# Shaoke Lou

## List of Publications by Year
## in descending order

| 22 papers | 1,790 citations | 759233 12 h-index | 642732 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. 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 |

| # | 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 |