Dajiang J Liu

List of Publications by Year
in descending order

41	5,724	318942	312153
papers	citations	23 h-index	41 g-index

51	51	51	14012
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic correlation, pleiotropy, and causal associations between substance use and psychiatric disorder. Psychological Medicine, 2022, 52, 968-978.	2.7	41
2	Association of Spinal Cord Stimulator Implantation With Persistent Opioid Use in Patients With Postlaminectomy Syndrome. JAMA Network Open, 2022, 5, e2145876.	2.8	10
3	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	2.6	24
4	Integrating 3D genomic and epigenomic data to enhance target gene discovery and drug repurposing in transcriptome-wide association studies. Nature Communications, 2022, 13, .	5.8	18
5	Model-based assessment of replicability for genome-wide association meta-analysis. Nature Communications, 2021, 12, 1964.	5.8	24
6	MetaPrism: A versatile toolkit for joint taxa/gene analysis of metagenomic sequencing data. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	1
7	Prothrombotic variants as modifiers of clinical phenotype in four related individuals with haemophilia A. Haemophilia, 2021, 27, e591-e595.	1.0	0
8	Causal Relationship and Shared Genetic Loci between Psoriasis and Type 2 Diabetes through Trans-Disease Meta-Analysis. Journal of Investigative Dermatology, 2021, 141, 1493-1502.	0.3	29
9	Inferring genes that escape X-Chromosome inactivation reveals important contribution of variable escape genes to sex-biased diseases. Genome Research, 2021, 31, 1629-1637.	2.4	25
10	Multivariate analysis of 1.5 million people identifies genetic associations with traits related to self-regulation and addiction. Nature Neuroscience, 2021, 24, 1367-1376.	7.1	137
11	MB-GAN: Microbiome Simulation via Generative Adversarial Network. GigaScience, 2021, 10, .	3.3	14
12	Medical Service Use and Charges for Cancer Care in 2018 for Privately Insured Patients Younger Than 65 Years in the US. JAMA Network Open, 2021, 4, e2127784.	2.8	12
13	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83
14	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
15	Seqminer2: an efficient tool to query and retrieve genotypes for statistical genetics analyses from biobank scale sequence dataset. Bioinformatics, 2020, 36, 4951-4954.	1.8	0
16	Prioritizing genetic variants in GWAS with lasso using permutation-assisted tuning. Bioinformatics, 2020, 36, 3811-3817.	1.8	15
17	Association Analysis and Meta-Analysis of Multi-Allelic Variants for Large-Scale Sequence Data. Genes, 2020, 11, 586.	1.0	3
18	Investigation of discordant phenotype in mild Hemophilia A using whole exome sequencing. Thrombosis Research, 2020, 193, 36-39.	0.8	1

#	Article	IF	Citations
19	Methods for the Analysis and Interpretation for Rare Variants Associated with Complex Traits. Current Protocols in Human Genetics, 2019, 101, e83.	3.5	11
20	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. Nature Genetics, 2019, 51, 237-244.	9.4	1,307
21	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	0.7	69
22	Bleeding in Mild Hemophilia A Due to a Splice-Site F8 Mutation May be Fully Abrogated By Prothrombotic Gene Variants. Blood, 2019, 134, 1125-1125.	0.6	0
23	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
24	Adaptive-weight burden test for associations between quantitative traits and genotype data with complex correlations. Annals of Applied Statistics, 2018, 12, 1558-1582.	0.5	3
25	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. Nature Genetics, 2018, 50, 1514-1523.	9.4	497
26	Proper conditional analysis in the presence of missing data: Application to large scale meta-analysis of tobacco use phenotypes. PLoS Genetics, 2018, 14, e1007452.	1.5	18
27	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
28	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
29	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. JAMA - Journal of the American Medical Association, 2017, 317, 937.	3.8	148
30	Robust and rapid algorithms facilitate large-scale whole genome sequencing downstream analysis in an integrative framework. Nucleic Acids Research, 2017, 45, gkx019.	6.5	36
31	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
32	Exome chip meta-analysis identifies novel loci and East Asianâ€“specific coding variants that contribute to lipid levels and coronary artery disease. Nature Genetics, 2017, 49, 1722-1730.	9.4	129
33	Clonal evolution in paired endometrial intraepithelial neoplasia/atypical hyperplasia and endometrioid adenocarcinoma. Human Pathology, 2017, 67, 69-77.	1.1	34
34	SEQSpark: A Complete Analysis Tool for Large-Scale Rare Variant Association Studies Using Whole-Genome and Exome Sequence Data. American Journal of Human Genetics, 2017, 101, 115-122.	2.6	9
35	Genetic variants inCETPincrease risk of intracerebral hemorrhage. Annals of Neurology, 2016, 80, 730-740.	2.8	33
36	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	2.6	82

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37	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
38	RVTESTS: an efficient and comprehensive tool for rare variant association analysis using sequence data. Bioinformatics, 2016, 32, 1423-1426.	1.8	366
39	SEQMINER: An Râ€Package to Facilitate the Functional Interpretation of Sequenceâ€Based Associations. Genetic Epidemiology, 2015, 39, 619-623.	0.6	31
40	RAREMETAL: fast and powerful meta-analysis for rare variants. Bioinformatics, 2014, 30, 2828-2829.	1.8	108
41	Meta-analysis of gene-level tests for rare variant association. Nature Genetics, 2014, 46, 200-204.	9.4	178