Baikang Pei

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.

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