# Hebing Chen

## List of Publications by Year
in descending order

| | | | |
|---|---|---|---|
| 20<br>papers | 458<br>citations | 1040056<br>9<br>h-index | 940533<br>16<br>g-index |
| 23<br>all docs | 23<br>docs citations | 23<br>times ranked | 851<br>citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Comprehensive Identification and Annotation of Cell Type-Specific and Ubiquitous CTCF-Binding Sites in the Human Genome. PLoS ONE, 2012, 7, e41374. | 2.5 | 119 |
| 2 | 3DSNP: a database for linking human noncoding SNPs to their three-dimensional interacting genes. Nucleic Acids Research, 2017, 45, D643-D649. | 14.5 | 90 |
| 3 | DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. PLoS Computational Biology, 2020, 16, e1007287. | 3.2 | 56 |
| 4 | A survey and evaluation of Web-based tools/databases for variant analysis of TCGA data. Briefings in Bioinformatics, 2019, 20, 1524-1541. | 6.5 | 48 |
| 5 | An integrative analysis of TFBS-clustered regions reveals new transcriptional regulation models on the accessible chromatin landscape. Scientific Reports, 2015, 5, 8465. | 3.3 | 41 |
| 6 | Functional annotation of HOT regions in the human genome: implications for human disease and cancer. Scientific Reports, 2015, 5, 11633. | 3.3 | 24 |
| 7 | Computational methods for the prediction of chromatin interaction and organization using sequence and epigenomic profiles. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 16 |
| 8 | Inferring transcription factor regulatory networks from single-cell ATAC-seq data based on graph neural networks. Nature Machine Intelligence, 2022, 4, 389-400. | 16.0 | 13 |
| 9 | Dynamic Interplay between Structural Variations and 3D Genome Organization in Pancreatic Cancer. Advanced Science, 2022, 9, e2200818. | 11.2 | 10 |
| 10 | ARDesigner: A web-based system for allosteric RNA design. Journal of Biotechnology, 2010, 150, 466-473. | 3.8 | 9 |
| 11 | CMTCN: a web tool for investigating cancer-specific microRNA and transcription factor co-regulatory networks. PeerJ, 2018, 6, e5951. | 2.0 | 9 |
| 12 | Exploration of prognosis-related microRNA and transcription factor co-regulatory networks across cancer types. RNA Biology, 2019, 16, 1010-1021. | 3.1 | 7 |
| 13 | Synergistic alterations in the multilevel chromatin structure anchor dysregulated genes in small cell lung cancer. Computational and Structural Biotechnology Journal, 2021, 19, 5946-5959. | 4.1 | 6 |
| 14 | Spatial density of open chromatin: an effective metric for the functional characterization of topologically associated domains. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 5 |
| 15 | Genome-wide identification and analysis of A-to-I RNA editing events in the malignantly transformed cell lines from bronchial epithelial cell line induced by α-particles radiation. PLoS ONE, 2019, 14, e0213047. | 2.5 | 3 |
| 16 | iFORM: Incorporating Find Occurrence of Regulatory Motifs. PLoS ONE, 2016, 11, e0168607. | 2.5 | 2 |
| 17 | DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. , 2020, 16, e1007287. | | 0 |
| 18 | DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. , 2020, 16, e1007287. | | 0 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|----|-----------| 
| 19 | DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. , 2020, 16, e1007287. | | 0 |
| 20 | DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. , 2020, 16, e1007287. | | 0 |