

# Baikang Pei

## List of Publications by Year in Descending Order

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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.

14  
papers

4,983  
citations

9  
h-index

14  
g-index

14  
ext. papers

6,887  
ext. citations

15.3  
avg, IF

3.95  
L-index

| #  | Paper   | IF   | Citations |
|----|---|------|-----------|
| 14 | GENCODE 2021. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D916-D923   | 20.1 | 82        |
| 13 | GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D766-D773   | 20.1 | 1140      |
| 12 | Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , <b>2015</b> , 6, 5903             | 17.4 | 56        |
| 11 | Comparative analysis of the transcriptome across distant species. <i>Nature</i> , <b>2014</b> , 512, 445-8  | 50.4 | 207       |
| 10 | Comparative analysis of pseudogenes across three phyla. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 13361-6 | 11.5 | 54        |
| 9  | A software framework integrating gene expression patterns, binding site analysis and gene ontology to hypothesize gene regulation relationships <b>2013</b> ,               |      | 4         |
| 8  | Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. <i>Genome Research</i> , <b>2013</b> , 23, 2042-52    | 9.7  | 41        |
| 7  | The GENCODE pseudogene resource. <i>Genome Biology</i> , <b>2012</b> , 13, R51  | 18.3 | 232       |
| 6  | GENCODE: the reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , <b>2012</b> , 22, 1760-74   | 9.7  | 3142      |
| 5  | Reconstruction of biological networks by incorporating prior knowledge into Bayesian network models. <i>Journal of Computational Biology</i> , <b>2012</b> , 19, 1324-34    | 1.7  | 10        |
| 4  | Learning Bayesian networks with integration of indirect prior knowledge. <i>International Journal of Data Mining and Bioinformatics</i> , <b>2010</b> , 4, 505-19           | 0.5  | 5         |
| 3  | PBC: A Software Framework Facilitating Pattern-Based Clustering for Microarray Data Analysis <b>2009</b> ,  |      | 4         |
| 2  | Meta Analysis of Microarray Data Using Gene Regulation Pathways <b>2008</b> ,   |      | 3         |
| 1  | Reverse Engineering of Gene Regulatory Network by Integration of Prior Global Gene Regulatory Information <b>2008</b> ,   |      | 3         |