

Shirley X Zhu

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

33,062
citations

66234

42
h-index

133063

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). <i>Genome Biology</i> , 2008, 9, R137. | 13.9 | 13,517 |
| 2 | TIMER: A Web Server for Comprehensive Analysis of Tumor-Infiltrating Immune Cells. <i>Cancer Research</i> , 2017, 77, e108-e110. | 0.4 | 4,049 |
| 3 | Signatures of T cell dysfunction and exclusion predict cancer immunotherapy response. <i>Nature Medicine</i> , 2018, 24, 1550-1558. | 15.2 | 2,791 |
| 4 | TIMER2.0 for analysis of tumor-infiltrating immune cells. <i>Nucleic Acids Research</i> , 2020, 48, W509-W514. | 6.5 | 2,546 |
| 5 | Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. <i>Genome Biology</i> , 2016, 17, 174. | 3.8 | 1,768 |
| 6 | A single-cell and spatially resolved atlas of human breast cancers. <i>Nature Genetics</i> , 2021, 53, 1334-1347. | 9.4 | 535 |
| 7 | Cistrome Data Browser: expanded datasets and new tools for gene regulatory analysis. <i>Nucleic Acids Research</i> , 2019, 47, D729-D735. | 6.5 | 527 |
| 8 | Sequence determinants of improved CRISPR sgRNA design. <i>Genome Research</i> , 2015, 25, 1147-1157. | 2.4 | 514 |
| 9 | Large-scale public data reuse to model immunotherapy response and resistance. <i>Genome Medicine</i> , 2020, 12, 21. | 3.6 | 514 |
| 10 | Response and resistance to BET bromodomain inhibitors in triple-negative breast cancer. <i>Nature</i> , 2016, 529, 413-417. | 13.7 | 490 |
| 11 | 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. | 6.5 | 451 |
| 12 | Overcoming Therapeutic Resistance in HER2-Positive Breast Cancers with CDK4/6 Inhibitors. <i>Cancer Cell</i> , 2016, 29, 255-269. | 7.7 | 356 |
| 13 | Quality control, modeling, and visualization of CRISPR screens with MAGeCK-VISPR. <i>Genome Biology</i> , 2015, 16, 281. | 3.8 | 330 |
| 14 | Identifying and mitigating bias in next-generation sequencing methods for chromatin biology. <i>Nature Reviews Genetics</i> , 2014, 15, 709-721. | 7.7 | 295 |
| 15 | Landscape of tumor-infiltrating T cell repertoire of human cancers. <i>Nature Genetics</i> , 2016, 48, 725-732. | 9.4 | 288 |
| 16 | Integrative analysis of pooled CRISPR genetic screens using MAGeCKFlute. <i>Nature Protocols</i> , 2019, 14, 756-780. | 5.5 | 260 |
| 17 | Stromal cell diversity associated with immune evasion in human triple-negative breast cancer. <i>EMBO Journal</i> , 2020, 39, e104063. | 3.5 | 224 |
| 18 | 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. | 3.3 | 218 |

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|----|---|------|-----------|
| 19 | Inhibitory CD161 receptor identified in glioma-infiltrating T cells by single-cell analysis. <i>Cell</i> , 2021, 184, 1281-1298.e26. | 13.5 | 210 |
| 20 | Allele-Specific Chromatin Recruitment and Therapeutic Vulnerabilities of ESR1 Activating Mutations. <i>Cancer Cell</i> , 2018, 33, 173-186.e5. | 7.7 | 201 |
| 21 | Applications of Immunogenomics to Cancer. <i>Cell</i> , 2017, 168, 600-612. | 13.5 | 198 |
| 22 | 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. | 4.6 | 182 |
| 23 | JARID1B Is a Luminal Lineage-Driving Oncogene in Breast Cancer. <i>Cancer Cell</i> , 2014, 25, 762-777. | 7.7 | 170 |
| 24 | VIPER: Visualization Pipeline for RNA-seq, a Snakemake workflow for efficient and complete RNA-seq analysis. <i>BMC Bioinformatics</i> , 2018, 19, 135. | 1.2 | 156 |
| 25 | Predicting Anticancer Drug Responses Using a Dual-Layer Integrated Cell Line-Drug Network Model. <i>PLoS Computational Biology</i> , 2015, 11, e1004498. | 1.5 | 152 |
| 26 | Cistrome Cancer: A Web Resource for Integrative Gene Regulation Modeling in Cancer. <i>Cancer Research</i> , 2017, 77, e19-e22. | 0.4 | 130 |
| 27 | ARv7 Represses Tumor-Suppressor Genes in Castration-Resistant Prostate Cancer. <i>Cancer Cell</i> , 2019, 35, 401-413.e6. | 7.7 | 127 |
| 28 | Integrative analyses of single-cell transcriptome and regulome using MAESTRO. <i>Genome Biology</i> , 2020, 21, 198. | 3.8 | 126 |
| 29 | Discovery of Biomarkers Predictive of GSI Response in Triple-Negative Breast Cancer and Adenoid Cystic Carcinoma. <i>Cancer Discovery</i> , 2014, 4, 1154-1167. | 7.7 | 123 |
| 30 | Mass cytometry of Hodgkin lymphoma reveals a CD4+ regulatory T-cell-rich and exhausted T-effector microenvironment. <i>Blood</i> , 2018, 132, 825-836. | 0.6 | 121 |
| 31 | Lysine-Specific Demethylase 1 Has Dual Functions as a Major Regulator of Androgen Receptor Transcriptional Activity. <i>Cell Reports</i> , 2014, 9, 1618-1627. | 2.9 | 115 |
| 32 | Synthetic Lethal and Resistance Interactions with BET Bromodomain Inhibitors in Triple-Negative Breast Cancer. <i>Molecular Cell</i> , 2020, 78, 1096-1113.e8. | 4.5 | 114 |
| 33 | ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline. <i>BMC Bioinformatics</i> , 2016, 17, 404. | 1.2 | 100 |
| 34 | Snail1-dependent p53 repression regulates expansion and activity of tumour-initiating cells in breast cancer. <i>Nature Cell Biology</i> , 2016, 18, 1221-1232. | 4.6 | 90 |
| 35 | 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. | 13.5 | 79 |
| 36 | Cistrome-GO: a web server for functional enrichment analysis of transcription factor ChIP-seq peaks. <i>Nucleic Acids Research</i> , 2019, 47, W206-W211. | 6.5 | 76 |

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|----|--|-----|-----------|
| 37 | Modeling <i>cis</i> -regulation with a compendium of genome-wide histone H3K27ac profiles. <i>Genome Research</i> , 2016, 26, 1417-1429. | 2.4 | 75 |
| 38 | Ultrasensitive detection of TCR hypervariable-region sequences in solid-tissue RNA-seq data. <i>Nature Genetics</i> , 2017, 49, 482-483. | 9.4 | 66 |
| 39 | Big data mining yields novel insights on cancer. <i>Nature Genetics</i> , 2015, 47, 103-104. | 9.4 | 64 |
| 40 | 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. | 3.2 | 60 |
| 41 | Immunostimulatory Cancer-Associated Fibroblast Subpopulations Can Predict Immunotherapy Response in Head and Neck Cancer. <i>Clinical Cancer Research</i> , 2022, 28, 2094-2109. | 3.2 | 60 |
| 42 | Subtype heterogeneity and epigenetic convergence in neuroendocrine prostate cancer. <i>Nature Communications</i> , 2021, 12, 5775. | 5.8 | 59 |
| 43 | MYC drives aggressive prostate cancer by disrupting transcriptional pause release at androgen receptor targets. <i>Nature Communications</i> , 2022, 13, 2559. | 5.8 | 56 |
| 44 | Network analysis of gene essentiality in functional genomics experiments. <i>Genome Biology</i> , 2015, 16, 239. | 3.8 | 50 |
| 45 | Getting Started in Tiling Microarray Analysis. <i>PLoS Computational Biology</i> , 2007, 3, e183. | 1.5 | 49 |
| 46 | Revisit linear regression-based deconvolution methods for tumor gene expression data. <i>Genome Biology</i> , 2017, 18, 127. | 3.8 | 45 |
| 47 | CARM1 Inhibition Enables Immunotherapy of Resistant Tumors by Dual Action on Tumor Cells and T Cells. <i>Cancer Discovery</i> , 2021, 11, 2050-2071. | 7.7 | 43 |
| 48 | 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. | 2.9 | 40 |
| 49 | Genome-wide identification and characterization of Notch transcription complex-binding sequence-paired sites in leukemia cells. <i>Science Signaling</i> , 2017, 10, . | 1.6 | 39 |
| 50 | 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. | 2.7 | 38 |
| 51 | Systematic characterization of mutations altering protein degradation in human cancers. <i>Molecular Cell</i> , 2021, 81, 1292-1308.e11. | 4.5 | 36 |
| 52 | Inhibition of MAN2A1 Enhances the Immune Response to Anti-PD-L1 in Human Tumors. <i>Clinical Cancer Research</i> , 2020, 26, 5990-6002. | 3.2 | 28 |
| 53 | Targeting the MIF/CXCR7/AKT Signaling Pathway in Castration-Resistant Prostate Cancer. <i>Molecular Cancer Research</i> , 2019, 17, 263-276. | 1.5 | 27 |
| 54 | 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. | 4.6 | 21 |

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|----|--|------|-----------|
| 55 | CoBRA: Containerized Bioinformatics Workflow for Reproducible ChIP/ATAC-seq Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 652-661. | 3.0 | 18 |
| 56 | PHF8 and REST/NRSF co-occupy gene promoters to regulate proximal gene expression. <i>Scientific Reports</i> , 2014, 4, 5008. | 1.6 | 16 |
| 57 | CRISPR Screens Identify Essential Cell Growth Mediators in BRAF Inhibitor-resistant Melanoma. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 26-40. | 3.0 | 14 |
| 58 | Topical therapy for regression and melanoma prevention of congenital giant nevi. <i>Cell</i> , 2022, 185, 2071-2085.e12. | 13.5 | 13 |
| 59 | ChIP-Chip: Algorithms for Calling Binding Sites. <i>Methods in Molecular Biology</i> , 2009, 556, 165-175. | 0.4 | 2 |
| 60 | 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. | 1.1 | 0 |
| 61 | Computational Approaches to Modeling Transcription Factor Activity and Gene Regulation. <i>Trends in Biochemical Sciences</i> , 2020, 45, 1094-1095. | 3.7 | 0 |
| 62 | Neural network architecture search with AMBER. <i>Nature Machine Intelligence</i> , 2021, 3, 372-373. | 8.3 | 0 |
| 63 | Analysis of ChIP-chip Data on Genome Tiling Microarrays. <i>Frontiers of Statistics</i> , 2009, , 239-257. | 0.2 | 0 |