Shirley X Zhu

List of Publications by Year
in descending order

63 papers	33,062 citations	66343 42 h-index	133252 59 g-index
63 all docs	63 docs citations	63 times ranked	47884 citing authors

#	ARTICLE	IF	CITATIONS
1	Model-based Analysis of ChIP-Seq (MACS). Genome Biology, 2008, 9, R137.	9.6	13,517
2	TIMER: A Web Server for Comprehensive Analysis of Tumor-Infiltrating Immune Cells. Cancer Research, 2017, 77, e108-e110.	0.9	4,049
3	Signatures of T cell dysfunction and exclusion predict cancer immunotherapy response. Nature Medicine, 2018, 24, 1550-1558.	30.7	2,791
4	TIMER2.0 for analysis of tumor-infiltrating immune cells. Nucleic Acids Research, 2020, 48, W509-W514.	14.5	2,546
5	Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. Genome Biology, 2016, 17, 174.	8.8	1,768
6	A single-cell and spatially resolved atlas of human breast cancers. Nature Genetics, 2021, 53, 1334-1347.	21.4	535
7	Cistrome Data Browser: expanded datasets and new tools for gene regulatory analysis. Nucleic Acids Research, 2019, 47, D729-D735.	14.5	527
8	Sequence determinants of improved CRISPR sgRNA design. Genome Research, 2015, 25, 1147-1157.	5.5	514
9	Large-scale public data reuse to model immunotherapy response and resistance. Genome Medicine, 2020, 12, 21.	8.2	514
10	Response and resistance to BET bromodomain inhibitors in triple-negative breast cancer. Nature, 2016, 529, 413-417.	27.8	490
11	Cistrome Data Browser: a data portal for ChIP-Seq and chromatin accessibility data in human and mouse. Nucleic Acids Research, 2017, 45, D658-D662.	14.5	451
12	Overcoming Therapeutic Resistance in HER2-Positive Breast Cancers with CDK4/6 Inhibitors. Cancer Cell, 2016, 29, 255-269.	16.8	356
13	Quality control, modeling, and visualization of CRISPR screens with MAGeCK-VISPR. Genome Biology, 2015, 16, 281.	8.8	330
14	Identifying and mitigating bias in next-generation sequencing methods for chromatin biology. Nature Reviews Genetics, 2014, 15, 709-721.	16.3	295
15	Landscape of tumor-infiltrating T cell repertoire of human cancers. Nature Genetics, 2016, 48, 725-732.	21.4	288
16	Integrative analysis of pooled CRISPR genetic screens using MAGeCKFlute. Nature Protocols, 2019, 14, 756-780.	12.0	260
17	Stromal cell diversity associated with immune evasion in human triple-negative breast cancer. EMBO Journal, 2020, 39, e104063.	7.8	224
18	NOTCH1–RBPJ complexes drive target gene expression through dynamic interactions with superenhancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 705-710.	7.1	218

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19	Inhibitory CD161 receptor identified in glioma-infiltrating T cells by single-cell analysis. Cell, 2021, 184, 1281-1298.e26.	28.9	210
20	Allele-Specific Chromatin Recruitment and Therapeutic Vulnerabilities of ESR1 Activating Mutations. Cancer Cell, 2018, 33, 173-186.e5.	16.8	201
21	Applications of Immunogenomics to Cancer. Cell, 2017, 168, 600-612.	28.9	198
22	Acetylation-dependent regulation of PD-L1 nuclear translocation dictates the efficacy of anti-PD-1 immunotherapy. Nature Cell Biology, 2020, 22, 1064-1075.	10.3	182
23	JARID1B Is a Luminal Lineage-Driving Oncogene in Breast Cancer. Cancer Cell, 2014, 25, 762-777.	16.8	170
24	VIPER: Visualization Pipeline for RNA-seq, a Snakemake workflow for efficient and complete RNA-seq analysis. BMC Bioinformatics, 2018, 19, 135.	2.6	156
25	Predicting Anticancer Drug Responses Using a Dual-Layer Integrated Cell Line-Drug Network Model. PLoS Computational Biology, 2015, 11, e1004498.	3.2	152
26	Cistrome Cancer: A Web Resource for Integrative Gene Regulation Modeling in Cancer. Cancer Research, 2017, 77, e19-e22.	0.9	130
27	ARv7 Represses Tumor-Suppressor Genes in Castration-Resistant Prostate Cancer. Cancer Cell, 2019, 35, 401-413.e6.	16.8	127
28	Integrative analyses of single-cell transcriptome and regulome using MAESTRO. Genome Biology, 2020, 21, 198.	8.8	126
29	Discovery of Biomarkers Predictive of GSI Response in Triple-Negative Breast Cancer and Adenoid Cystic Carcinoma. Cancer Discovery, 2014, 4, 1154-1167.	9.4	123
30	Mass cytometry of Hodgkin lymphoma reveals a CD4+ regulatory T-cell–rich and exhausted T-effector microenvironment. Blood, 2018, 132, 825-836.	1.4	121
31	Lysine-Specific Demethylase 1 Has Dual Functions as a Major Regulator of Androgen Receptor Transcriptional Activity. Cell Reports, 2014, 9, 1618-1627.	6.4	115
32	Synthetic Lethal and Resistance Interactions with BET Bromodomain Inhibitors in Triple-Negative Breast Cancer. Molecular Cell, 2020, 78, 1096-1113.e8.	9.7	114
33	ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline. BMC Bioinformatics, 2016, 17, 404.	2.6	100
34	Snail1-dependent p53 repression regulates expansion and activity of tumour-initiating cells in breast cancer. Nature Cell Biology, 2016, 18, 1221-1232.	10.3	90
35	In vivo CRISPR screens identify the E3 ligase Cop1 as a modulator of macrophage infiltration and cancer immunotherapy target. Cell, 2021, 184, 5357-5374.e22.	28.9	79
36	Cistrome-GO: a web server for functional enrichment analysis of transcription factor ChIP-seq peaks. Nucleic Acids Research, 2019, 47, W206-W211.	14.5	76

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37	Modeling *cis*-regulation with a compendium of genome-wide histone H3K27ac profiles. Genome Research, 2016, 26, 1417-1429.	5.5	75
38	Ultrasensitive detection of TCR hypervariable-region sequences in solid-tissue RNA–seq data. Nature Genetics, 2017, 49, 482-483.	21.4	66
39	Big data mining yields novel insights on cancer. Nature Genetics, 2015, 47, 103-104.	21.4	64
40	Kidney Cancer Is Characterized by Aberrant Methylation of Tissue-Specific Enhancers That Are Prognostic for Overall Survival. Clinical Cancer Research, 2014, 20, 4349-4360.	7.0	60
41	Immunostimulatory Cancer-Associated Fibroblast Subpopulations Can Predict Immunotherapy Response in Head and Neck Cancer. Clinical Cancer Research, 2022, 28, 2094-2109.	7.0	60
42	Subtype heterogeneity and epigenetic convergence in neuroendocrine prostate cancer. Nature Communications, 2021, 12, 5775.	12.8	59
43	MYC drives aggressive prostate cancer by disrupting transcriptional pause release at androgen receptor targets. Nature Communications, 2022, 13, 2559.	12.8	56
44	Network analysis of gene essentiality in functional genomics experiments. Genome Biology, 2015, 16, 239.	8.8	50
45	Getting Started in Tiling Microarray Analysis. PLoS Computational Biology, 2007, 3, e183.	3.2	49
46	Revisit linear regression-based deconvolution methods for tumor gene expression data. Genome Biology, 2017, 18, 127.	8.8	45
47	CARM1 Inhibition Enables Immunotherapy of Resistant Tumors by Dual Action on Tumor Cells and T Cells. Cancer Discovery, 2021, 11, 2050-2071.	9.4	43
48	Genome-Scale Signatures of Gene Interaction from Compound Screens Predict Clinical Efficacy of Targeted Cancer Therapies. Cell Systems, 2018, 6, 343-354.e5.	6.2	40
49	Genome-wide identification and characterization of Notch transcription complex–binding sequence-paired sites in leukemia cells. Science Signaling, 2017, 10, .	3.6	39
50	Active enhancers are delineated de novo during hematopoiesis, with limited lineage fidelity among specified primary blood cells. Genes and Development, 2014, 28, 1827-1839.	5.9	38
51	Systematic characterization of mutations altering protein degradation in human cancers. Molecular Cell, 2021, 81, 1292-1308.e11.	9.7	36
52	Inhibition of MAN2A1 Enhances the Immune Response to Anti–PD-L1 in Human Tumors. Clinical Cancer Research, 2020, 26, 5990-6002.	7.0	28
53	Targeting the MIF/CXCR7/AKT Signaling Pathway in Castration-Resistant Prostate Cancer. Molecular Cancer Research, 2019, 17, 263-276.	3.4	27
54	FGFR-inhibitor-mediated dismissal of SWI/SNF complexes from YAP-dependent enhancers induces adaptive therapeutic resistance. Nature Cell Biology, 2021, 23, 1187-1198.	10.3	21

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55	CoBRA: Containerized Bioinformatics Workflow for Reproducible ChIP/ATAC-seq Analysis. Genomics, Proteomics and Bioinformatics, 2021, 19, 652-661.	6.9	18
56	PHF8 and REST/NRSF co-occupy gene promoters to regulate proximal gene expression. Scientific Reports, 2014, 4, 5008.	3.3	16
57	CRISPR Screens Identify Essential Cell Growth Mediators in BRAF Inhibitor-resistant Melanoma. Genomics, Proteomics and Bioinformatics, 2020, 18, 26-40.	6.9	14
58	Topical therapy for regression and melanoma prevention of congenital giant nevi. Cell, 2022, 185, 2071-2085.e12.	28.9	13
59	ChIP-Chip: Algorithms for Calling Binding Sites. Methods in Molecular Biology, 2009, 556, 165-175.	0.9	2
60	Erratum for Verzi et al., Intestinal Master Transcription Factor CDX2 Controls Chromatin Access for Partner Transcription Factor Binding. Molecular and Cellular Biology, 2015, 35, 496-496.	2.3	0
61	Computational Approaches to Modeling Transcription Factor Activity and Gene Regulation. Trends in Biochemical Sciences, 2020, 45, 1094-1095.	7.5	0
62	Neural network architecture search with AMBER. Nature Machine Intelligence, 2021, 3, 372-373.	16.0	0
63	Analysis of ChIP-chip Data on Genome Tiling Microarrays. Frontiers of Statistics, 2009, , 239-257.	0.2	0