

# Xiaoyi Cao

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1063624/publications.pdf>

Version: 2024-02-01

24  
papers

2,720  
citations

687363

13  
h-index

642732

23  
g-index

28  
all docs

28  
docs citations

28  
times ranked

6385  
citing authors

#	ARTICLE	IF	CITATIONS
1	EpiAlignment: alignment with both DNA sequence and epigenomic data. <i>Nucleic Acids Research</i> , 2019, 47, W11-W19.	14.5	3
2	A likelihood approach to testing hypotheses on the co-evolution of epigenome and genome. <i>PLoS Computational Biology</i> , 2018, 14, e1006673.	3.2	4
3	GIVE: portable genome browsers for personal websites. <i>Genome Biology</i> , 2018, 19, 92.	8.8	15
4	Systematic Mapping of RNA-Chromatin Interactions In Vivo. <i>Current Biology</i> , 2017, 27, 602-609.	3.9	144
5	Transcriptomic insights into the genetic basis of mammalian limb diversity. <i>BMC Evolutionary Biology</i> , 2017, 17, 86.	3.2	19
6	SMARCAD1 Contributes to the Regulation of Naive Pluripotency by Interacting with Histone Citrullination. <i>Cell Reports</i> , 2017, 18, 3117-3128.	6.4	40
7	Pattern-based Search of Epigenomic Data Using GeNemo. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	0
8	GeNemo: a search engine for web-based functional genomic data. <i>Nucleic Acids Research</i> , 2016, 44, W122-W127.	14.5	11
9	Mapping RNA-RNA interactome and RNA structure in vivo by MARIO. <i>Nature Communications</i> , 2016, 7, 12023.	12.8	135
10	Comparative epigenomics: defining and utilizing epigenomic variations across species, time-course, and individuals. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2014, 6, 345-352.	6.6	10
11	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	27.8	1,444
12	Time-variant clustering model for understanding cell fate decisions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4797-806.	7.1	29
13	Cell fate inclination within 2-cell and 4-cell mouse embryos revealed by single-cell RNA sequencing. <i>Genome Research</i> , 2014, 24, 1787-1796.	5.5	263
14	Intronic Non-CG DNA hydroxymethylation and alternative mRNA splicing in honey bees. <i>BMC Genomics</i> , 2013, 14, 666.	2.8	62
15	Understanding Variation in Transcription Factor Binding by Modeling Transcription Factor Genome-Epigenome Interactions. <i>PLoS Computational Biology</i> , 2013, 9, e1003367.	3.2	26
16	Enabling interspecies epigenomic comparison with CEpBrowser. <i>Bioinformatics</i> , 2013, 29, 1223-1225.	4.1	9
17	Comparative Epigenomic Annotation of Regulatory DNA. <i>Cell</i> , 2012, 149, 1381-1392.	28.9	188
18	Molecular determinants of marsupial limb integration and constraint. , 2012, , 257-278.		6

#	ARTICLE	IF	CITATIONS
19	Disparate <i>Isl1</i> Expression and Growth in the Fore- and Hind Limbs of a Marsupial Mammal ( <i>Monodelphis domestica</i> ). <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2012, 318, 279-293.	1.3	24
20	Mapping personal functional data to personal genomes. <i>Bioinformatics</i> , 2011, 27, 3427-3429.	4.1	8
21	Towards an Evolutionary Model of Transcription Networks. <i>PLoS Computational Biology</i> , 2011, 7, e1002064.	3.2	10
22	Network-based comparison of temporal gene expression patterns. <i>Bioinformatics</i> , 2010, 26, 2944-2951.	4.1	8
23	Rewirable gene regulatory networks in the preimplantation embryonic development of three mammalian species. <i>Genome Research</i> , 2010, 20, 804-815.	5.5	204
24	Dissecting Early Differentially Expressed Genes in a Mixture of Differentiating Embryonic Stem Cells. <i>PLoS Computational Biology</i> , 2009, 5, e1000607.	3.2	13