Shaojie Zhang

List of Publications by Year in descending order

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54 papers	1,805 citations	586496 16 h-index	371746 37 g-index
67 all docs	67 docs citations	67 times ranked	2570 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.	1.5	7
2	Repressing Ago2 mRNA translation by Trim71 maintains pluripotency through inhibiting let-7 microRNAs. ELife, 2021, 10, .	2.8	19
3	d-PBWT: dynamic positional Burrowsâ€“Wheeler transform. Bioinformatics, 2021, 37, 2390-2397.	1.8	10
4	Personalized genealogical history of UK individuals inferred from biobank-scale IBD segments. BMC Biology, 2021, 19, 32.	1.7	12
5	RNAMotifContrast: a method to discover and visualize RNA structural motif subfamilies. Nucleic Acids Research, 2021, 49, e61-e61.	6.5	5
6	Simultaneous epigenetic perturbation and genome imaging reveal distinct roles of H3K9me3 in chromatin architecture and transcription. Genome Biology, 2020, 21, 296.	3.8	37
7	LocalSTAR3D: a local stack-based RNA 3D structural alignment tool. Nucleic Acids Research, 2020, 48, e77.	6.5	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.	1.0	3
10	Efficient haplotype matching between a query and a panel for genealogical search. Bioinformatics, 2019, 35, i233-i241.	1.8	14
11	RaPID: ultra-fast, powerful, and accurate detection of segments identical by descent (IBD) in biobank-scale cohorts. Genome Biology, 2019, 20, 143.	3.8	48
12	Accurate and Efficient Mapping of the Cross-Linked microRNA-mRNA Duplex Reads. IScience, 2019, 18, 11-19.	1.9	7
13	NETA. , 2019, , .		10
14	Multi-allelic positional Burrows-Wheeler transform. BMC Bioinformatics, 2019, 20, 279.	1.2	7
15	Cell cycleâ€“ and genomic distanceâ€“dependent dynamics of a discrete chromosomal region. Journal of Cell Biology, 2019, 218, 1467-1477.	2.3	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.	1.9	12
18	De novo discovery of structural motifs in RNA 3D structures through clustering. Nucleic Acids Research, 2018, 46, 4783-4793.	6.5	14

#	Article	IF	Citations
19	The Old Frontier of Reverse Engineering: Netlist Partitioning. Journal of Hardware and Systems Security, 2018, 2, 201-213.	0.8	15
20	Hardware Trojan Detection and Functionality Determination for Soft IPs. , 2018, , .		4
21	CRISPR-Sirius: RNA scaffolds for signal amplification in genome imaging. Nature Methods, 2018, 15, 928-931.	9.0	118
22	The long noncoding RNA SPRIGHTLY acts as an intranuclear organizing hub for pre-mRNA molecules. Science Advances, 2017, 3, e1602505.	4.7	31
23	CompAnnotate: a comparative approach to annotate base-pairing interactions in RNA 3D structures. Nucleic Acids Research, 2017, 45, e136-e136.	6.5	4
24	IP protection through gate-level netlist security enhancement. The Integration VLSI Journal, 2017, 58, 563-570.	1.3	8
25	Multi-allelic positional burrows-wheeler transform. , 2017, , .		0
26	DRREP: deep ridge regressed epitope predictor. BMC Genomics, 2017, 18, 676.	1.2	26
27	Translation repression via modulation of the cytoplasmic poly(A)-binding protein in the inflammatory response. ELife, 2017, 6, .	2.8	32
28	Interrogation of CRISPR Dynamics with Fluorescent Single Guide RNAs in Live Cells. Biophysical Journal, 2016, 110, 362a-363a.	0.2	1
29	Multiplexed labeling of genomic loci with dCas9 and engineered sgRNAs using CRISPRainbow. Nature Biotechnology, 2016, 34, 528-530.	9.4	365
30	The Non-Coding RNA Ontology (NCRO): a comprehensive resource for the unification of non-coding RNA biology. Journal of Biomedical Semantics, 2016, 7, 24.	0.9	10
31	WebSTAR3D: a web server for RNA 3D structural alignment. Bioinformatics, 2016, 32, btw502.	1.8	0
32	CRISPR-Cas9 nuclear dynamics and target recognition in living cells. Journal of Cell Biology, 2016, 214, 529-537.	2.3	165
33	Gate-level netlist reverse engineering for hardware security: Control logic register identification. , 2016, , .		34
34	The development of non-coding RNA ontology. International Journal of Data Mining and Bioinformatics, 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. Methods, 2015, 79-80, 60-66.	1.9	26

#	ARTICLE	IF	CITATIONS
37	RNAMotifScanX: a graph alignment approach for RNA structural motif identification. Rna, 2015, 21, 333-346.	1.6	53
38	Multicolor CRISPR labeling of chromosomal loci in human cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3002-3007.	3.3	363
39	STAR3D: a stack-based RNA 3D structural alignment tool. Nucleic Acids Research, 2015, 43, gkv697.	6.5	11
40	Finding consensus stable local optimal structures for aligned RNA sequences and its application to discovering riboswitch elements. International Journal of Bioinformatics Research and Applications, 2014, 10, 498.	0.1	2
41	FIGHT-Metric. , 2014, , .		27
42	Discovering non-coding RNA elements in Drosophila 3' untranslated regions. International Journal of Bioinformatics Research and Applications, 2014, 10, 479.	0.1	2
43	ProbeAlign: incorporating high-throughput sequencing-based structure probing information into ncRNA homology search. BMC Bioinformatics, 2014, 15, S15.	1.2	6
44	Clustering RNA structural motifs in ribosomal RNAs using secondary structural alignment. Nucleic Acids Research, 2012, 40, 1307-1317.	6.5	22
45	Discovering non-coding RNA elements in drosophila 3&#x2032; 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. Bioinformatics, 2011, 27, 2994-3001.	1.8	17
49	RNAMotifScan: automatic identification of RNA structural motifs using secondary structural alignment. Nucleic Acids Research, 2010, 38, e176-e176.	6.5	41
50	PMFastR: A New Approach to Multiple RNA Structure Alignment. Lecture Notes in Computer Science, 2009, , 49-61.	1.0	3
51	A sequence-based filtering method for ncRNA identification and its application to searching for riboswitch elements. Bioinformatics, 2006, 22, e557-e565.	1.8	30
52	EXPLORING THE OCEAN'S MICROBES: SEQUENCING THE SEVEN SEAS. , 2006, , .		0
53	Searching Genomes for Noncoding RNA Using FastR. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 366-379.	1.9	48
54	FastR: fast database search tool for non-coding RNA. , 2004, , 52-61.		19