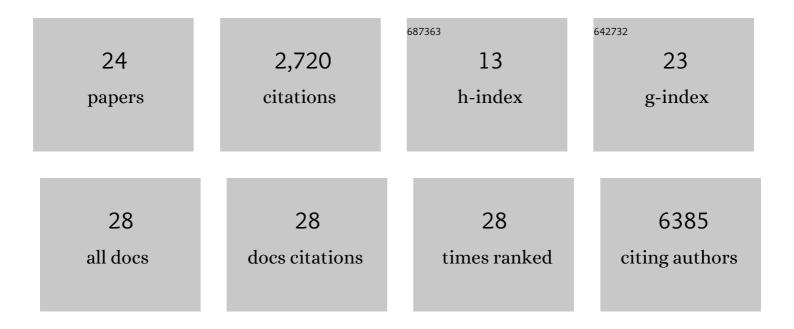
## Xiaoyi Cao

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1063624/publications.pdf Version: 2024-02-01



Χιλογι Cλο

#	Article	lF	CITATIONS
1	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444
2	Cell fate inclination within 2-cell and 4-cell mouse embryos revealed by single-cell RNA sequencing. Genome Research, 2014, 24, 1787-1796.	5.5	263
3	Rewirable gene regulatory networks in the preimplantation embryonic development of three mammalian species. Genome Research, 2010, 20, 804-815.	5.5	204
4	Comparative Epigenomic Annotation of Regulatory DNA. Cell, 2012, 149, 1381-1392.	28.9	188
5	Systematic Mapping of RNA-Chromatin Interactions InÂVivo. Current Biology, 2017, 27, 602-609.	3.9	144
6	Mapping RNA–RNA interactome and RNA structure in vivo by MARIO. Nature Communications, 2016, 7, 12023.	12.8	135
7	Intronic Non-CG DNA hydroxymethylation and alternative mRNA splicing in honey bees. BMC Genomics, 2013, 14, 666.	2.8	62
8	SMARCAD1 Contributes to the Regulation of Naive Pluripotency by Interacting with Histone Citrullination. Cell Reports, 2017, 18, 3117-3128.	6.4	40
9	Time-variant clustering model for understanding cell fate decisions. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4797-806.	7.1	29
10	Understanding Variation in Transcription Factor Binding by Modeling Transcription Factor Genome-Epigenome Interactions. PLoS Computational Biology, 2013, 9, e1003367.	3.2	26
11	Disparate <i><scp>I</scp>gf1</i> Expression and Growth in the Fore―and Hind Limbs of a Marsupial Mammal ( <i><scp>M</scp>onodelphis domestica</i> ). Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2012, 318, 279-293.	1.3	24
12	Transcriptomic insights into the genetic basis of mammalian limb diversity. BMC Evolutionary Biology, 2017, 17, 86.	3.2	19
13	GIVE: portable genome browsers for personal websites. Genome Biology, 2018, 19, 92.	8.8	15
14	Dissecting Early Differentially Expressed Genes in a Mixture of Differentiating Embryonic Stem Cells. PLoS Computational Biology, 2009, 5, e1000607.	3.2	13
15	GeNemo: a search engine for web-based functional genomic data. Nucleic Acids Research, 2016, 44, W122-W127.	14.5	11
16	Towards an Evolutionary Model of Transcription Networks. PLoS Computational Biology, 2011, 7, e1002064.	3.2	10
17	Comparative epigenomics: defining and utilizing epigenomic variations across species, time-course, and individuals. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2014, 6, 345-352.	6.6	10
18	Enabling interspecies epigenomic comparison with CEpBrowser. Bioinformatics, 2013, 29, 1223-1225.	4.1	9

Χιλογι ζλο

#	Article	IF	CITATIONS
19	Network-based comparison of temporal gene expression patterns. Bioinformatics, 2010, 26, 2944-2951.	4.1	8
20	Mapping personal functional data to personal genomes. Bioinformatics, 2011, 27, 3427-3429.	4.1	8
21	Molecular determinants of marsupial limb integration and constraint. , 2012, , 257-278.		6
22	A likelihood approach to testing hypotheses on the co-evolution of epigenome and genome. PLoS Computational Biology, 2018, 14, e1006673.	3.2	4
23	EpiAlignment: alignment with both DNA sequence and epigenomic data. Nucleic Acids Research, 2019, 47, W11-W19.	14.5	3
24	Pattern-based Search of Epigenomic Data Using GeNemo. Journal of Visualized Experiments, 2017, , .	0.3	0