

Xiwei Wu

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

4,222
citations

147801

31
h-index

118850

62
g-index

85
all docs

85
docs citations

85
times ranked

8346
citing authors

#	ARTICLE	IF	CITATIONS
1	Unbiased detection of off-target cleavage by CRISPR-Cas9 and TALENs using integrase-defective lentiviral vectors. <i>Nature Biotechnology</i> , 2015, 33, 175-178.	17.5	395
2	Targeting FTO Suppresses Cancer Stem Cell Maintenance and Immune Evasion. <i>Cancer Cell</i> , 2020, 38, 79-96.e11.	16.8	389
3	Cancer-cell-secreted exosomal miR-105 promotes tumour growth through the MYC-dependent metabolic reprogramming of stromal cells. <i>Nature Cell Biology</i> , 2018, 20, 597-609.	10.3	306
4	De novo sequencing of circulating miRNAs identifies novel markers predicting clinical outcome of locally advanced breast cancer. <i>Journal of Translational Medicine</i> , 2012, 10, 42.	4.4	208
5	IDH2 R172 mutations define a unique subgroup of patients with angioimmunoblastic T-cell lymphoma. <i>Blood</i> , 2015, 126, 1741-1752.	1.4	184
6	Epigenomic profiling reveals an association between persistence of DNA methylation and metabolic memory in the DCCT/EDIC type 1 diabetes cohort. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3002-11.	7.1	179
7	Gpr124 is essential for blood-brain barrier integrity in central nervous system disease. <i>Nature Medicine</i> , 2017, 23, 450-460.	30.7	177
8	Genome-wide Analysis of Histone Lysine Methylation Variations Caused by Diabetic Conditions in Human Monocytes. <i>Journal of Biological Chemistry</i> , 2007, 282, 13854-13863.	3.4	161
9	Regulation of Inflammatory Phenotype in Macrophages by a Diabetes-Induced Long Noncoding RNA. <i>Diabetes</i> , 2014, 63, 4249-4261.	0.6	155
10	Chemotherapy-Induced Extracellular Vesicle miRNAs Promote Breast Cancer Stemness by Targeting <i>ONECUT2</i> . <i>Cancer Research</i> , 2019, 79, 3608-3621.	0.9	129
11	CpG Island Hypermethylation in Human Astrocytomas. <i>Cancer Research</i> , 2010, 70, 2718-2727.	0.9	122
12	Tet3 Reads 5-Carboxylcytosine through Its CXXC Domain and Is a Potential Guardian against Neurodegeneration. <i>Cell Reports</i> , 2016, 14, 493-505.	6.4	109
13	Regulation of angiotensin II actions by enhancers and super-enhancers in vascular smooth muscle cells. <i>Nature Communications</i> , 2017, 8, 1467.	12.8	89
14	Primary T Cells from Cutaneous T-cell Lymphoma Skin Explants Display an Exhausted Immune Checkpoint Profile. <i>Cancer Immunology Research</i> , 2018, 6, 900-909.	3.4	73
15	JMJD1B Demethylates H4R3me2s and H3K9me2 to Facilitate Gene Expression for Development of Hematopoietic Stem and Progenitor Cells. <i>Cell Reports</i> , 2018, 23, 389-403.	6.4	71
16	SIRT1 Activation Disrupts Maintenance of Myelodysplastic Syndrome Stem and Progenitor Cells by Restoring TET2 Function. <i>Cell Stem Cell</i> , 2018, 23, 355-369.e9.	11.1	68
17	High throughput sequencing analysis of RNA libraries reveals the influences of initial library and PCR methods on SELEX efficiency. <i>Scientific Reports</i> , 2016, 6, 33697.	3.3	66
18	Pharmacodynamic and pharmacogenomic study of the nanoparticle conjugate of camptothecin CRLX101 for the treatment of cancer. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2014, 10, 1477-1486.	3.3	58

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19	Extrafollicular CD4+ T-B interactions are sufficient for inducing autoimmune-like chronic graft-versus-host disease. <i>Nature Communications</i> , 2017, 8, 978.	12.8	58
20	Metastatic breast cancer cells overexpress and secrete miR-218 to regulate type I collagen deposition by osteoblasts. <i>Breast Cancer Research</i> , 2018, 20, 127.	5.0	56
21	The DNA methylation landscape of human melanoma. <i>Genomics</i> , 2015, 106, 322-330.	2.9	50
22	Characterization of Arginase Expression in Glioma-Associated Microglia and Macrophages. <i>PLoS ONE</i> , 2016, 11, e0165118.	2.5	47
23	Dynamics of RNA Polymerase II Pausing and Bivalent Histone H3 Methylation during Neuronal Differentiation in Brain Development. <i>Cell Reports</i> , 2017, 20, 1307-1318.	6.4	47
24	KIF20A/MKLP2 regulates the division modes of neural progenitor cells during cortical development. <i>Nature Communications</i> , 2018, 9, 2707.	12.8	46
25	Loss of the Polycomb Mark from Bivalent Promoters Leads to Activation of Cancer-Promoting Genes in Colorectal Tumors. <i>Cancer Research</i> , 2014, 74, 3617-3629.	0.9	43
26	Genetic Gastric Cancer Susceptibility in the International Clinical Cancer Genomics Community Research Network. <i>Cancer Genetics</i> , 2017, 216-217, 111-119.	0.4	42
27	<sc>hDNA</sc> 2 nuclease/helicase promotes centromeric <sc>DNA</sc> replication and genome stability. <i>EMBO Journal</i> , 2018, 37, .	7.8	42
28	RNA-seq Reveals Aurora Kinase-Driven mTOR Pathway Activation in Patients with Sarcomatoid Metastatic Renal Cell Carcinoma. <i>Molecular Cancer Research</i> , 2015, 13, 130-137.	3.4	38
29	Fen1 mutations that specifically disrupt its interaction with PCNA cause aneuploidy-associated cancer. <i>Cell Research</i> , 2011, 21, 1052-1067.	12.0	35
30	Cancer-cell-secreted extracellular vesicles suppress insulin secretion through miR-122 to impair systemic glucose homeostasis and contribute to tumour growth. <i>Nature Cell Biology</i> , 2022, 24, 954-967.	10.3	35
31	Identification of Tissue-Specific DNA Methylation Signatures for Thyroid Nodule Diagnostics. <i>Clinical Cancer Research</i> , 2019, 25, 544-551.	7.0	34
32	Exosomal miRNAs species in the blood of small cell and non-small cell lung cancer patients. <i>Oncotarget</i> , 2018, 9, 19793-19806.	1.8	34
33	Detailed comparison of two popular variant calling packages for exome and targeted exon studies. <i>PeerJ</i> , 2014, 2, e600.	2.0	33
34	Reprogramming of DNA methylation at NEUROD2-bound sequences during cortical neuron differentiation. <i>Science Advances</i> , 2019, 5, eaax0080.	10.3	32
35	ATRA-Induced Cellular Differentiation and CD38 Expression Inhibits Acquisition of BCR-ABL Mutations for CML Acquired Resistance. <i>PLoS Genetics</i> , 2014, 10, e1004414.	3.5	31
36	Disruption of microRNA-21 by TALEN leads to diminished cell transformation and increased expression of cell-environment interaction genes. <i>Cancer Letters</i> , 2015, 356, 506-516.	7.2	31

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37	Underexpression of LKB1 tumor suppressor is associated with enhanced Wnt signaling and malignant characteristics of human intrahepatic cholangiocarcinoma. <i>Oncotarget</i> , 2015, 6, 18905-18920.	1.8	30
38	TDRD3 promotes DHX9 chromatin recruitment and R-loop resolution. <i>Nucleic Acids Research</i> , 2021, 49, 8573-8591.	14.5	30
39	The spectrum of genetic variants in hereditary pancreatic cancer includes Fanconi anemia genes. <i>Familial Cancer</i> , 2018, 17, 235-245.	1.9	29
40	Loss of H2B monoubiquitination is associated with poor differentiation and enhanced malignancy of lung adenocarcinoma. <i>International Journal of Cancer</i> , 2017, 141, 766-777.	5.1	27
41	Targeting miR-126 in inv(16) acute myeloid leukemia inhibits leukemia development and leukemia stem cell maintenance. <i>Nature Communications</i> , 2021, 12, 6154.	12.8	27
42	Vitamin K epoxide reductase regulation of androgen receptor activity. <i>Oncotarget</i> , 2017, 8, 13818-13831.	1.8	25
43	State-Transition Analysis of Time-Sequential Gene Expression Identifies Critical Points That Predict Development of Acute Myeloid Leukemia. <i>Cancer Research</i> , 2020, 80, 3157-3169.	0.9	25
44	Targeting the metabolic vulnerability of acute myeloid leukemia blasts with a combination of venetoclax and 8-chloro-adenosine. <i>Journal of Hematology and Oncology</i> , 2021, 14, 70.	17.0	25
45	Double-hit Signature with <i>TP53</i> Abnormalities Predicts Poor Survival in Patients with Germinal Center Type Diffuse Large B-cell Lymphoma Treated with R-CHOP. <i>Clinical Cancer Research</i> , 2021, 27, 1671-1680.	7.0	24
46	Analysis of Liver Tumor-Prone Mouse Models of the Hippo Kinase Scaffold Proteins RASSF1A and SAV1. <i>Cancer Research</i> , 2016, 76, 2824-2835.	0.9	22
47	Tissue-resident PSGL1 ^{lo} CD4 ⁺ T cells promote B cell differentiation and chronic graft-versus-host disease-associated autoimmunity. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	21
48	UVB irradiation does not directly induce detectable changes of DNA methylation in human keratinocytes. <i>F1000Research</i> , 2013, 2, 45.	1.6	21
49	A germline missense mutation in COQ6 is associated with susceptibility to familial schwannomatosis. <i>Genetics in Medicine</i> , 2014, 16, 787-792.	2.4	20
50	Leflunomide Synergizes with Gemcitabine in Growth Inhibition of PC Cells and Impairs c-Myc Signaling through PIM Kinase Targeting. <i>Molecular Therapy - Oncolytics</i> , 2019, 14, 149-158.	4.4	17
51	Cancer-secreted miRNAs regulate amino acid-induced mTORC1 signaling and fibroblast protein synthesis. <i>EMBO Reports</i> , 2021, 22, e51239.	4.5	17
52	Alternative RNA Splicing Associated With Mammalian Neuronal Differentiation. <i>Cerebral Cortex</i> , 2018, 28, 2810-2816.	2.9	16
53	LncRNA DRAIR is downregulated in diabetic monocytes and modulates inflammatory phenotype via epigenetic mechanisms. <i>JCI Insight</i> , 2021, 6, .	5.0	15
54	Leflunomide regulates c-Myc expression in myeloma cells through PIM targeting. <i>Blood Advances</i> , 2019, 3, 1027-1032.	5.2	14

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55	Prospective separation and transcriptome analyses of cortical projection neurons and interneurons based on lineage tracing by <i>scp>T</scp>br2</i> (Eomes) <i>â€œscp>GFP</scp>/<scp>D</scp>cxâ€œm<scp>RFP</scp></i> reporters. <i>Developmental Neurobiology</i> , 2016, 76, 587-599.	3.0	13
56	SNPs in inflammatory genes CCL11, CCL4 and MEFV in a fibromyalgia family study. <i>PLoS ONE</i> , 2018, 13, e0198625.	2.5	12
57	Immune Mediated Mechanisms of Resistance to Daratumumab. <i>Blood</i> , 2018, 132, 3201-3201.	1.4	11
58	MicroRNA Regulation of T-Cell Exhaustion in Cutaneous T Cell Lymphoma. <i>Journal of Investigative Dermatology</i> , 2022, 142, 603-612.e7.	0.7	9
59	Error-prone, stress-induced 3â€² flapâ€œbased Okazaki fragment maturation supports cell survival. <i>Science</i> , 2021, 374, 1252-1258.	12.6	9
60	Dynamic patterns of microRNA expression during acute myeloid leukemia state-transition. <i>Science Advances</i> , 2022, 8, eabj1664.	10.3	9
61	Role of FEN1 S187 phosphorylation in counteracting oxygenâ€œinduced stress and regulating postnatal heart development. <i>FASEB Journal</i> , 2017, 31, 132-147.	0.5	8
62	Identification of a Distinct miRNA Regulatory Network in the Tumor Microenvironment of Transformed Mycosis Fungoides. <i>Cancers</i> , 2021, 13, 5854.	3.7	7
63	A comprehensive preclinical study supporting clinical trial of oncolytic chimeric poxvirus CF33-hNIS-anti-PD-L1 to treat breast cancer. <i>Molecular Therapy - Methods and Clinical Development</i> , 2022, 24, 102-116.	4.1	7
64	Loss of SIRT1 inhibits hematopoietic stem cell aging and age-dependent mixed phenotype acute leukemia. <i>Communications Biology</i> , 2022, 5, 396.	4.4	7
65	New Genomic Model Integrating Clinical Factors and Gene Mutations to Predict Overall Survival in Patients with Diffuse Large B-Cell Lymphoma Treated with R-CHOP. <i>Blood</i> , 2018, 132, 346-346.	1.4	6
66	Molecular divergence of mammalian astrocyte progenitor cells at early gliogenesis. <i>Development (Cambridge)</i> , 2022, 149, .	2.5	6
67	Fatty acid synthase reprograms the epigenome in uterine leiomyosarcomas. <i>PLoS ONE</i> , 2017, 12, e0179692.	2.5	5
68	Synergy of Venetoclax and 8-Chloro-Adenosine in AML: The Interplay of rRNA Inhibition and Fatty Acid Metabolism. <i>Cancers</i> , 2022, 14, 1446.	3.7	5
69	The miRNA Profile of Cutaneous T Cell Lymphoma Correlates with the Dysfunctional Immunophenotype of the Disease. <i>Blood</i> , 2016, 128, 4132-4132.	1.4	4
70	Clinical and immunologic responses to extracorporeal photopheresis and low-dose IL-2 in patients with steroid refractory chronic graft-versus host disease. <i>Bone Marrow Transplantation</i> , 2022, 57, 1045-1047.	2.4	4
71	Cytokine gene polymorphisms are associated with response to blinatumomab in Bâ€œcell acute lymphoblastic leukemia. <i>European Journal of Haematology</i> , 2021, 106, 851-858.	2.2	2
72	Single-Cell Transcriptomics of Human <i><i>TET2</i></i> Knockout CD4 T-Cells and Their Clonal Evolution. <i>Blood</i> , 2020, 136, 22-23.	1.4	2

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73	Genomic Analysis of Cutaneous CD30-Positive Lymphoproliferative Disorders. JID Innovations, 2022, 2, 100068.	2.4	2
74	Tnfr1± Promotes an Immunosuppressive Microenvironment in Cutaneous T Cell Lymphoma and Regulates PD-L1 Expression. Blood, 2020, 136, 33-34.	1.4	2
75	Double-Hit Signature with <i>TP53</i> Abnormalities Predicts Poor Survival in Patients with Germinal Center Type Diffuse Large B-Cell Lymphoma Treated with R-CHOP. Blood, 2020, 136, 25-26.	1.4	1
76	Role of p38 ^β - NFATc4 - IL17A Pathway As a Potential Therapeutic Target in Cutaneous T Cell Lymphoma. Blood, 2016, 128, 2725-2725.	1.4	1
77	Driver Mutations Affecting Natural Killer/T Cell Lymphoma. Blood, 2016, 128, 4109-4109.	1.4	1
78	Time Sequential Transcriptome Analysis Identifies Mir-126 As an Early Biomarker for Inv(16) Acute Myeloid Leukemia (AML) Disease Progression. Blood, 2016, 128, 773-773.	1.4	0
79	Cytokine Gene Polymorphisms Are Associated with Disease Response to Blinatumomab in Patients with B-Cell Acute Lymphoblastic Leukemia. Blood, 2018, 132, 1549-1549.	1.4	0
80	Suppressing Synthesis of the Long Isoform of the Prolactin Receptor Is a Targeted Strategy to Prevent and Treat B Cell Malignancies. Blood, 2021, 138, 1135-1135.	1.4	0
81	The Involvement of STAT/SOCS Signaling in miRNA-Induced T Cell Exhaustion in Cutaneous T-Cell Lymphoma. Blood, 2020, 136, 1-1.	1.4	0