

Fulai Jin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7193253/publications.pdf>

Version: 2024-02-01

16
papers

3,743
citations

840776

11
h-index

996975

15
g-index

20
all docs

20
docs citations

20
times ranked

8972
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	21.4	2,224
2	A high-resolution map of the three-dimensional chromatin interactome in human cells. <i>Nature</i> , 2013, 503, 290-294.	27.8	1,074
3	Robust Hi-C Maps of Enhancer-Promoter Interactions Reveal the Function of Non-coding Genome in Neural Development and Diseases. <i>Molecular Cell</i> , 2020, 79, 521-534.e15.	9.7	110
4	Single-Cell Heterogeneity Analysis and CRISPR Screen Identify Key $\hat{2}$ -Cell-Specific Disease Genes. <i>Cell Reports</i> , 2019, 26, 3132-3144.e7.	6.4	90
5	A hidden Markov random field-based Bayesian method for the detection of long-range chromosomal interactions in Hi-C data. <i>Bioinformatics</i> , 2016, 32, 650-656.	4.1	47
6	53BP1 regulates heterochromatin through liquid phase separation. <i>Nature Communications</i> , 2022, 13, 360.	12.8	46
7	Single-cell lineage analysis reveals extensive multimodal transcriptional control during directed beta-cell differentiation. <i>Nature Metabolism</i> , 2020, 2, 1443-1458.	11.9	39
8	Chemical Screening Identifies Enhancers of Mutant Oligodendrocyte Survival and Unmasks a Distinct Pathological Phase in Pelizaeus-Merzbacher Disease. <i>Stem Cell Reports</i> , 2018, 11, 711-726.	4.8	28
9	DeepLoop robustly maps chromatin interactions from sparse allele-resolved or single-cell Hi-C data at kilobase resolution. <i>Nature Genetics</i> , 2022, 54, 1013-1025.	21.4	19
10	A locus at 19q13.31 significantly reduces the ApoE $\hat{4}$ risk for Alzheimer's Disease in African Ancestry. <i>PLoS Genetics</i> , 2022, 18, e1009977.	3.5	19
11	Identifying differential regulatory control of <i>APOE</i> $\hat{4}$ on African versus European haplotypes as potential therapeutic targets. <i>Alzheimer's and Dementia</i> , 2022, 18, 1930-1942.	0.8	12
12	TWO $\hat{\Sigma}$: A novel two-component single cell model-based association method for single-cell RNA-seq data. <i>Genetic Epidemiology</i> , 2021, 45, 142-153.	1.3	11
13	HiView: an integrative genome browser to leverage Hi-C results for the interpretation of GWAS variants. <i>BMC Research Notes</i> , 2016, 9, 159.	1.4	10
14	Aberrant methylation underlies insulin gene expression in human insulinoma. <i>Nature Communications</i> , 2020, 11, 5210.	12.8	9
15	INFIMA leverages multi-omics model organism data to identify effector genes of human GWAS variants. <i>Genome Biology</i> , 2021, 22, 241.	8.8	3
16	Abstract 10865: Elucidating the Variant-to-Function Relationship for LIPA, a Risk Locus of Coronary Artery Diseases. <i>Circulation</i> , 2021, 144, .	1.6	0