

Zheng Xia

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

61
papers

5,629
citations

30
h-index

68
g-index

68
ext. papers

7,456
ext. citations

15.4
avg, IF

5.04
L-index

#	Paper	IF	Citations
61	Androgen receptor activity in T cells limits checkpoint blockade efficacy.. <i>Nature</i> , 2022 ,	50.4	13
60	Postpartum breast cancer has a distinct molecular profile that predicts poor outcomes. <i>Nature Communications</i> , 2021 , 12, 6341	17.4	3
59	Mammary collagen is under reproductive control with implications for breast cancer. <i>Matrix Biology</i> , 2021 , 105, 104-104	11.4	1
58	Pregnancy and weaning regulate human maternal liver size and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
57	Reversible cardiac disease features in an inducible CUG repeat RNA-expressing mouse model of myotonic dystrophy. <i>JCI Insight</i> , 2021 , 6,	9.9	2
56	A Distinct Innate Immune Signature of Early Onset Colorectal Cancer. <i>ImmunoHorizons</i> , 2021 , 5, 489-499	2.7	4
55	BET Bromodomain Inhibition Blocks an AR-Repressed, E2F1-Activated Treatment-Emergent Neuroendocrine Prostate Cancer Lineage Plasticity Program. <i>Clinical Cancer Research</i> , 2021 , 27, 4923-4936	12.9	6
54	Pharmacologic Targeting of Mcl-1 Induces Mitochondrial Dysfunction and Apoptosis in B-Cell Lymphoma Cells in a and Dependent Manner. <i>Clinical Cancer Research</i> , 2021 , 27, 4910-4922	12.9	3
53	Mesenchymal Lineage Heterogeneity Underlies Non-Redundant Functions of Pancreatic Cancer-Associated Fibroblasts. <i>Cancer Discovery</i> , 2021 ,	24.4	12
52	Transcriptional profiling identifies an androgen receptor activity-low, stemness program associated with enzalutamide resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 12315-12323	11.5	28
51	Alternative splicing of LSD1+8a in neuroendocrine prostate cancer is mediated by SRRM4. <i>Neoplasia</i> , 2020 , 22, 253-262	6.4	9
50	Increased nuclear but not cytoplasmic activities of CELF1 protein leads to muscle wasting. <i>Human Molecular Genetics</i> , 2020 , 29, 1729-1744	5.6	8
49	Tgf β signaling is critical for maintenance of the tendon cell fate. <i>ELife</i> , 2020 , 9,	8.9	33
48	Copy Number Loss of 17q22 Is Associated with Enzalutamide Resistance and Poor Prognosis in Metastatic Castration-Resistant Prostate Cancer. <i>Clinical Cancer Research</i> , 2020 , 26, 4616-4624	12.9	4
47	Nudt21 regulates the alternative polyadenylation of Pak1 and is predictive in the prognosis of glioblastoma patients. <i>Oncogene</i> , 2019 , 38, 4154-4168	9.2	30
46	BET bromodomain inhibition blocks the function of a critical AR-independent master regulator network in lethal prostate cancer. <i>Oncogene</i> , 2019 , 38, 5658-5669	9.2	19
45	Genomic Drivers of Poor Prognosis and Enzalutamide Resistance in Metastatic Castration-resistant Prostate Cancer. <i>European Urology</i> , 2019 , 76, 562-571	10.2	49

44	MEK-ERK signaling is a therapeutic target in metastatic castration resistant prostate cancer. <i>Prostate Cancer and Prostatic Diseases</i> , 2019 , 22, 531-538	6.2	32
43	The genomic landscape of estrogen receptor binding sites in mouse mammary gland. <i>PLoS ONE</i> , 2019 , 14, e0220311	3.7	13
42	Cleavage factor 25 deregulation contributes to pulmonary fibrosis through alternative polyadenylation. <i>Journal of Clinical Investigation</i> , 2019 , 129, 1984-1999	15.9	32
41	RNA-seq from archival FFPE breast cancer samples: molecular pathway fidelity and novel discovery. <i>BMC Medical Genomics</i> , 2019 , 12, 195	3.7	12
40	Highly scalable generation of DNA methylation profiles in single cells. <i>Nature Biotechnology</i> , 2018 , 36, 428-431	44.5	125
39	3'UTR lengthening as a novel mechanism in regulating cellular senescence. <i>Genome Research</i> , 2018 ,	9.7	49
38	miR-205 Regulates Basal Cell Identity and Stem Cell Regenerative Potential During Mammary Reconstitution. <i>Stem Cells</i> , 2018 , 36, 1875-1889	5.8	7
37	3'UTR shortening represses tumor-suppressor genes in trans by disrupting ceRNA crosstalk. <i>Nature Genetics</i> , 2018 , 50, 783-789	36.3	85
36	Gleason Score 7 Prostate Cancers Emerge through Branched Evolution of Clonal Gleason Pattern 3 and 4. <i>Clinical Cancer Research</i> , 2017 , 23, 3823-3833	12.9	30
35	Poly(A)-ClickSeq: click-chemistry for next-generation 3'end sequencing without RNA enrichment or fragmentation. <i>Nucleic Acids Research</i> , 2017 , 45, e112	20.1	32
34	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
33	Aberrant plasticity of peripheral sensory axons in a painful neuropathy. <i>Scientific Reports</i> , 2017 , 7, 3407	4.9	23
32	Human mutations in integrator complex subunits link transcriptome integrity to brain development. <i>PLoS Genetics</i> , 2017 , 13, e1006809	6	41
31	Extensive alternative splicing transitions during postnatal skeletal muscle development are required for calcium handling functions. <i>ELife</i> , 2017 , 6,	8.9	31
30	Neonatal cardiac dysfunction and transcriptome changes caused by the absence of Celf1. <i>Scientific Reports</i> , 2016 , 6, 35550	4.9	11
29	KDM5 lysine demethylases are involved in maintenance of 3'UTR length. <i>Science Advances</i> , 2016 , 2, e1501662	16.2	16
28	CFIm25 regulates glutaminase alternative terminal exon definition to modulate miR-23 function. <i>Rna</i> , 2016 , 22, 830-8	5.8	25
27	PRMT9 is a type II methyltransferase that methylates the splicing factor SAP145. <i>Nature Communications</i> , 2015 , 6, 6428	17.4	128

26	Myc and SAGA rewire an alternative splicing network during early somatic cell reprogramming. <i>Genes and Development</i> , 2015 , 29, 803-16	12.6	55
25	Long non-coding RNAs control hematopoietic stem cell function. <i>Cell Stem Cell</i> , 2015 , 16, 426-38	18	115
24	Broad H3K4me3 is associated with increased transcription elongation and enhancer activity at tumor-suppressor genes. <i>Nature Genetics</i> , 2015 , 47, 1149-57	36.3	183
23	Whole transcriptome sequencing reveals extensive unspliced mRNA in metastatic castration-resistant prostate cancer. <i>Molecular Cancer Research</i> , 2015 , 13, 98-106	6.6	69
22	The Overlooked Fact: Fundamental Need for Spike-In Control for Virtually All Genome-Wide Analyses. <i>Molecular and Cellular Biology</i> , 2015 , 36, 662-7	4.8	94
21	ZMYND11 links histone H3.3K36me3 to transcription elongation and tumour suppression. <i>Nature</i> , 2014 , 508, 263-8	50.4	202
20	CFIm25 links alternative polyadenylation to glioblastoma tumour suppression. <i>Nature</i> , 2014 , 510, 412-6	50.4	243
19	Dynamic analyses of alternative polyadenylation from RNA-seq reveal a 3'UTR landscape across seven tumour types. <i>Nature Communications</i> , 2014 , 5, 5274	17.4	260
18	Rbfox2-coordinated alternative splicing of Mef2d and Rock2 controls myoblast fusion during myogenesis. <i>Molecular Cell</i> , 2014 , 55, 592-603	17.6	78
17	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. <i>Cell</i> , 2014 , 158, 929-944	56.2	935
16	Dnmt3a and Dnmt3b have overlapping and distinct functions in hematopoietic stem cells. <i>Cell Stem Cell</i> , 2014 , 15, 350-364	18	217
15	Alternative splicing regulates vesicular trafficking genes in cardiomyocytes during postnatal heart development. <i>Nature Communications</i> , 2014 , 5, 3603	17.4	98
14	Epigenomic profiling of young and aged HSCs reveals concerted changes during aging that reinforce self-renewal. <i>Cell Stem Cell</i> , 2014 , 14, 673-88	18	399
13	The histone-H3K4-specific demethylase KDM5B binds to its substrate and product through distinct PHD fingers. <i>Cell Reports</i> , 2014 , 6, 325-35	10.6	113
12	Nucleosome loss leads to global transcriptional up-regulation and genomic instability during yeast aging. <i>Genes and Development</i> , 2014 , 28, 396-408	12.6	196
11	A novel network and sparsity constraint regression model for functional module identification in genomic data analysis. <i>International Journal of Data Mining and Bioinformatics</i> , 2013 , 8, 311-25	0.5	2
10	Computer-assisted lip diagnosis on Traditional Chinese Medicine using multi-class support vector machines. <i>BMC Complementary and Alternative Medicine</i> , 2012 , 12, 127	4.7	38
9	NSMAP: a method for spliced isoforms identification and quantification from RNA-Seq. <i>BMC Bioinformatics</i> , 2011 , 12, 162	3.6	26

8	Semi-supervised drug-protein interaction prediction from heterogeneous biological spaces. <i>BMC Systems Biology</i> , 2010 , 4 Suppl 2, S6	3.5	224
7	An Image Based System Biology Approach for Alzheimer's Disease Pathway Analysis 2009 , 2009, 128-132		1
6	Registration of 3-D CT and 2-D flat images of mouse via affine transformation. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2008 , 12, 569-78		13
5	Fault Diagnosis Based on Fuzzy Support Vector Machine with Parameter Tuning and Feature Selection. <i>Chinese Journal of Chemical Engineering</i> , 2007 , 15, 233-239	3.2	14
4	Automated Recognition of Cellular Phenotypes by Support Vector Machines with Feature Reduction. <i>Lecture Notes in Computer Science</i> , 2006 , 171-178	0.9	
3	Extensive alternative splicing transitions during postnatal skeletal muscle development are required for calcium handling functions		1
2	Phenotype-guided subpopulation identification from single-cell sequencing data		1
1	Poly(A)-ClickSeq: click-chemistry for next-generation 3'-end sequencing without RNA enrichment or fragmentation		1