

Shaojie Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4335691/publications.pdf>

Version: 2024-02-01

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	Multiplexed labeling of genomic loci with dCas9 and engineered sgRNAs using CRISPRainbow. <i>Nature Biotechnology</i> , 2016, 34, 528-530.	17.5	365
2	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
3	CRISPR-Cas9 nuclear dynamics and target recognition in living cells. <i>Journal of Cell Biology</i> , 2016, 214, 529-537.	5.2	165
4	CRISPR-Sirius: RNA scaffolds for signal amplification in genome imaging. <i>Nature Methods</i> , 2018, 15, 928-931.	19.0	118
5	RNAMotifScanX: a graph alignment approach for RNA structural motif identification. <i>Rna</i> , 2015, 21, 333-346.	3.5	53
6	Netlist reverse engineering for high-level functionality reconstruction. , 2016, , .		50
7	Searching Genomes for Noncoding RNA Using FastR. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005, 2, 366-379.	3.0	48
8	RaPID: ultra-fast, powerful, and accurate detection of segments identical by descent (IBD) in biobank-scale cohorts. <i>Genome Biology</i> , 2019, 20, 143.	8.8	48
9	RNAMotifScan: automatic identification of RNA structural motifs using secondary structural alignment. <i>Nucleic Acids Research</i> , 2010, 38, e176-e176.	14.5	41
10	Cell cycleâ€“ and genomic distanceâ€“dependent dynamics of a discrete chromosomal region. <i>Journal of Cell Biology</i> , 2019, 218, 1467-1477.	5.2	40
11	Simultaneous epigenetic perturbation and genome imaging reveal distinct roles of H3K9me3 in chromatin architecture and transcription. <i>Genome Biology</i> , 2020, 21, 296.	8.8	37
12	Gate-level netlist reverse engineering for hardware security: Control logic register identification. , 2016, , .		34
13	Translation repression via modulation of the cytoplasmic poly(A)-binding protein in the inflammatory response. <i>ELife</i> , 2017, 6, .	6.0	32
14	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
15	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
16	FIGHT-Metric. , 2014, , .		27
17	Computational analysis of RNA structures with chemical probing data. <i>Methods</i> , 2015, 79-80, 60-66.	3.8	26
18	DRREP: deep ridge regressed epitope predictor. <i>BMC Genomics</i> , 2017, 18, 676.	2.8	26

#	ARTICLE	IF	CITATIONS
19	Clustering RNA structural motifs in ribosomal RNAs using secondary structural alignment. <i>Nucleic Acids Research</i> , 2012, 40, 1307-1317.	14.5	22
20	FastR: fast database search tool for non-coding RNA. , 2004, , 52-61.		19
21	Repressing Ago2 mRNA translation by Trim71 maintains pluripotency through inhibiting let-7 microRNAs. <i>ELife</i> , 2021, 10, .	6.0	19
22	Finding stable local optimal RNA secondary structures. <i>Bioinformatics</i> , 2011, 27, 2994-3001.	4.1	17
23	The Old Frontier of Reverse Engineering: Netlist Partitioning. <i>Journal of Hardware and Systems Security</i> , 2018, 2, 201-213.	1.3	15
24	De novo discovery of structural motifs in RNA 3D structures through clustering. <i>Nucleic Acids Research</i> , 2018, 46, 4783-4793.	14.5	14
25	Efficient haplotype matching between a query and a panel for genealogical search. <i>Bioinformatics</i> , 2019, 35, i233-i241.	4.1	14
26	Practical considerations on performing and analyzing CLIP-seq experiments to identify transcriptomic-wide RNA-protein interactions. <i>Methods</i> , 2019, 155, 49-57.	3.8	12
27	Personalized genealogical history of UK individuals inferred from biobank-scale IBD segments. <i>BMC Biology</i> , 2021, 19, 32.	3.8	12
28	STAR3D: a stack-based RNA 3D structural alignment tool. <i>Nucleic Acids Research</i> , 2015, 43, gkv697.	14.5	11
29	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
30	NETA. , 2019, , .		10
31	d-PBWT: dynamic positional Burrows-Wheeler transform. <i>Bioinformatics</i> , 2021, 37, 2390-2397.	4.1	10
32	The development of non-coding RNA ontology. <i>International Journal of Data Mining and Bioinformatics</i> , 2016, 15, 214.	0.1	9
33	IP protection through gate-level netlist security enhancement. <i>The Integration VLSI Journal</i> , 2017, 58, 563-570.	2.1	8
34	Accurate and Efficient Mapping of the Cross-Linked microRNA-mRNA Duplex Reads. <i>IScience</i> , 2019, 18, 11-19.	4.1	7
35	Multi-allelic positional Burrows-Wheeler transform. <i>BMC Bioinformatics</i> , 2019, 20, 279.	2.6	7
36	RAFFI: Accurate and fast familial relationship inference in large scale biobank studies using RaPID. <i>PLoS Genetics</i> , 2021, 17, e1009315.	3.5	7

#	ARTICLE	IF	CITATIONS
37	ProbeAlign: incorporating high-throughput sequencing-based structure probing information into ncRNA homology search. BMC Bioinformatics, 2014, 15, S15.	2.6	6
38	RNAMotifContrast: a method to discover and visualize RNA structural motif subfamilies. Nucleic Acids Research, 2021, 49, e61-e61.	14.5	5
39	CompAnnotate: a comparative approach to annotate base-pairing interactions in RNA 3D structures. Nucleic Acids Research, 2017, 45, e136-e136.	14.5	4
40	Hardware Trojan Detection and Functionality Determination for Soft IPs. , 2018, , .		4
41	LocalSTAR3D: a local stack-based RNA 3D structural alignment tool. Nucleic Acids Research, 2020, 48, e77.	14.5	4
42	PMFastR: A New Approach to Multiple RNA Structure Alignment. Lecture Notes in Computer Science, 2009, , 49-61.	1.3	3
43	d-PBWT: Dynamic Positional Burrows-Wheeler Transform. Lecture Notes in Computer Science, 2020, , 269-270.	1.3	3
44	Finding consensus stable local optimal structures for aligned RNA sequences. , 2012, , .		2
45	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.	0.2	2
46	Discovering non-coding RNA elements in Drosophila 3' untranslated regions. International Journal of Bioinformatics Research and Applications, 2014, 10, 479.	0.2	2
47	Discovering non-coding RNA elements in drosophila 3' untranslated regions. , 2012, , .		1
48	Interrogation of CRISPR Dynamics with Fluorescent Single Guide RNAs in Live Cells. Biophysical Journal, 2016, 110, 362a-363a.	0.5	1
49	RERTL: Finite State Transducer Logic Recovery at Register Transfer Level. , 2019, , .		1
50	Genealogical search using whole-genome genotype profiles. , 2020, , 51-94.		1
51	EXPLORING THE OCEAN'S MICROBES: SEQUENCING THE SEVEN SEAS. , 2006, , .		0
52	Predicting folding pathways between RNA conformational structures guided by RNA stacks. , 2011, , .		0
53	WebSTAR3D: a web server for RNA 3D structural alignment. Bioinformatics, 2016, 32, btw502.	4.1	0
54	Multi-allelic positional burrows-wheeler transform. , 2017, , .		0