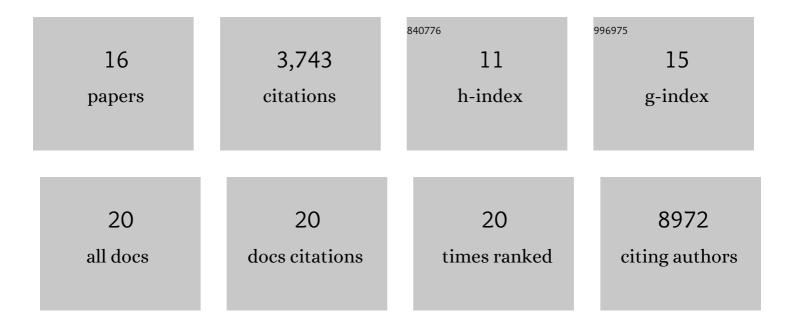
Fulai Jin

List of Publications by Year in descending order

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FULATIN

#	Article	IF	CITATIONS
1	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	21.4	2,224
2	A high-resolution map of the three-dimensional chromatin interactome in human cells. Nature, 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. Molecular Cell, 2020, 79, 521-534.e15.	9.7	110
4	Single-Cell Heterogeneity Analysis and CRISPR Screen Identify Key β-Cell-Specific Disease Genes. Cell Reports, 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. Bioinformatics, 2016, 32, 650-656.	4.1	47
6	53BP1 regulates heterochromatin through liquid phase separation. Nature Communications, 2022, 13, 360.	12.8	46
7	Single-cell lineage analysis reveals extensive multimodal transcriptional control during directed beta-cell differentiation. Nature Metabolism, 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. Stem Cell Reports, 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. Nature Genetics, 2022, 54, 1013-1025.	21.4	19
10	A locus at 19q13.31 significantly reduces the ApoE ε4 risk for Alzheimer's Disease in African Ancestry. PLoS Genetics, 2022, 18, e1009977.	3.5	19
11	Identifying differential regulatory control of <i>APOE</i> É>4 on African versus European haplotypes as potential therapeutic targets. Alzheimer's and Dementia, 2022, 18, 1930-1942.	0.8	12
12	TWOâ€&IGMA: A novel twoâ€component single cell modelâ€based association method for singleâ€cell RNAâ€sec data. Genetic Epidemiology, 2021, 45, 142-153.	1.3 1.3	11
13	HiView: an integrative genome browser to leverage Hi-C results for the interpretation of GWAS variants. BMC Research Notes, 2016, 9, 159.	1.4	10
14	Aberrant methylation underlies insulin gene expression in human insulinoma. Nature Communications, 2020, 11, 5210.	12.8	9
15	INFIMA leverages multi-omics model organism data to identify effector genes of human GWAS variants. Genome Biology, 2021, 22, 241.	8.8	3
16	Abstract 10865: Elucidating the Variant-to-Function Relationship for LIPA, a Risk Locus of Coronary Artery Diseases. Circulation, 2021, 144, .	1.6	0