Shaoke Lou

List of Publications by Year
in descending order

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	Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, .	6.0	618
2	FunSeq2: a framework for prioritizing noncoding regulatory variants in cancer. Genome Biology, 2014, 15, 480.	3.8	291
3	The real cost of sequencing: scaling computation to keep pace with data generation. Genome Biology, 2016, 17, 53.	3.8	264
4	Whole-genome bisulfite sequencing of multiple individuals reveals complementary roles of promoter and gene body methylation in transcriptional regulation. Genome Biology, 2014, 15, 408.	3.8	173
5	Passenger Mutations in More Than 2,500 Cancer Genomes: Overall Molecular Functional Impact and Consequences. Cell, 2020, 180, 915-927.e16.	13.5	98
6	An integrative ENCODE resource for cancer genomics. Nature Communications, 2020, 11, 3696.	5.8	95
7	Combined in vivo imaging and omics approaches reveal metabolism of icaritin and its glycosides in zebrafish larvae. Molecular BioSystems, 2011, 7, 2128.	2.9	43
8	MrTADFinder: A network modularity based approach to identify topologically associating domains in multiple resolutions. PLoS Computational Biology, 2017, 13, e1005647.	1.5	42
9	Regulators Associated with Clinical Outcomes Revealed by DNA Methylation Data in Breast Cancer. PLoS Computational Biology, 2015, 11, e1004269.	1.5	34
10	Transcriptional profiling of angiogenesis activities of calycosin in zebrafish. Molecular BioSystems, 2011, 7, 3112.	2.9	29
11	Microarray analysis of differentially expressed genes in mouse bone marrow tissues after ionizing radiation. International Journal of Radiation Biology, 2006, 82, 511-521.	1.0	17
12	Selection of antisense oligonucleotides based on multiple predicted target mRNA structures. BMC Bioinformatics, 2006, 7, 122.	1.2	12
13	AOBase: a database for antisense oligonucleotides selection and design. Nucleic Acids Research, 2006, 34, D664-D667.	6.5	12
14	RADAR: annotation and prioritization of variants in the post-transcriptional regulome of RNA-binding proteins. Genome Biology, 2020, 21, 151.	3.8	9
15	Bayesian structural time series for biomedical sensor data: A flexible modeling framework for evaluating interventions. PLoS Computational Biology, 2021, 17, e1009303.	1.5	8
16	Building a Hybrid Physical-Statistical Classifier for Predicting the Effect of Variants Related to Protein-Drug Interactions. Structure, 2019, 27, 1469-1481.e3.	1.6	6
17	Approaches for integrating heterogeneous RNA-seq data reveal cross-talk between microbes and genes in asthmatic patients. Genome Biology, 2020, 21, 150.	3.8	5
18	DiNeR: a Differential graphical model for analysis of co-regulation Network Rewiring. BMC Bioinformatics, 2020, 21, 281.	1.2	5

#	Article	IF	Citations
19	Integrative Genomic Analyses Yield Cell-Cycle Regulatory Programs with Prognostic Value. Molecular Cancer Research, 2016, 14, 332-343.	1.5	4
20	GRAM: A GeneRAlized Model to predict the molecular effect of a non-coding variant in a cell-type specific manner. PLoS Genetics, 2019, 15, e1007860.	1.5	1
21	Latent-space embedding of expression data identifies gene signatures from sputum samples of asthmatic patients. BMC Bioinformatics, 2020, 21, 457.	1.2	1
22	Gene Tracer: a smart, interactive, voice-controlled Alexa skill For gene information retrieval and browsing, mutation annotation and network visualization. Bioinformatics, 2021, 37, 2998-3000.	1.8	1