

# Xiaole Shirley Liu

## List of Publications by Year in descending order

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Version: 2024-02-01

80  
papers

38,028  
citations

50170

46  
h-index

62479

80  
g-index

91  
all docs

91  
docs citations

91  
times ranked

52492  
citing authors

#	ARTICLE	IF	CITATIONS
1	TISMO: syngeneic mouse tumor database to model tumor immunity and immunotherapy response. <i>Nucleic Acids Research</i> , 2022, 50, D1391-D1397.	6.5	41
2	Inhibition of EZH2 transactivation function sensitizes solid tumors to genotoxic stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	22
3	A high-resolution view of intra-tumoral B cell immunity. <i>Immunity</i> , 2022, 55, 387-389.	6.6	4
4	IKAROS and MENIN coordinate therapeutically actionable leukemogenic gene expression in MLL-r acute myeloid leukemia. <i>Nature Cancer</i> , 2022, 3, 595-613.	5.7	16
5	MYC drives aggressive prostate cancer by disrupting transcriptional pause release at androgen receptor targets. <i>Nature Communications</i> , 2022, 13, 2559.	5.8	56
6	Comprehensive Characterizations of Immune Receptor Repertoire in Tumors and Cancer Immunotherapy Studies. <i>Cancer Immunology Research</i> , 2022, 10, 788-799.	1.6	10
7	Enhanced Efficacy of Simultaneous PD-1 and PD-L1 Immune Checkpoint Blockade in High-Grade Serous Ovarian Cancer. <i>Cancer Research</i> , 2021, 81, 158-173.	0.4	85
8	Integrin $\alpha 6 \beta 1$ -TGF $\beta$ -SOX4 Pathway Drives Immune Evasion in Triple-Negative Breast Cancer. <i>Cancer Cell</i> , 2021, 39, 54-67.e9.	7.7	99
9	Therapeutically Increasing MHC-I Expression Potentiates Immune Checkpoint Blockade. <i>Cancer Discovery</i> , 2021, 11, 1524-1541.	7.7	103
10	Systematic characterization of mutations altering protein degradation in human cancers. <i>Molecular Cell</i> , 2021, 81, 1292-1308.e11.	4.5	36
11	TRUST4: immune repertoire reconstruction from bulk and single-cell RNA-seq data. <i>Nature Methods</i> , 2021, 18, 627-630.	9.0	126
12	Neural network architecture search with AMBER. <i>Nature Machine Intelligence</i> , 2021, 3, 372-373.	8.3	0
13	CoBRA: Containerized Bioinformatics Workflow for Reproducible ChIP/ATAC-seq Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 652-661.	3.0	18
14	A single-cell and spatially resolved atlas of human breast cancers. <i>Nature Genetics</i> , 2021, 53, 1334-1347.	9.4	535
15	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
16	Subtype heterogeneity and epigenetic convergence in neuroendocrine prostate cancer. <i>Nature Communications</i> , 2021, 12, 5775.	5.8	59
17	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
18	Genetic fusions favor tumorigenesis through degron loss in oncogenes. <i>Nature Communications</i> , 2021, 12, 6704.	5.8	14

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19	Fast alignment and preprocessing of chromatin profiles with Chromap. Nature Communications, 2021, 12, 6566.	5.8	39
20	Stromal cell diversity associated with immune evasion in human triple-negative breast cancer. EMBO Journal, 2020, 39, e104063.	3.5	224
21	Integrative analyses of single-cell transcriptome and regulome using MAESTRO. Genome Biology, 2020, 21, 198.	3.8	126
22	A peripheral immune signature of responsiveness to PD-1 blockade in patients with classical Hodgkin lymphoma. Nature Medicine, 2020, 26, 1468-1479.	15.2	87
23	Inhibition of MAN2A1 Enhances the Immune Response to Anti-PD-L1 in Human Tumors. Clinical Cancer Research, 2020, 26, 5990-6002.	3.2	28
24	An integrative ENCODE resource for cancer genomics. Nature Communications, 2020, 11, 3696.	5.8	95
25	Clonal tracing reveals diverse patterns of response to immune checkpoint blockade. Genome Biology, 2020, 21, 263.	3.8	15
26	Acetylation-dependent regulation of PD-L1 nuclear translocation dictates the efficacy of anti-PD-1 immunotherapy. Nature Cell Biology, 2020, 22, 1064-1075.	4.6	182
27	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	9.4	146
28	Determinants of transcription factor regulatory range. Nature Communications, 2020, 11, 2472.	5.8	28
29	CRISPR Screens Identify Essential Cell Growth Mediators in BRAF Inhibitor-resistant Melanoma. Genomics, Proteomics and Bioinformatics, 2020, 18, 26-40.	3.0	14
30	Loss of H3K36 Methyltransferase SETD2 Impairs V(D)J Recombination during Lymphoid Development. IScience, 2020, 23, 100941.	1.9	6
31	Lisa: inferring transcriptional regulators through integrative modeling of public chromatin accessibility and ChIP-seq data. Genome Biology, 2020, 21, 32.	3.8	161
32	Large-scale public data reuse to model immunotherapy response and resistance. Genome Medicine, 2020, 12, 21.	3.6	514
33	Mammalian SWI/SNF Complex Genomic Alterations and Immune Checkpoint Blockade in Solid Tumors. Cancer Immunology Research, 2020, 8, 1075-1084.	1.6	47
34	TIMER2.0 for analysis of tumor-infiltrating immune cells. Nucleic Acids Research, 2020, 48, W509-W514.	6.5	2,546
35	Integrative analysis of pooled CRISPR genetic screens using MAGeCKFlute. Nature Protocols, 2019, 14, 756-780.	5.5	260
36	Cistrome-GO: a web server for functional enrichment analysis of transcription factor ChIP-seq peaks. Nucleic Acids Research, 2019, 47, W206-W211.	6.5	76

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37	Landscape of B cell immunity and related immune evasion in human cancers. <i>Nature Genetics</i> , 2019, 51, 560-567.	9.4	115
38	Deciphering essential cistromes using genome-wide CRISPR screens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25186-25195.	3.3	33
39	Immune receptor repertoires in pediatric and adult acute myeloid leukemia. <i>Genome Medicine</i> , 2019, 11, 73.	3.6	38
40	Cistrome Data Browser: expanded datasets and new tools for gene regulatory analysis. <i>Nucleic Acids Research</i> , 2019, 47, D729-D735.	6.5	527
41	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
42	A major chromatin regulator determines resistance of tumor cells to T cell-mediated killing. <i>Science</i> , 2018, 359, 770-775.	6.0	641
43	Evaluation of immune repertoire inference methods from RNA-seq data. <i>Nature Biotechnology</i> , 2018, 36, 1034-1034.	9.4	7
44	Improved design and analysis of CRISPR knockout screens. <i>Bioinformatics</i> , 2018, 34, 4095-4101.	1.8	44
45	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
46	Big Data Approaches for Modeling Response and Resistance to Cancer Drugs. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 1-27.	2.8	27
47	Signatures of T cell dysfunction and exclusion predict cancer immunotherapy response. <i>Nature Medicine</i> , 2018, 24, 1550-1558.	15.2	2,791
48	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
49	Applications of Immunogenomics to Cancer. <i>Cell</i> , 2017, 168, 600-612.	13.5	198
50	Exploring genetic associations with ceRNA regulation in the human genome. <i>Nucleic Acids Research</i> , 2017, 45, 5653-5665.	6.5	39
51	Ultrasensitive detection of TCR hypervariable-region sequences in solid-tissue RNA-seq data. <i>Nature Genetics</i> , 2017, 49, 482-483.	9.4	66
52	Cistrome Cancer: A Web Resource for Integrative Gene Regulation Modeling in Cancer. <i>Cancer Research</i> , 2017, 77, e19-e22.	0.4	130
53	Topological analysis reveals a PD-L1-associated microenvironmental niche for Reed-Sternberg cells in Hodgkin lymphoma. <i>Blood</i> , 2017, 130, 2420-2430.	0.6	262
54	TIMER: A Web Server for Comprehensive Analysis of Tumor-Infiltrating Immune Cells. <i>Cancer Research</i> , 2017, 77, e108-e110.	0.4	4,049

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55	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
56	Revisit linear regression-based deconvolution methods for tumor gene expression data. <i>Genome Biology</i> , 2017, 18, 127.	3.8	45
57	CRISPR-FOCUS: A web server for designing focused CRISPR screening experiments. <i>PLoS ONE</i> , 2017, 12, e0184281.	1.1	16
58	ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline. <i>BMC Bioinformatics</i> , 2016, 17, 404.	1.2	100
59	CRISPR-DO for genome-wide CRISPR design and optimization. <i>Bioinformatics</i> , 2016, 32, 3336-3338.	1.8	46
60	Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. <i>Genome Biology</i> , 2016, 17, 174.	3.8	1,768
61	Genome-scale deletion screening of human long non-coding RNAs using a paired-guide RNA CRISPR-Cas9 library. <i>Nature Biotechnology</i> , 2016, 34, 1279-1286.	9.4	380
62	Landscape of tumor-infiltrating T cell repertoire of human cancers. <i>Nature Genetics</i> , 2016, 48, 725-732.	9.4	288
63	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
64	Inference of transcriptional regulation in cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7731-7736.	3.3	84
65	Sequence determinants of improved CRISPR sgRNA design. <i>Genome Research</i> , 2015, 25, 1147-1157.	2.4	514
66	Quality control, modeling, and visualization of CRISPR screens with MAGeCK-VISPR. <i>Genome Biology</i> , 2015, 16, 281.	3.8	330
67	SETDB1 modulates PRC2 activity at developmental genes independently of H3K9 trimethylation in mouse ES cells. <i>Genome Research</i> , 2015, 25, 1325-1335.	2.4	33
68	Network analysis of gene essentiality in functional genomics experiments. <i>Genome Biology</i> , 2015, 16, 239.	3.8	50
69	MAGeCK enables robust identification of essential genes from genome-scale CRISPR/Cas9 knockout screens. <i>Genome Biology</i> , 2014, 15, 554.	3.8	1,614
70	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , 2014, 512, 449-452.	13.7	363
71	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
72	Enhancer RNAs participate in androgen receptor-driven looping that selectively enhances gene activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7319-7324.	3.3	332

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73	Target analysis by integration of transcriptome and ChIP-seq data with BETA. Nature Protocols, 2013, 8, 2502-2515.	5.5	428
74	Amplitude modulation of androgen signaling by c-MYC. Genes and Development, 2013, 27, 734-748.	2.7	78
75	EZH2 Oncogenic Activity in Castration-Resistant Prostate Cancer Cells Is Polycomb-Independent. Science, 2012, 338, 1465-1469.	6.0	748
76	Model-based Analysis of ChIP-Seq (MACS). Genome Biology, 2008, 9, R137.	13.9	13,517
77	Getting Started in Tiling Microarray Analysis. PLoS Computational Biology, 2007, 3, e183.	1.5	49
78	CEAS: cis-regulatory element annotation system. Nucleic Acids Research, 2006, 34, W551-W554.	6.5	170
79	Chromosome-Wide Mapping of Estrogen Receptor Binding Reveals Long-Range Regulation Requiring the Forkhead Protein FoxA1. Cell, 2005, 122, 33-43.	13.5	1,208
80	<i>In vivo</i> CRISPR Screens Identify E3 Ligase <i>Cop1</i> as a Modulator of Macrophage Infiltration and Cancer Immunotherapy Target. SSRN Electronic Journal, 0, , .	0.4	0