nucleic Acids Research, 2009, 37, e106-e106.	6.5	152
7	Critical role of histone demethylase Jmjd3 in the regulation of CD4+ T-cell differentiation. Nature Communications, 2014, 5, 5780.	5.8	136
8	Dynamic regulation of alternative splicing and chromatin structure in Drosophila gonads revealed by RNA-seq. Cell Research, 2010, 20, 763-783.	5.7	107
9	Cell Fate Determination Factor Dachshund Reprograms Breast Cancer Stem Cell Function. Journal of Biological Chemistry, 2011, 286, 2132-2142.	1.6	74
10	Common inversion polymorphism at 17q21.31 affects expression of multiple genes in tissue-specific manner. BMC Genomics, 2012, 13, 458.	1.2	62
11	Attenuation of Forkhead signaling by the retinal determination factor DACH1. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6864-6869.	3.3	58
12	CTCF boundary remodels chromatin domain and drives aberrant HOX gene transcription in acute myeloid leukemia. Blood, 2018, 132, 837-848.	0.6	56
13	Mapping of INS promoter interactions reveals its role in long-range regulation of SYT8 transcription. Nature Structural and Molecular Biology, 2011, 18, 372-378.	3.6	55
14	Stage-Dependent and Locus-Specific Role of Histone Demethylase Jumonji D3 (JMJD3) in the Embryonic Stages of Lung Development. PLoS Genetics, 2014, 10, e1004524.	1.5	50
15	Long-distance interactions ofD-brane bound states and longitudinal five-brane inM(atrix) theory. Physical Review D, 1997, 56, 3672-3685.	1.6	32
16	Response: Mapping Nucleosome Positions Using ChIP-Seq Data. Cell, 2007, 131, 832-833.	13.5	32
17	Epsteinâ€“Barr virus nuclear antigen 2 extensively rewires the human chromatin landscape at autoimmune risk loci. Genome Research, 2021, 31, 2185-2198.	2.4	24
18	The Effect of Inversion at 8p23 on BLK Association with Lupus in Caucasian Population. PLoS ONE, 2014, 9, e115614.	1.1	23

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19	Alternative splicing switching in stem cell lineages. Frontiers in Biology, 2013, 8, 50-59.	0.7	22
20	Cyclin D1 integrates G9a-mediated histone methylation. Oncogene, 2019, 38, 4232-4249.	2.6	20
21	A Barrier-Only Boundary Element Delimits the Formation of Facultative Heterochromatin in Drosophila melanogaster and Vertebrates. Molecular and Cellular Biology, 2011, 31, 2729-2741.	1.1	19
22	Alteration of CTCF-associated chromatin neighborhood inhibits TAL1-driven oncogenic transcription program and leukemogenesis. Nucleic Acids Research, 2020, 48, 3119-3133.	6.5	19
23	Genomeâ€wide chromatin occupancy of BRDT and gene expression analysis suggest transcriptional partners and specific epigenetic landscapes that regulate gene expression during spermatogenesis. Molecular Reproduction and Development, 2021, 88, 141-157.	1.0	9
24	Tissue-specific expression of IL-15RA alternative splicing transcripts and its regulation by DNA methylation. European Cytokine Network, 2010, 21, 308-18.	1.1	8
25	Validation of lowâ€coverage wholeâ€genome sequencing for mitochondrial DNA variants suggests mitochondrial DNA as a genetic cause of preterm birth. Human Mutation, 2021, 42, 1602-1614.	1.1	5