Yi Xing

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2039603/publications.pdf

Version: 2024-02-01

48	6,263	186265	223800
papers	citations	28 h-index	46 g-index

50	50	50	11021
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	rMATS: Robust and flexible detection of differential alternative splicing from replicate RNA-Seq data. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5593-601.	7.1	1,774
2	m6A RNA Modification Controls Cell Fate Transition in Mammalian Embryonic Stem Cells. Cell Stem Cell, 2014, 15, 707-719.	11.1	990
3	An ESRP-regulated splicing programme is abrogated during the epithelialâ€“mesenchymal transition. EMBO Journal, 2010, 29, 3286-3300.	7.8	346
4	Genome-Wide Maps of m6A circRNAs Identify Widespread and Cell-Type-Specific Methylation Patterns that Are Distinct from mRNAs. Cell Reports, 2017, 20, 2262-2276.	6.4	315
5	m6A-LAIC-seq reveals the census and complexity of the m6A epitranscriptome. Nature Methods, 2016, 13, 692-698.	19.0	310
6	The Expanding Landscape of Alternative Splicing Variation in Human Populations. American Journal of Human Genetics, 2018, 102, 11-26.	6.2	290
7	BS69/ZMYND11 Reads and Connects Histone H3.3 Lysine 36 Trimethylation-Decorated Chromatin to Regulated Pre-mRNA Processing. Molecular Cell, 2014, 56, 298-310.	9.7	194
8	Transcriptome-wide Discovery of microRNA Binding Sites in Human Brain. Neuron, 2014, 81, 294-305.	8.1	179
9	Rbfox Proteins Regulate Splicing as Part of a Large Multiprotein Complex LASR. Cell, 2016, 165, 606-619.	28.9	158
10	Genome-Wide Determination of a Broad ESRP-Regulated Posttranscriptional Network by High-Throughput Sequencing. Molecular and Cellular Biology, 2012, 32, 1468-1482.	2.3	127
11	The splicing regulators Esrp1 and Esrp2 direct an epithelial splicing program essential for mammalian development. ELife, 2015, 4, .	6.0	118
12	Determination of a Comprehensive Alternative Splicing Regulatory Network and Combinatorial Regulation by Key Factors during the Epithelial-to-Mesenchymal Transition. Molecular and Cellular Biology, 2016, 36, 1704-1719.	2.3	118
13	Transcriptome sequencing reveals aberrant alternative splicing in Huntington's disease. Human Molecular Genetics, 2016, 25, 3454-3466.	2.9	102
14	isoCirc catalogs full-length circular RNA isoforms in human transcriptomes. Nature Communications, 2021, 12, 266.	12.8	87
15	SURVIV for survival analysis of mRNA isoform variation. Nature Communications, 2016, 7, 11548.	12.8	85
16	METTL4 is an snRNA m6Am methyltransferase that regulates RNA splicing. Cell Research, 2020, 30, 544-547.	12.0	84
17	GLiMMPS: Robust statistical model for regulatory variation of alternative splicing using RNA-seq data. Genome Biology, 2013, 14, R74.	9.6	76
18	Multiphasic and Dynamic Changes in Alternative Splicing during Induction of Pluripotency Are Coordinated by Numerous RNA-Binding Proteins. Cell Reports, 2016, 15, 247-255.	6.4	75

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19	Deep-learning augmented RNA-seq analysis of transcript splicing. Nature Methods, 2019, 16, 307-310.	19.0	74
20	Transcriptome-wide Landscape of Pre-mRNA Alternative Splicing Associated with Metastatic Colonization. Molecular Cancer Research, 2015, 13, 305-318.	3.4	63
21	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	7.0	57
22	rMAPS: RNA map analysis and plotting server for alternative exon regulation. Nucleic Acids Research, 2016, 44, W333-W338.	14.5	54
23	Pathway-guided analysis identifies Myc-dependent alternative pre-mRNA splicing in aggressive prostate cancers. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5269-5279.	7.1	44
24	Genetic variation of preâ€mRNA alternative splicing in human populations. Wiley Interdisciplinary Reviews RNA, 2012, 3, 581-592.	6.4	42
25	Cleft lip and cleft palate (CL/P) in Esrp1 KO mice is associated with alterations in epithelial-mesenchymal crosstalk. Development (Cambridge), 2020, 147, .	2.5	42
26	Population and allelic variation of A-to-I RNA editing in human transcriptomes. Genome Biology, 2017, 18, 143.	8.8	41
27	The contribution of Alu exons to the human proteome. Genome Biology, 2016, 17, 15.	8.8	39
28	RNA Dysregulation: An Expanding Source of Cancer Immunotherapy Targets. Trends in Pharmacological Sciences, 2021, 42, 268-282.	8.7	39
29	Î±CP binding to a cytosine-rich subset of polypyrimidine tracts drives a novel pathway of cassette exon splicing in the mammalian transcriptome. Nucleic Acids Research, 2016, 44, 2283-2297.	14.5	32
30	Tracking pre-mRNA maturation across subcellular compartments identifies developmental gene regulation through intron retention and nuclear anchoring. Genome Research, 2021, 31, 1106-1119.	5.5	31
31	Regional Variation of Splicing QTLs in Human Brain. American Journal of Human Genetics, 2020, 107, 196-210.	6.2	26
32	Genetic variation and microRNA targeting of A-to-I RNA editing fine tune human tissue transcriptomes. Genome Biology, 2021, 22, 77.	8.8	26
33	Systems Biology With High-Throughput Sequencing Reveals Genetic Mechanisms Underlying the Metabolic Syndrome in the Lyon Hypertensive Rat. Circulation: Cardiovascular Genetics, 2015, 8, 316-326.	5.1	24
34	rMATS-DVR: rMATS discovery of differential variants in RNA. Bioinformatics, 2017, 33, 2216-2217.	4.1	24
35	TideHunter: efficient and sensitive tandem repeat detection from noisy long-reads using seed-and-chain. Bioinformatics, 2019, 35, i200-i207.	4.1	23
36	Ablation of the epithelialâ€specific splicing factor Esrp1 results in ureteric branching defects and reduced nephron number. Developmental Dynamics, 2016, 245, 991-1000.	1.8	20

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37	abPOA: an SIMD-based C library for fast partial order alignment using adaptive band. Bioinformatics, 2021, 37, 2209-2211.	4.1	20
38	SEASTAR: systematic evaluation of alternative transcription start sites in RNA. Nucleic Acids Research, 2018, 46, e45-e45.	14.5	17
39	Discovery of Allele-Specific Protein-RNA Interactions in Human Transcriptomes. American Journal of Human Genetics, 2019, 104, 492-502.	6.2	17
40	PrimerSeq: Design and Visualization of RT-PCR Primers for Alternative Splicing Using RNA-seq Data. Genomics, Proteomics and Bioinformatics, 2014, 12, 105-109.	6.9	15
41	â€œRADIOTRANSCRIPTOMICSâ€• A synergy of imaging and transcriptomics in clinical assessment. Quantitative Biology, 2016, 4, 1-12.	0.5	15
42	Detecting Allele-Specific Alternative Splicing from Population-Scale RNA-Seq Data. American Journal of Human Genetics, 2020, 107, 461-472.	6.2	14
43	Discover hidden splicing variations by mapping personal transcriptomes to personal genomes. Nucleic Acids Research, 2015, 43, 10612-10622.	14.5	13
44	Species-Specific Exon Loss in Human Transcriptomes. Molecular Biology and Evolution, 2015, 32, 481-494.	8.9	7
45	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
46	Using RNA-Seq to Discover Genetic Polymorphisms That Produce Hidden Splice Variants. Methods in Molecular Biology, 2017, 1648, 129-142.	0.9	2
47	Longitudinal Large-Scale Semiquantitative Proteomic Data Stability Across Multiple Instrument Platforms. Journal of Proteome Research, 2021, 20, 5203-5211.	3.7	1
48	Mis-splicing in Huntingtonâ€™s disease: harnessing the power of comparative transcriptomics. Trends in Neurosciences, 2021, , .	8.6	0