

Yanxiao Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2211906/publications.pdf>

Version: 2024-02-01

26
papers

2,321
citations

586496

16
h-index

759306

22
g-index

36
all docs

36
docs citations

36
times ranked

4848
citing authors

#	ARTICLE	IF	CITATIONS
1	Joint profiling of histone modifications and transcriptome in single cells from mouse brain. <i>Nature Methods</i> , 2021, 18, 283-292.	9.0	171
2	Comprehensive analysis of single cell ATAC-seq data with SnapATAC. <i>Nature Communications</i> , 2021, 12, 1337.	5.8	253
3	CTCF mediates dosage- and sequence-context-dependent transcriptional insulation by forming local chromatin domains. <i>Nature Genetics</i> , 2021, 53, 1064-1074.	9.4	90
4	Cardiac cell type-specific gene regulatory programs and disease risk association. <i>Science Advances</i> , 2021, 7, .	4.7	63
5	SnapHiC: a computational pipeline to identify chromatin loops from single-cell Hi-C data. <i>Nature Methods</i> , 2021, 18, 1056-1059.	9.0	46
6	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	13.7	257
7	Significant association between host transcriptome-derived HPV oncogene E6 * influence score and carcinogenic pathways, tumor size, and survival in head and neck cancer. <i>Head and Neck</i> , 2020, 42, 2375-2389.	0.9	9
8	Genome-wide association and multi-omic analyses reveal ACTN2 as a gene linked to heart failure. <i>Nature Communications</i> , 2020, 11, 1122.	5.8	57
9	Transcriptionally active HERV-H retrotransposons demarcate topologically associating domains in human pluripotent stem cells. <i>Nature Genetics</i> , 2019, 51, 1380-1388.	9.4	236
10	Joint profiling of DNA methylation and chromatin architecture in single cells. <i>Nature Methods</i> , 2019, 16, 991-993.	9.0	155
11	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. <i>PLoS Computational Biology</i> , 2019, 15, e1006982.	1.5	94
12	Degeneration of Injured Axons and Dendrites Requires Restraint of a Protective JNK Signaling Pathway by the Transmembrane Protein Raw. <i>Journal of Neuroscience</i> , 2019, 39, 8457-8470.	1.7	11
13	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. <i>Nature Neuroscience</i> , 2018, 21, 432-439.	7.1	290
14	HPV Integration in HNSCC Correlates with Survival Outcomes, Immune Response Signatures, and Candidate Drivers. <i>Molecular Cancer Research</i> , 2018, 16, 90-102.	1.5	151
15	Expressed HNSCC variants by HPV-status in a well-characterized Michigan cohort. <i>Scientific Reports</i> , 2018, 8, 11458.	1.6	18
16	A Scalable Epitope Tagging Approach for High Throughput ChIP-Seq Analysis. <i>ACS Synthetic Biology</i> , 2017, 6, 1034-1042.	1.9	19
17	Genomic binding of PAX8-PPARG fusion protein regulates cancer-related pathways and alters the immune landscape of thyroid cancer. <i>Oncotarget</i> , 2017, 8, 5761-5773.	0.8	14
18	Subtypes of HPV-Positive Head and Neck Cancers Are Associated with HPV Characteristics, Copy Number Alterations, PIK3CA Mutation, and Pathway Signatures. <i>Clinical Cancer Research</i> , 2016, 22, 4735-4745.	3.2	107

#	ARTICLE	IF	CITATIONS
19	Adipogenic Differentiation of Thyroid Cancer Cells Through the Pax8-PPAR γ Fusion Protein Is Regulated by Thyroid Transcription Factor 1 (TTF-1). <i>Journal of Biological Chemistry</i> , 2016, 291, 19274-19286.	1.6	14
20	Abstract 1511: Mutational signatures from RNA-seq data distinguish HPV(+) and HPV(-) HNSCC. , 2016, , .		0
21	Abstract 1515: Identification and characterization of HPV-host fusion transcripts in HNSCCs. , 2016, , .		0
22	Genomic binding and regulation of gene expression by the thyroid carcinoma-associated PAX8-PPARG fusion protein. <i>Oncotarget</i> , 2015, 6, 40418-40432.	0.8	19
23	Abstract 2180: Immune, keratinocyte, and fibroblast expression signatures distinguish HNSCC samples by HPV status. , 2015, , .		0
24	Abstract 4808: Identification of genes with variants in HPV-associated head and neck squamous cell carcinoma. , 2015, , .		0
25	Abstract 2184: Gene expression analysis of human papillomavirus positive head and neck cancer primary tumor samples reveals two distinct subgroups. , 2015, , .		0
26	PePr: a peak-calling prioritization pipeline to identify consistent or differential peaks from replicated ChIP-Seq data. <i>Bioinformatics</i> , 2014, 30, 2568-2575.	1.8	114