

# Xinshu Xiao

## List of Publications by Year in descending order

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76  
papers

7,015  
citations

108046

37  
h-index

87275

74  
g-index

85  
all docs

85  
docs citations

85  
times ranked

12025  
citing authors

#	ARTICLE	IF	CITATIONS
1	Extracellular microRNA 3' end modification across diverse body fluids. <i>Epigenetics</i> , 2021, 16, 1000-1015.	1.3	7
2	Allele-specific alternative splicing and its functional genetic variants in human tissues. <i>Genome Research</i> , 2021, 31, 359-371.	2.4	17
3	Long-term maturation of human cortical organoids matches key early postnatal transitions. <i>Nature Neuroscience</i> , 2021, 24, 331-342.	7.1	188
4	Genetics of white color and iridophoroma in "Lemon Frost" leopard geckos. <i>PLoS Genetics</i> , 2021, 17, e1009580.	1.5	13
5	Lipin 1 modulates mRNA splicing during fasting adaptation in liver. <i>JCI Insight</i> , 2021, 6, .	2.3	7
6	RNA editing in cancer impacts mRNA abundance in immune response pathways. <i>Genome Biology</i> , 2020, 21, 268.	3.8	27
7	Statistical inference of differential RNA-editing sites from RNA-sequencing data by hierarchical modeling. <i>Bioinformatics</i> , 2020, 36, 2796-2804.	1.8	14
8	p38 Mitogen-activated protein kinase regulates chamber-specific perinatal growth in heart. <i>Journal of Clinical Investigation</i> , 2020, 130, 5287-5301.	3.9	19
9	Molecular consequences of fetal alcohol exposure on amniotic exosomal miRNAs with functional implications for stem cell potency and differentiation. <i>PLoS ONE</i> , 2020, 15, e0242276.	1.1	11
10	mountainClimber Identifies Alternative Transcription Start and Polyadenylation Sites in RNA-Seq. <i>Cell Systems</i> , 2019, 9, 393-400.e6.	2.9	15
11	DeepPASTA: deep neural network based polyadenylation site analysis. <i>Bioinformatics</i> , 2019, 35, 4577-4585.	1.8	35
12	Allele-specific binding of RNA-binding proteins reveals functional genetic variants in the RNA. <i>Nature Communications</i> , 2019, 10, 1338.	5.8	38
13	Widespread RNA editing dysregulation in brains from autistic individuals. <i>Nature Neuroscience</i> , 2019, 22, 25-36.	7.1	161
14	A Multiplexed Assay for Exon Recognition Reveals that an Unappreciated Fraction of Rare Genetic Variants Cause Large-Effect Splicing Disruptions. <i>Molecular Cell</i> , 2019, 73, 183-194.e8.	4.5	88
15	Regulation of RNA editing by RNA-binding proteins in human cells. <i>Communications Biology</i> , 2019, 2, 19.	2.0	97
16	TAPAS: tool for alternative polyadenylation site analysis. <i>Bioinformatics</i> , 2018, 34, 2521-2529.	1.8	62
17	Characterization of Human Salivary Extracellular RNA by Next-generation Sequencing. <i>Clinical Chemistry</i> , 2018, 64, 1085-1095.	1.5	33
18	Novel approaches for bioinformatic analysis of salivary RNA sequencing data for development. <i>Bioinformatics</i> , 2018, 34, 1-8.	1.8	24

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19	Coregulation of alternative splicing by hnRNPM and ESRP1 during EMT. <i>Rna</i> , 2018, 24, 1326-1338.	1.6	53
20	Loss of MECP2 Leads to Activation of P53 and Neuronal Senescence. <i>Stem Cell Reports</i> , 2018, 10, 1453-1463.	2.3	56
21	RNA editing in nascent RNA affects pre-mRNA splicing. <i>Genome Research</i> , 2018, 28, 812-823.	2.4	107
22	FoxP2 isoforms delineate spatiotemporal transcriptional networks for vocal learning in the zebra finch. <i>ELife</i> , 2018, 7, .	2.8	19
23	Extensive translation of circular RNAs driven by N6-methyladenosine. <i>Cell Research</i> , 2017, 27, 626-641.	5.7	1,367
24	Structure-mediated modulation of mRNA abundance by A-to-I editing. <i>Nature Communications</i> , 2017, 8, 1255.	5.8	65
25	Wnt11 regulates cardiac chamber development and disease during perinatal maturation. <i>JCI Insight</i> , 2017, 2, .	2.3	21
26	Catabolic Defect of Branched-Chain Amino Acids Promotes Heart Failure. <i>Circulation</i> , 2016, 133, 2038-2049.	1.6	390
27	Systems Nutrigenomics Reveals Brain Gene Networks Linking Metabolic and Brain Disorders. <i>EBioMedicine</i> , 2016, 7, 157-166.	2.7	59
28	Decoding the Long Noncoding RNA During Cardiac Maturation. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 395-407.	5.1	39
29	The long noncoding RNA Chaer defines an epigenetic checkpoint in cardiac hypertrophy. <i>Nature Medicine</i> , 2016, 22, 1131-1139.	15.2	331
30	Global analyses of endonucleolytic cleavage in mammals reveal expanded repertoires of cleavage-inducing small RNAs and their targets. <i>Nucleic Acids Research</i> , 2016, 44, 3253-3263.	6.5	8
31	Alternative splicing modulated by genetic variants demonstrates accelerated evolution regulated by highly conserved proteins. <i>Genome Research</i> , 2016, 26, 440-450.	2.4	50
32	Research Resource: Hormones, Genes, and Athleticism: Effect of Androgens on the Avian Muscular Transcriptome. <i>Molecular Endocrinology</i> , 2016, 30, 254-271.	3.7	37
33	Global Approaches to Alternative Splicing and Its Regulation—Recent Advances and Open Questions. <i>Translational Bioinformatics</i> , 2016, , 37-71.	0.0	2
34	Hypothalamic transcriptomes of 99 mouse strains reveal trans eQTL hotspots, splicing QTLs and novel non-coding genes. <i>ELife</i> , 2016, 5, .	2.8	35
35	Regulation of NF- $\kappa$ B signaling by oxidized glycerophospholipid and IL-1 $\beta$ induced miRs-21-3p and -27a-5p in human aortic endothelial cells. <i>Journal of Lipid Research</i> , 2015, 56, 38-50.	2.0	33
36	Noncoding RNAs in human saliva as potential disease biomarkers. <i>Frontiers in Genetics</i> , 2015, 6, 175.	1.1	44

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37	The Sm protein methyltransferase <scp>PRMT</scp>5 is not required for primordial germ cell specification in mice. EMBO Journal, 2015, 34, 748-758.	3.5	41
38	Genomic analysis of ADAR1 binding and its involvement in multiple RNA processing pathways. Nature Communications, 2015, 6, 6355.	5.8	127
39	Genome sequence-independent identification of RNA editing sites. Nature Methods, 2015, 12, 347-350.	9.0	102
40	ESRP2 controls an adult splicing programme in hepatocytes to support postnatal liver maturation. Nature Communications, 2015, 6, 8768.	5.8	83
41	RASER: reads aligner for SNPs and editing sites of RNA. Bioinformatics, 2015, 31, 3906-3913.	1.8	21
42	The Landscape of MicroRNA, Piwi-Interacting RNA, and Circular RNA in Human Saliva. Clinical Chemistry, 2015, 61, 221-230.	1.5	573
43	RBFox1-mediated RNA splicing regulates cardiac hypertrophy and heart failure. Journal of Clinical Investigation, 2015, 126, 195-206.	3.9	114
44	Abstract 15: Global RNA Splicing Regulation in Cardiac Maturation. Circulation Research, 2015, 117, .	2.0	0
45	Cell type-restricted activity of hnRNPM promotes breast cancer metastasis via regulating alternative splicing. Genes and Development, 2014, 28, 1191-1203.	2.7	193
46	Decoding the Noncoding Transcripts in Human Heart Failure. Circulation, 2014, 129, 958-960.	1.6	9
47	A complex network of factors with overlapping affinities represses splicing through intronic elements. Nature Structural and Molecular Biology, 2013, 20, 36-45.	3.6	90
48	Modeling Associated Protein-DNA Pattern Discovery with Unified Scores. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 696-707.	1.9	5
49	Analysis and design of RNA sequencing experiments for identifying RNA editing and other single-nucleotide variants. Rna, 2013, 19, 725-732.	1.6	60
50	Abstract 235: Global RNA Splicing and Regulation in Cardiac Maturation and Diseases. Circulation Research, 2013, 113, .	2.0	0
51	Identification of allele-specific alternative mRNA processing via transcriptome sequencing. Nucleic Acids Research, 2012, 40, e104-e104.	6.5	74
52	Accurate identification of A-to-I RNA editing in human by transcriptome sequencing. Genome Research, 2012, 22, 142-150.	2.4	297
53	The cardiotoxic steroid digitoxin regulates alternative splicing through depletion of the splicing factors SRSF3 and TRA2B. Rna, 2012, 18, 1041-1049.	1.6	53
54	Intronic splicing enhancers, cognate splicing factors and context-dependent regulation rules. Nature Structural and Molecular Biology, 2012, 19, 1044-1052.	3.6	142

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55	Identification of Vascular and Hematopoietic Genes Downstream of etsrp by Deep Sequencing in Zebrafish. PLoS ONE, 2012, 7, e31658.	1.1	26
56	Analysis of Transcriptome Complexity Through RNA Sequencing in Normal and Failing Murine Hearts. Circulation Research, 2011, 109, 1332-1341.	2.0	194
57	Systems analysis of alternative splicing and its regulation. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 550-565.	6.6	14
58	Detection of two distinct forms of apoC-I in great apes. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2010, 5, 73-79.	0.4	15
59	Splice site strengthâ€“dependent activity and genetic buffering by poly-G runs. Nature Structural and Molecular Biology, 2009, 16, 1094-1100.	3.6	112
60	A postnatal switch of CELF and MBNL proteins reprograms alternative splicing in the developing heart. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20333-20338.	3.3	433
61	Global analysis of alternative splicing differences between humans and chimpanzees. Genes and Development, 2007, 21, 2963-2975.	2.7	130
62	Coevolutionary networks of splicing <i>cis</i>-regulatory elements. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18583-18588.	3.3	52
63	General and Specific Functions of Exonic Splicing Silencers in Splicing Control. Molecular Cell, 2006, 23, 61-70.	4.5	164
64	Why is Orthostatic Tolerance Lower in Women than in Men? Renal and Cardiovascular Responses to Simulated Microgravity and the Role of Midodrine. Journal of Investigative Medicine, 2006, 54, 180-190.	0.7	26
65	A weighted-principal component regression method for the identification of physiologic systems. IEEE Transactions on Biomedical Engineering, 2006, 53, 1521-1530.	2.5	6
66	Inference of Splicing Regulatory Activities by Sequence Neighborhood Analysis. PLoS Genetics, 2006, 2, e191.	1.5	71
67	Readaptation from Simulated Microgravity as a Stimulus for Improved Orthostatic Tolerance: Role of the Renal, Cardioendocrine, and Cardiovascular Systems. Journal of Investigative Medicine, 2005, 53, 82-91.	0.7	7
68	Simulated Microgravity Induces Microvolt T Wave Alternans. Annals of Noninvasive Electrocardiology, 2005, 10, 363-370.	0.5	16
69	A Model Order Selection Criterion With Applications to Cardio-Respiratory-Renal Systems. IEEE Transactions on Biomedical Engineering, 2005, 52, 445-453.	2.5	9
70	System identification: a multi-signal approach for probing neural cardiovascular regulation. Physiological Measurement, 2005, 26, R41-R71.	1.2	56
71	Bed rest effects on human calf hemodynamics and orthostatic intolerance: a model-based analysis. Aviation, Space, and Environmental Medicine, 2005, 76, 1037-45.	0.6	4
72	Effects of simulated microgravity on closed-loop cardiovascular regulation and orthostatic intolerance: analysis by means of system identification. Journal of Applied Physiology, 2004, 96, 489-497.	1.2	24

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73	Sleep restriction does not affect orthostatic tolerance in the simulated microgravity environment. Journal of Applied Physiology, 2004, 97, 1660-1666.	1.2	2
74	Model-Based Assessment of Cardiovascular Health from Noninvasive Measurements. Annals of Biomedical Engineering, 2002, 30, 612-623.	1.3	19
75	Numerical Simulation of Enhanced External Counterpulsation. Annals of Biomedical Engineering, 2001, 29, 284-297.	1.3	36
76	A weighted principal component regression approach for system identification. , 0, , .		1