

Shaoke Lou

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

1,790
citations

759055

12
h-index

642610

23
g-index

27
all docs

27
docs citations

27
times ranked

5362
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene Tracer: a smart, interactive, voice-controlled Alexa skill For gene information retrieval and browsing, mutation annotation and network visualization. <i>Bioinformatics</i> , 2021, 37, 2998-3000.	1.8	1
2	Bayesian structural time series for biomedical sensor data: A flexible modeling framework for evaluating interventions. <i>PLoS Computational Biology</i> , 2021, 17, e1009303.	1.5	8
3	An integrative ENCODE resource for cancer genomics. <i>Nature Communications</i> , 2020, 11, 3696.	5.8	95
4	RADAR: annotation and prioritization of variants in the post-transcriptional regulome of RNA-binding proteins. <i>Genome Biology</i> , 2020, 21, 151.	3.8	9
5	Latent-space embedding of expression data identifies gene signatures from sputum samples of asthmatic patients. <i>BMC Bioinformatics</i> , 2020, 21, 457.	1.2	1
6	Approaches for integrating heterogeneous RNA-seq data reveal cross-talk between microbes and genes in asthmatic patients. <i>Genome Biology</i> , 2020, 21, 150.	3.8	5
7	DiNeR: a Differential graphical model for analysis of co-regulation Network Rewiring. <i>BMC Bioinformatics</i> , 2020, 21, 281.	1.2	5
8	Passenger Mutations in More Than 2,500 Cancer Genomes: Overall Molecular Functional Impact and Consequences. <i>Cell</i> , 2020, 180, 915-927.e16.	13.5	98
9	Building a Hybrid Physical-Statistical Classifier for Predicting the Effect of Variants Related to Protein-Drug Interactions. <i>Structure</i> , 2019, 27, 1469-1481.e3.	1.6	6
10	GRAM: A GeneRALized Model to predict the molecular effect of a non-coding variant in a cell-type specific manner. <i>PLoS Genetics</i> , 2019, 15, e1007860.	1.5	1
11	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, .	6.0	618
12	MrTADFinder: A network modularity based approach to identify topologically associating domains in multiple resolutions. <i>PLoS Computational Biology</i> , 2017, 13, e1005647.	1.5	42
13	The real cost of sequencing: scaling computation to keep pace with data generation. <i>Genome Biology</i> , 2016, 17, 53.	3.8	264
14	Integrative Genomic Analyses Yield Cell-Cycle Regulatory Programs with Prognostic Value. <i>Molecular Cancer Research</i> , 2016, 14, 332-343.	1.5	4
15	Regulators Associated with Clinical Outcomes Revealed by DNA Methylation Data in Breast Cancer. <i>PLoS Computational Biology</i> , 2015, 11, e1004269.	1.5	34
16	FunSeq2: a framework for prioritizing noncoding regulatory variants in cancer. <i>Genome Biology</i> , 2014, 15, 480.	3.8	291
17	Whole-genome bisulfite sequencing of multiple individuals reveals complementary roles of promoter and gene body methylation in transcriptional regulation. <i>Genome Biology</i> , 2014, 15, 408.	3.8	173
18	Combined in vivo imaging and omics approaches reveal metabolism of icaritin and its glycosides in zebrafish larvae. <i>Molecular BioSystems</i> , 2011, 7, 2128.	2.9	43

#	ARTICLE	IF	CITATIONS
19	Transcriptional profiling of angiogenesis activities of calycosin in zebrafish. <i>Molecular BioSystems</i> , 2011, 7, 3112.	2.9	29
20	Microarray analysis of differentially expressed genes in mouse bone marrow tissues after ionizing radiation. <i>International Journal of Radiation Biology</i> , 2006, 82, 511-521.	1.0	17
21	Selection of antisense oligonucleotides based on multiple predicted target mRNA structures. <i>BMC Bioinformatics</i> , 2006, 7, 122.	1.2	12
22	AOBase: a database for antisense oligonucleotides selection and design. <i>Nucleic Acids Research</i> , 2006, 34, D664-D667.	6.5	12