

Xiaoyun Xing

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

3,902
citations

394421

19
h-index

477307

29
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docs citations

31
times ranked

8046
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome profiling of DNA methylation and hydroxymethylation identifies distinct regulatory programs among innate lymphocytes. <i>Nature Immunology</i> , 2022, 23, 619-631.	14.5	14
2	A genome-wide CRISPR-Cas9 knockout screen identifies essential and growth-restricting genes in human trophoblast stem cells. <i>Nature Communications</i> , 2022, 13, 2548.	12.8	25
3	Common DNA methylation dynamics in endometriod adenocarcinoma and glioblastoma suggest universal epigenomic alterations in tumorigenesis. <i>Communications Biology</i> , 2021, 4, 607.	4.4	9
4	Abstract 2225: Transposable elements are an abundant and pan-cancer source of shared tumor-specific antigens and membrane targets. , 2021, , .		0
5	OCT4 cooperates with distinct ATP-dependent chromatin remodelers in na ⁺ and primed pluripotent states in human. <i>Nature Communications</i> , 2021, 12, 5123.	12.8	17
6	Epigenetic dynamics shaping melanophore and iridophore cell fate in zebrafish. <i>Genome Biology</i> , 2021, 22, 282.	8.8	8
7	Requisite Chromatin Remodeling for Myeloid and Erythroid Lineage Differentiation from Erythromyeloid Progenitors. <i>Cell Reports</i> , 2020, 33, 108395.	6.4	6
8	A map of cis-regulatory elements and 3D genome structures in zebrafish. <i>Nature</i> , 2020, 588, 337-343.	27.8	80
9	Comparison of differential accessibility analysis strategies for ATAC-seq data. <i>Scientific Reports</i> , 2020, 10, 10150.	3.3	32
10	DeepH&M: Estimating single-CpG hydroxymethylation and methylation levels from enrichment and restriction enzyme sequencing methods. <i>Science Advances</i> , 2020, 6, .	10.3	8
11	Derivation of trophoblast stem cells from na ⁺ human pluripotent stem cells. <i>ELife</i> , 2020, 9, .	6.0	203
12	Transposable elements drive widespread expression of oncogenes in human cancers. <i>Nature Genetics</i> , 2019, 51, 611-617.	21.4	253
13	Soluble inflammatory mediators induce transcriptional re-organization that is independent of dna methylation changes in cultured human chorionic villous trophoblasts. <i>Journal of Reproductive Immunology</i> , 2018, 128, 2-8.	1.9	3
14	Whole-Genome DNA Methylation Profiling Identifies Epigenetic Signatures of Uterine Carcinosarcoma. <i>Neoplasia</i> , 2017, 19, 100-111.	5.3	27
15	Functional cis-regulatory modules encoded by mouse-specific endogenous retrovirus. <i>Nature Communications</i> , 2017, 8, 14550.	12.8	73
16	MicroRNAs Induce a Permissive Chromatin Environment that Enables Neuronal Subtype-Specific Reprogramming of Adult Human Fibroblasts. <i>Cell Stem Cell</i> , 2017, 21, 332-348.e9.	11.1	112
17	Uncovering the transcriptomic and epigenomic landscape of nicotinic receptor genes in non-neuronal tissues. <i>BMC Genomics</i> , 2017, 18, 439.	2.8	15
18	Tissue-specific DNA methylation is conserved across human, mouse, and rat, and driven by primary sequence conservation. <i>BMC Genomics</i> , 2017, 18, 724.	2.8	71

#	ARTICLE	IF	CITATIONS
19	Inhibition of DNA Methyltransferases Blocks Mutant Huntingtin-Induced Neurotoxicity. <i>Scientific Reports</i> , 2016, 6, 31022.	3.3	28
20	Mapping of Variable DNA Methylation Across Multiple Cell Types Defines a Dynamic Regulatory Landscape of the Human Genome. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 973-986.	1.8	41
21	Perinatal deiodinase 2 expression in hepatocytes defines epigenetic susceptibility to liver steatosis and obesity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14018-14023.	7.1	34
22	Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015, 6, 6363.	12.8	91
23	Combining MeDIP-seq and MRE-seq to investigate genome-wide CpG methylation. <i>Methods</i> , 2015, 72, 29-40.	3.8	93
24	Comparative DNA methylome analysis of endometrial carcinoma reveals complex and distinct deregulation of cancer promoters and enhancers. <i>BMC Genomics</i> , 2014, 15, 868.	2.8	49
25	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.	27.8	259
26	Widespread contribution of transposable elements to the innovation of gene regulatory networks. <i>Genome Research</i> , 2014, 24, 1963-1976.	5.5	408
27	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. <i>Nature Genetics</i> , 2013, 45, 836-841.	21.4	207
28	Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. <i>Genome Research</i> , 2013, 23, 1522-1540.	5.5	162
29	Conserved role of intragenic DNA methylation in regulating alternative promoters. <i>Nature</i> , 2010, 466, 253-257.	27.8	1,568