

# Shirley X Zhu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1719206/publications.pdf>

Version: 2024-02-01

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	Immunostimulatory Cancer-Associated Fibroblast Subpopulations Can Predict Immunotherapy Response in Head and Neck Cancer. <i>Clinical Cancer Research</i> , 2022, 28, 2094-2109.	7.0	60
2	Topical therapy for regression and melanoma prevention of congenital giant nevi. <i>Cell</i> , 2022, 185, 2071-2085.e12.	28.9	13
3	MYC drives aggressive prostate cancer by disrupting transcriptional pause release at androgen receptor targets. <i>Nature Communications</i> , 2022, 13, 2559.	12.8	56
4	CARM1 Inhibition Enables Immunotherapy of Resistant Tumors by Dual Action on Tumor Cells and T Cells. <i>Cancer Discovery</i> , 2021, 11, 2050-2071.	9.4	43
5	Systematic characterization of mutations altering protein degradation in human cancers. <i>Molecular Cell</i> , 2021, 81, 1292-1308.e11.	9.7	36
6	Inhibitory CD161 receptor identified in glioma-infiltrating T cells by single-cell analysis. <i>Cell</i> , 2021, 184, 1281-1298.e26.	28.9	210
7	Neural network architecture search with AMBER. <i>Nature Machine Intelligence</i> , 2021, 3, 372-373.	16.0	0
8	CoBRA: Containerized Bioinformatics Workflow for Reproducible CHIP/ATAC-seq Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 652-661.	6.9	18
9	A single-cell and spatially resolved atlas of human breast cancers. <i>Nature Genetics</i> , 2021, 53, 1334-1347.	21.4	535
10	In vivo CRISPR screens identify the E3 ligase Cop1 as a modulator of macrophage infiltration and cancer immunotherapy target. <i>Cell</i> , 2021, 184, 5357-5374.e22.	28.9	79
11	Subtype heterogeneity and epigenetic convergence in neuroendocrine prostate cancer. <i>Nature Communications</i> , 2021, 12, 5775.	12.8	59
12	FGFR-inhibitor-mediated dismissal of SWI/SNF complexes from YAP-dependent enhancers induces adaptive therapeutic resistance. <i>Nature Cell Biology</i> , 2021, 23, 1187-1198.	10.3	21
13	Stromal cell diversity associated with immune evasion in human triple-negative breast cancer. <i>EMBO Journal</i> , 2020, 39, e104063.	7.8	224
14	Computational Approaches to Modeling Transcription Factor Activity and Gene Regulation. <i>Trends in Biochemical Sciences</i> , 2020, 45, 1094-1095.	7.5	0
15	Integrative analyses of single-cell transcriptome and regulome using MAESTRO. <i>Genome Biology</i> , 2020, 21, 198.	8.8	126
16	Inhibition of MAN2A1 Enhances the Immune Response to Anti-PD-L1 in Human Tumors. <i>Clinical Cancer Research</i> , 2020, 26, 5990-6002.	7.0	28
17	Acetylation-dependent regulation of PD-L1 nuclear translocation dictates the efficacy of anti-PD-1 immunotherapy. <i>Nature Cell Biology</i> , 2020, 22, 1064-1075.	10.3	182
18	CRISPR Screens Identify Essential Cell Growth Mediators in BRAF Inhibitor-resistant Melanoma. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 26-40.	6.9	14

#	ARTICLE	IF	CITATIONS
19	Large-scale public data reuse to model immunotherapy response and resistance. <i>Genome Medicine</i> , 2020, 12, 21.	8.2	514
20	Synthetic Lethal and Resistance Interactions with BET Bromodomain Inhibitors in Triple-Negative Breast Cancer. <i>Molecular Cell</i> , 2020, 78, 1096-1113.e8.	9.7	114
21	TIMER2.0 for analysis of tumor-infiltrating immune cells. <i>Nucleic Acids Research</i> , 2020, 48, W509-W514.	14.5	2,546
22	Integrative analysis of pooled CRISPR genetic screens using MAGeCKFlute. <i>Nature Protocols</i> , 2019, 14, 756-780.	12.0	260
23	Cistrome-GO: a web server for functional enrichment analysis of transcription factor ChIP-seq peaks. <i>Nucleic Acids Research</i> , 2019, 47, W206-W211.	14.5	76
24	ARv7 Represses Tumor-Suppressor Genes in Castration-Resistant Prostate Cancer. <i>Cancer Cell</i> , 2019, 35, 401-413.e6.	16.8	127
25	Targeting the MIF/CXCR7/AKT Signaling Pathway in Castration-Resistant Prostate Cancer. <i>Molecular Cancer Research</i> , 2019, 17, 263-276.	3.4	27
26	Cistrome Data Browser: expanded datasets and new tools for gene regulatory analysis. <i>Nucleic Acids Research</i> , 2019, 47, D729-D735.	14.5	527
27	Allele-Specific Chromatin Recruitment and Therapeutic Vulnerabilities of ESR1 Activating Mutations. <i>Cancer Cell</i> , 2018, 33, 173-186.e5.	16.8	201
28	Genome-Scale Signatures of Gene Interaction from Compound Screens Predict Clinical Efficacy of Targeted Cancer Therapies. <i>Cell Systems</i> , 2018, 6, 343-354.e5.	6.2	40
29	VIPER: Visualization Pipeline for RNA-seq, a Snakemake workflow for efficient and complete RNA-seq analysis. <i>BMC Bioinformatics</i> , 2018, 19, 135.	2.6	156
30	Signatures of T cell dysfunction and exclusion predict cancer immunotherapy response. <i>Nature Medicine</i> , 2018, 24, 1550-1558.	30.7	2,791
31	Mass cytometry of Hodgkin lymphoma reveals a CD4+ regulatory T-cell "rich and exhausted T-effector microenvironment. <i>Blood</i> , 2018, 132, 825-836.	1.4	121
32	Applications of Immunogenomics to Cancer. <i>Cell</i> , 2017, 168, 600-612.	28.9	198
33	Genome-wide identification and characterization of Notch transcription complex "binding sequence-paired sites in leukemia cells. <i>Science Signaling</i> , 2017, 10, .	3.6	39
34	Ultrasensitive detection of TCR hypervariable-region sequences in solid-tissue RNA "seq data. <i>Nature Genetics</i> , 2017, 49, 482-483.	21.4	66
35	Cistrome Cancer: A Web Resource for Integrative Gene Regulation Modeling in Cancer. <i>Cancer Research</i> , 2017, 77, e19-e22.	0.9	130
36	TIMER: A Web Server for Comprehensive Analysis of Tumor-Infiltrating Immune Cells. <i>Cancer Research</i> , 2017, 77, e108-e110.	0.9	4,049

#	ARTICLE	IF	CITATIONS
37	Cistrome Data Browser: a data portal for ChIP-Seq and chromatin accessibility data in human and mouse. <i>Nucleic Acids Research</i> , 2017, 45, D658-D662.	14.5	451
38	Revisit linear regression-based deconvolution methods for tumor gene expression data. <i>Genome Biology</i> , 2017, 18, 127.	8.8	45
39	ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline. <i>BMC Bioinformatics</i> , 2016, 17, 404.	2.6	100
40	Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. <i>Genome Biology</i> , 2016, 17, 174.	8.8	1,768
41	Modeling cis-regulation with a compendium of genome-wide histone H3K27ac profiles. <i>Genome Research</i> , 2016, 26, 1417-1429.	5.5	75
42	Snail1-dependent p53 repression regulates expansion and activity of tumour-initiating cells in breast cancer. <i>Nature Cell Biology</i> , 2016, 18, 1221-1232.	10.3	90
43	Landscape of tumor-infiltrating T cell repertoire of human cancers. <i>Nature Genetics</i> , 2016, 48, 725-732.	21.4	288
44	Overcoming Therapeutic Resistance in HER2-Positive Breast Cancers with CDK4/6 Inhibitors. <i>Cancer Cell</i> , 2016, 29, 255-269.	16.8	356
45	Response and resistance to BET bromodomain inhibitors in triple-negative breast cancer. <i>Nature</i> , 2016, 529, 413-417.	27.8	490
46	Predicting Anticancer Drug Responses Using a Dual-Layer Integrated Cell Line-Drug Network Model. <i>PLoS Computational Biology</i> , 2015, 11, e1004498.	3.2	152
47	Sequence determinants of improved CRISPR sgRNA design. <i>Genome Research</i> , 2015, 25, 1147-1157.	5.5	514
48	Quality control, modeling, and visualization of CRISPR screens with MAGeCK-VISPR. <i>Genome Biology</i> , 2015, 16, 281.	8.8	330
49	Big data mining yields novel insights on cancer. <i>Nature Genetics</i> , 2015, 47, 103-104.	21.4	64
50	Erratum for Verzi et al., Intestinal Master Transcription Factor CDX2 Controls Chromatin Access for Partner Transcription Factor Binding. <i>Molecular and Cellular Biology</i> , 2015, 35, 496-496.	2.3	0
51	Network analysis of gene essentiality in functional genomics experiments. <i>Genome Biology</i> , 2015, 16, 239.	8.8	50
52	NOTCH1-RBPJ complexes drive target gene expression through dynamic interactions with superenhancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 705-710.	7.1	218
53	Kidney Cancer Is Characterized by Aberrant Methylation of Tissue-Specific Enhancers That Are Prognostic for Overall Survival. <i>Clinical Cancer Research</i> , 2014, 20, 4349-4360.	7.0	60
54	Lysine-Specific Demethylase 1 Has Dual Functions as a Major Regulator of Androgen Receptor Transcriptional Activity. <i>Cell Reports</i> , 2014, 9, 1618-1627.	6.4	115

#	ARTICLE	IF	CITATIONS
55	Active enhancers are delineated de novo during hematopoiesis, with limited lineage fidelity among specified primary blood cells. <i>Genes and Development</i> , 2014, 28, 1827-1839.	5.9	38
56	JARID1B Is a Luminal Lineage-Driving Oncogene in Breast Cancer. <i>Cancer Cell</i> , 2014, 25, 762-777.	16.8	170
57	Identifying and mitigating bias in next-generation sequencing methods for chromatin biology. <i>Nature Reviews Genetics</i> , 2014, 15, 709-721.	16.3	295
58	Discovery of Biomarkers Predictive of GSI Response in Triple-Negative Breast Cancer and Adenoid Cystic Carcinoma. <i>Cancer Discovery</i> , 2014, 4, 1154-1167.	9.4	123
59	PHF8 and REST/NRSF co-occupy gene promoters to regulate proximal gene expression. <i>Scientific Reports</i> , 2014, 4, 5008.	3.3	16
60	ChIP-Chip: Algorithms for Calling Binding Sites. <i>Methods in Molecular Biology</i> , 2009, 556, 165-175.	0.9	2
61	Analysis of ChIP-chip Data on Genome Tiling Microarrays. <i>Frontiers of Statistics</i> , 2009, , 239-257.	0.2	0
62	Model-based Analysis of ChIP-Seq (MACS). <i>Genome Biology</i> , 2008, 9, R137.	9.6	13,517
63	Getting Started in Tiling Microarray Analysis. <i>PLoS Computational Biology</i> , 2007, 3, e183.	3.2	49