

# Shaojie Zhang

## List of Publications by Year in descending order

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54  
papers

1,805  
citations

516710

16  
h-index

330143

37  
g-index

67  
all docs

67  
docs citations

67  
times ranked

2258  
citing authors

#	ARTICLE	IF	CITATIONS
1	RAFFI: Accurate and fast familial relationship inference in large scale biobank studies using RaPID. PLoS Genetics, 2021, 17, e1009315.	3.5	7
2	Repressing Ago2 mRNA translation by Trim71 maintains pluripotency through inhibiting let-7 microRNAs. ELife, 2021, 10, .	6.0	19
3	d-PBWT: dynamic positional Burrows-Wheeler transform. Bioinformatics, 2021, 37, 2390-2397.	4.1	10
4	Personalized genealogical history of UK individuals inferred from biobank-scale IBD segments. BMC Biology, 2021, 19, 32.	3.8	12
5	RNAMotifContrast: a method to discover and visualize RNA structural motif subfamilies. Nucleic Acids Research, 2021, 49, e61-e61.	14.5	5
6	Simultaneous epigenetic perturbation and genome imaging reveal distinct roles of H3K9me3 in chromatin architecture and transcription. Genome Biology, 2020, 21, 296.	8.8	37
7	LocalSTAR3D: a local stack-based RNA 3D structural alignment tool. Nucleic Acids Research, 2020, 48, e77.	14.5	4
8	Genealogical search using whole-genome genotype profiles. , 2020, , 51-94.		1
9	d-PBWT: Dynamic Positional Burrows-Wheeler Transform. Lecture Notes in Computer Science, 2020, , 269-270.	1.3	3
10	Efficient haplotype matching between a query and a panel for genealogical search. Bioinformatics, 2019, 35, i233-i241.	4.1	14
11	RaPID: ultra-fast, powerful, and accurate detection of segments identical by descent (IBD) in biobank-scale cohorts. Genome Biology, 2019, 20, 143.	8.8	48
12	Accurate and Efficient Mapping of the Cross-Linked microRNA-mRNA Duplex Reads. IScience, 2019, 18, 11-19.	4.1	7
13	NETA. , 2019, , .		10
14	Multi-allelic positional Burrows-Wheeler transform. BMC Bioinformatics, 2019, 20, 279.	2.6	7
15	Cell cycle- and genomic distance-dependent dynamics of a discrete chromosomal region. Journal of Cell Biology, 2019, 218, 1467-1477.	5.2	40
16	RERTL: Finite State Transducer Logic Recovery at Register Transfer Level. , 2019, , .		1
17	Practical considerations on performing and analyzing CLIP-seq experiments to identify transcriptomic-wide RNA-protein interactions. Methods, 2019, 155, 49-57.	3.8	12
18	De novo discovery of structural motifs in RNA 3D structures through clustering. Nucleic Acids Research, 2018, 46, 4783-4793.	14.5	14

#	ARTICLE	IF	CITATIONS
19	The Old Frontier of Reverse Engineering: Netlist Partitioning. <i>Journal of Hardware and Systems Security</i> , 2018, 2, 201-213.	1.3	15
20	Hardware Trojan Detection and Functionality Determination for Soft IPs. , 2018, , .		4
21	CRISPR-Sirius: RNA scaffolds for signal amplification in genome imaging. <i>Nature Methods</i> , 2018, 15, 928-931.	19.0	118
22	The long noncoding RNA SPRIGHTLY acts as an intranuclear organizing hub for pre-mRNA molecules. <i>Science Advances</i> , 2017, 3, e1602505.	10.3	31
23	CompAnnotate: a comparative approach to annotate base-pairing interactions in RNA 3D structures. <i>Nucleic Acids Research</i> , 2017, 45, e136-e136.	14.5	4
24	IP protection through gate-level netlist security enhancement. <i>The Integration VLSI Journal</i> , 2017, 58, 563-570.	2.1	8
25	Multi-allelic positional burrows-wheeler transform. , 2017, , .		0
26	DRREP: deep ridge regressed epitope predictor. <i>BMC Genomics</i> , 2017, 18, 676.	2.8	26
27	Translation repression via modulation of the cytoplasmic poly(A)-binding protein in the inflammatory response. <i>ELife</i> , 2017, 6, .	6.0	32
28	Interrogation of CRISPR Dynamics with Fluorescent Single Guide RNAs in Live Cells. <i>Biophysical Journal</i> , 2016, 110, 362a-363a.	0.5	1
29	Multiplexed labeling of genomic loci with dCas9 and engineered sgRNAs using CRISPRainbow. <i>Nature Biotechnology</i> , 2016, 34, 528-530.	17.5	365
30	The Non-Coding RNA Ontology (NCRO): a comprehensive resource for the unification of non-coding RNA biology. <i>Journal of Biomedical Semantics</i> , 2016, 7, 24.	1.6	10
31	WebSTAR3D: a web server for RNA 3D structural alignment. <i>Bioinformatics</i> , 2016, 32, btw502.	4.1	0
32	CRISPR-Cas9 nuclear dynamics and target recognition in living cells. <i>Journal of Cell Biology</i> , 2016, 214, 529-537.	5.2	165
33	Gate-level netlist reverse engineering for hardware security: Control logic register identification. , 2016, , .		34
34	The development of non-coding RNA ontology. <i>International Journal of Data Mining and Bioinformatics</i> , 2016, 15, 214.	0.1	9
35	Netlist reverse engineering for high-level functionality reconstruction. , 2016, , .		50
36	Computational analysis of RNA structures with chemical probing data. <i>Methods</i> , 2015, 79-80, 60-66.	3.8	26

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37	RNAMotifScanX: a graph alignment approach for RNA structural motif identification. <i>Rna</i> , 2015, 21, 333-346.	3.5	53
38	Multicolor CRISPR labeling of chromosomal loci in human cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3002-3007.	7.1	363
39	STAR3D: a stack-based RNA 3D structural alignment tool. <i>Nucleic Acids Research</i> , 2015, 43, gkv697.	14.5	11
40	Finding consensus stable local optimal structures for aligned RNA sequences and its application to discovering riboswitch elements. <i>International Journal of Bioinformatics Research and Applications</i> , 2014, 10, 498.	0.2	2
41	FIGHT-Metric. , 2014, , .		27
42	Discovering non-coding RNA elements in <i>Drosophila</i> 3' untranslated regions. <i>International Journal of Bioinformatics Research and Applications</i> , 2014, 10, 479.	0.2	2
43	ProbeAlign: incorporating high-throughput sequencing-based structure probing information into ncRNA homology search. <i>BMC Bioinformatics</i> , 2014, 15, S15.	2.6	6
44	Clustering RNA structural motifs in ribosomal RNAs using secondary structural alignment. <i>Nucleic Acids Research</i> , 2012, 40, 1307-1317.	14.5	22
45	Discovering non-coding RNA elements in <i>drosophila</i> 3' untranslated regions. , 2012, , .		1
46	Finding consensus stable local optimal structures for aligned RNA sequences. , 2012, , .		2
47	Predicting folding pathways between RNA conformational structures guided by RNA stacks. , 2011, , .		0
48	Finding stable local optimal RNA secondary structures. <i>Bioinformatics</i> , 2011, 27, 2994-3001.	4.1	17
49	RNAMotifScan: automatic identification of RNA structural motifs using secondary structural alignment. <i>Nucleic Acids Research</i> , 2010, 38, e176-e176.	14.5	41
50	PMFastR: A New Approach to Multiple RNA Structure Alignment. <i>Lecture Notes in Computer Science</i> , 2009, , 49-61.	1.3	3
51	A sequence-based filtering method for ncRNA identification and its application to searching for riboswitch elements. <i>Bioinformatics</i> , 2006, 22, e557-e565.	4.1	30
52	EXPLORING THE OCEAN'S MICROBES: SEQUENCING THE SEVEN SEAS. , 2006, , .		0
53	Searching Genomes for Noncoding RNA Using FastR. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005, 2, 366-379.	3.0	48
54	FastR: fast database search tool for non-coding RNA. , 2004, , 52-61.		19