

# Yang Li

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

9

papers

63

citations

5

h-index

7

g-index

10

ext. papers

132

ext. citations

8.2

avg, IF

2.18

L-index

| # | Paper   | IF   | Citations |
|---|---|------|-----------|
| 9 | An algorithmic perspective of de novo cis-regulatory motif finding based on ChIP-seq data. <i>Briefings in Bioinformatics</i> , <b>2018</b> , 19, 1069-1081                               | 13.4 | 15        |
| 8 | Prediction of regulatory motifs from human Chip-sequencing data using a deep learning framework. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 7809-7824                              | 20.1 | 13        |
| 7 | Elucidation of Biological Networks across Complex Diseases Using Single-Cell Omics. <i>Trends in Genetics</i> , <b>2020</b> , 36, 951-966   | 8.5  | 12        |
| 6 | Identification of driver modules in pan-cancer via coordinating coverage and exclusivity. <i>Oncotarget</i> , <b>2017</b> , 8, 36115-36126  | 3.3  | 6         |
| 5 | ProSampler: an ultrafast and accurate motif finder in large ChIP-seq datasets for combinatory motif discovery. <i>Bioinformatics</i> , <b>2019</b> , 35, 4632-4639                        | 7.2  | 5         |
| 4 | Prediction of Driver Modules via Balancing Exclusive Coverages of Mutations in Cancer Samples. <i>Advanced Science</i> , <b>2019</b> , 6, 1801384   | 13.6 | 5         |
| 3 | Block-based characterization of protease specificity from substrate sequence profile. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 438   | 3.6  | 4         |
| 2 | MiMod: A New Algorithm for Mining Biological Network Modules. <i>IEEE Access</i> , <b>2019</b> , 7, 49492-49503   | 3.5  | 2         |
| 1 | Revealing favorable and unfavorable residues in cooperative positions in protease cleavage sites. <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 519, 714-720 | 3.4  |           |