

# Yi Xing

## List of Publications by Year in descending order

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Version: 2024-02-01

48  
papers

6,263  
citations

186265

28  
h-index

223800

46  
g-index

50  
all docs

50  
docs citations

50  
times ranked

11021  
citing authors

#	ARTICLE	IF	CITATIONS
1	abPOA: an SIMD-based C library for fast partial order alignment using adaptive band. <i>Bioinformatics</i> , 2021, 37, 2209-2211.	4.1	20
2	isoCirc catalogs full-length circular RNA isoforms in human transcriptomes. <i>Nature Communications</i> , 2021, 12, 266.	12.8	87
3	Genetic variation and microRNA targeting of A-to-I RNA editing fine tune human tissue transcriptomes. <i>Genome Biology</i> , 2021, 22, 77.	8.8	26
4	RNA Dysregulation: An Expanding Source of Cancer Immunotherapy Targets. <i>Trends in Pharmacological Sciences</i> , 2021, 42, 268-282.	8.7	39
5	Tracking pre-mRNA maturation across subcellular compartments identifies developmental gene regulation through intron retention and nuclear anchoring. <i>Genome Research</i> , 2021, 31, 1106-1119.	5.5	31
6	Longitudinal Large-Scale Semiquantitative Proteomic Data Stability Across Multiple Instrument Platforms. <i>Journal of Proteome Research</i> , 2021, 20, 5203-5211.	3.7	1
7	Mis-splicing in Huntington's disease: harnessing the power of comparative transcriptomics. <i>Trends in Neurosciences</i> , 2021, , .	8.6	0
8	METTL4 is an snRNA m6Am methyltransferase that regulates RNA splicing. <i>Cell Research</i> , 2020, 30, 544-547.	12.0	84
9	Detecting Allele-Specific Alternative Splicing from Population-Scale RNA-Seq Data. <i>American Journal of Human Genetics</i> , 2020, 107, 461-472.	6.2	14
10	Cancer Moonshot Immuno-Oncology Translational Network (IOTN): accelerating the clinical translation of basic discoveries for improving immunotherapy and immunoprevention of cancer. , 2020, 8, e000796.		7
11	Regional Variation of Splicing QTLs in Human Brain. <i>American Journal of Human Genetics</i> , 2020, 107, 196-210.	6.2	26
12	Pathway-guided analysis identifies Myc-dependent alternative pre-mRNA splicing in aggressive prostate cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5269-5279.	7.1	44
13	Cleft lip and cleft palate (CL/P) in <i>Esrp1</i> KO mice is associated with alterations in epithelial-mesenchymal crosstalk. <i>Development (Cambridge)</i> , 2020, 147, .	2.5	42
14	TideHunter: efficient and sensitive tandem repeat detection from noisy long-reads using seed-and-chain. <i>Bioinformatics</i> , 2019, 35, i200-i207.	4.1	23
15	Discovery of Allele-Specific Protein-RNA Interactions in Human Transcriptomes. <i>American Journal of Human Genetics</i> , 2019, 104, 492-502.	6.2	17
16	Deep-learning augmented RNA-seq analysis of transcript splicing. <i>Nature Methods</i> , 2019, 16, 307-310.	19.0	74
17	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , 2019, 49, 10-29.	7.0	57
18	The Expanding Landscape of Alternative Splicing Variation in Human Populations. <i>American Journal of Human Genetics</i> , 2018, 102, 11-26.	6.2	290

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19	SEASTAR: systematic evaluation of alternative transcription start sites in RNA. <i>Nucleic Acids Research</i> , 2018, 46, e45-e45.	14.5	17
20	rMATS-DVR: rMATS discovery of differential variants in RNA. <i>Bioinformatics</i> , 2017, 33, 2216-2217.	4.1	24
21	Genome-Wide Maps of m6A circRNAs Identify Widespread and Cell-Type-Specific Methylation Patterns that Are Distinct from mRNAs. <i>Cell Reports</i> , 2017, 20, 2262-2276.	6.4	315
22	Using RNA-Seq to Discover Genetic Polymorphisms That Produce Hidden Splice Variants. <i>Methods in Molecular Biology</i> , 2017, 1648, 129-142.	0.9	2
23	Population and allelic variation of A-to-I RNA editing in human transcriptomes. <i>Genome Biology</i> , 2017, 18, 143.	8.8	41
24	m6A-LAIC-seq reveals the census and complexity of the m6A epitranscriptome. <i>Nature Methods</i> , 2016, 13, 692-698.	19.0	310
25	Transcriptome sequencing reveals aberrant alternative splicing in Huntington's disease. <i>Human Molecular Genetics</i> , 2016, 25, 3454-3466.	2.9	102
26	Multiphasic and Dynamic Changes in Alternative Splicing during Induction of Pluripotency Are Coordinated by Numerous RNA-Binding Proteins. <i>Cell Reports</i> , 2016, 15, 247-255.	6.4	75
27	Î±CP binding to a cytosine-rich subset of polypyrimidine tracts drives a novel pathway of cassette exon splicing in the mammalian transcriptome. <i>Nucleic Acids Research</i> , 2016, 44, 2283-2297.	14.5	32
28	Determination of a Comprehensive Alternative Splicing Regulatory Network and Combinatorial Regulation by Key Factors during the Epithelial-to-Mesenchymal Transition. <i>Molecular and Cellular Biology</i> , 2016, 36, 1704-1719.	2.3	118
29	Rbfox Proteins Regulate Splicing as Part of a Large Multiprotein Complex LASR. <i>Cell</i> , 2016, 165, 606-619.	28.9	158
30	SURVIV for survival analysis of mRNA isoform variation. <i>Nature Communications</i> , 2016, 7, 11548.	12.8	85
31	Ablation of the epithelial-specific splicing factor <i>Esrp1</i> results in ureteric branching defects and reduced nephron number. <i>Developmental Dynamics</i> , 2016, 245, 991-1000.	1.8	20
32	â€œRADIOTRANSCRIPTOMICSâ€ A synergy of imaging and transcriptomics in clinical assessment. <i>Quantitative Biology</i> , 2016, 4, 1-12.	0.5	15
33	rMAPS: RNA map analysis and plotting server for alternative exon regulation. <i>Nucleic Acids Research</i> , 2016, 44, W333-W338.	14.5	54
34	The contribution of Alu exons to the human proteome. <i>Genome Biology</i> , 2016, 17, 15.	8.8	39
35	The splicing regulators <i>Esrp1</i> and <i>Esrp2</i> direct an epithelial splicing program essential for mammalian development. <i>ELife</i> , 2015, 4, .	6.0	118
36	Discover hidden splicing variations by mapping personal transcriptomes to personal genomes. <i>Nucleic Acids Research</i> , 2015, 43, 10612-10622.	14.5	13

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37	Systems Biology With High-Throughput Sequencing Reveals Genetic Mechanisms Underlying the Metabolic Syndrome in the Lyon Hypertensive Rat. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 316-326.	5.1	24
38	Species-Specific Exon Loss in Human Transcriptomes. <i>Molecular Biology and Evolution</i> , 2015, 32, 481-494.	8.9	7
39	Transcriptome-wide Landscape of Pre-mRNA Alternative Splicing Associated with Metastatic Colonization. <i>Molecular Cancer Research</i> , 2015, 13, 305-318.	3.4	63
40	rMATS: Robust and flexible detection of differential alternative splicing from replicate RNA-Seq data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5593-601.	7.1	1,774
41	PrimerSeq: Design and Visualization of RT-PCR Primers for Alternative Splicing Using RNA-seq Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 105-109.	6.9	15
42	Transcriptome-wide Discovery of microRNA Binding Sites in Human Brain. <i>Neuron</i> , 2014, 81, 294-305.	8.1	179
43	m6A RNA Modification Controls Cell Fate Transition in Mammalian Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2014, 15, 707-719.	11.1	990
44	BS69/ZMYND11 Reads and Connects Histone H3.3 Lysine 36 Trimethylation-Decorated Chromatin to Regulated Pre-mRNA Processing. <i>Molecular Cell</i> , 2014, 56, 298-310.	9.7	194
45	GLiMMPS: Robust statistical model for regulatory variation of alternative splicing using RNA-seq data. <i>Genome Biology</i> , 2013, 14, R74.	9.6	76
46	Genome-Wide Determination of a Broad ESRP-Regulated Posttranscriptional Network by High-Throughput Sequencing. <i>Molecular and Cellular Biology</i> , 2012, 32, 1468-1482.	2.3	127
47	Genetic variation of pre-mRNA alternative splicing in human populations. <i>Wiley Interdisciplinary Reviews RNA</i> , 2012, 3, 581-592.	6.4	42
48	An ESRP-regulated splicing programme is abrogated during the epithelial-to-mesenchymal transition. <i>EMBO Journal</i> , 2010, 29, 3286-3300.	7.8	346