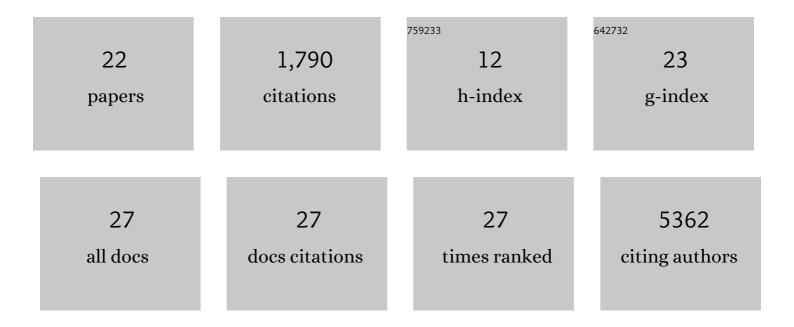
Shaoke Lou

List of Publications by Year in descending order

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SHAOKELOU

#	Article	IF	CITATIONS
1	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.	4.1	1
2	Bayesian structural time series for biomedical sensor data: A flexible modeling framework for evaluating interventions. PLoS Computational Biology, 2021, 17, e1009303.	3.2	8
3	An integrative ENCODE resource for cancer genomics. Nature Communications, 2020, 11, 3696.	12.8	95
4	RADAR: annotation and prioritization of variants in the post-transcriptional regulome of RNA-binding proteins. Genome Biology, 2020, 21, 151.	8.8	9
5	Latent-space embedding of expression data identifies gene signatures from sputum samples of asthmatic patients. BMC Bioinformatics, 2020, 21, 457.	2.6	1
6	Approaches for integrating heterogeneous RNA-seq data reveal cross-talk between microbes and genes in asthmatic patients. Genome Biology, 2020, 21, 150.	8.8	5
7	DiNeR: a Differential graphical model for analysis of co-regulation Network Rewiring. BMC Bioinformatics, 2020, 21, 281.	2.6	5
8	Passenger Mutations in More Than 2,500 Cancer Genomes: Overall Molecular Functional Impact and Consequences. Cell, 2020, 180, 915-927.e16.	28.9	98
9	Building a Hybrid Physical-Statistical Classifier for Predicting the Effect of Variants Related to Protein-Drug Interactions. Structure, 2019, 27, 1469-1481.e3.	3.3	6
10	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.	3.5	1
11	Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, .	12.6	618
12	MrTADFinder: A network modularity based approach to identify topologically associating domains in multiple resolutions. PLoS Computational Biology, 2017, 13, e1005647.	3.2	42
13	The real cost of sequencing: scaling computation to keep pace with data generation. Genome Biology, 2016, 17, 53.	8.8	264
14	Integrative Genomic Analyses Yield Cell-Cycle Regulatory Programs with Prognostic Value. Molecular Cancer Research, 2016, 14, 332-343.	3.4	4
15	Regulators Associated with Clinical Outcomes Revealed by DNA Methylation Data in Breast Cancer. PLoS Computational Biology, 2015, 11, e1004269.	3.2	34
16	FunSeq2: a framework for prioritizing noncoding regulatory variants in cancer. Genome Biology, 2014, 15, 480.	8.8	291
17	Whole-genome bisulfite sequencing of multiple individuals reveals complementary roles of promoter and gene body methylation in transcriptional regulation. Genome Biology, 2014, 15, 408.	8.8	173
18	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

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#	ARTICLE	IF	CITATIONS
19	Transcriptional profiling of angiogenesis activities of calycosin in zebrafish. Molecular BioSystems, 2011, 7, 3112.	2.9	29
20	Microarray analysis of differentially expressed genes in mouse bone marrow tissues after ionizing radiation. International Journal of Radiation Biology, 2006, 82, 511-521.	1.8	17
21	Selection of antisense oligonucleotides based on multiple predicted target mRNA structures. BMC Bioinformatics, 2006, 7, 122.	2.6	12
22	AOBase: a database for antisense oligonucleotides selection and design. Nucleic Acids Research, 2006, 34, D664-D667.	14.5	12