

Shuai Wang

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

1,546
citations

933447

10
h-index

839539

18
g-index

22
all docs

22
docs citations

22
times ranked

5484
citing authors

#	ARTICLE	IF	CITATIONS
1	The relationship between interstitial lung abnormalities, mortality, and multimorbidity: a cohort study. <i>Thorax</i> , 2023, 78, 559-565.	5.6	2
2	Impute the missing data using retrieved dropouts. <i>BMC Medical Research Methodology</i> , 2022, 22, 82.	3.1	2
3	Efficacy and Safety of Ertugliflozin in Patients With Diabetes Mellitus Inadequately Controlled by Sulfonylurea Monotherapy: a Substudy of VERTIS CV. <i>Diabetes Therapy</i> , 2021, 12, 1175-1192.	2.5	4
4	Genetic association tests in family samples for multi-category phenotypes. <i>BMC Genomics</i> , 2021, 22, 873.	2.8	1
5	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. <i>Diabetes</i> , 2020, 69, 2806-2818.	0.6	26
6	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. <i>American Journal of Human Genetics</i> , 2019, 105, 15-28.	6.2	21
7	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.	27.8	248
8	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	21.4	89
9	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	21.4	286
10	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
11	Joint association analysis of a binary and a quantitative trait in family samples. <i>European Journal of Human Genetics</i> , 2017, 25, 130-136.	2.8	4
12	A candidate transacting modulator of fetal hemoglobin gene expression in the Arab-Indian haplotype of sickle cell anemia. <i>American Journal of Hematology</i> , 2016, 91, 1118-1122.	4.1	16
13	General Framework for Meta-Analysis of Haplotype Association Tests. <i>Genetic Epidemiology</i> , 2016, 40, 244-252.	1.3	0
14	A genomic approach to therapeutic target validation identifies a glucose-lowering <i>GLP1R</i> variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016, 8, 341ra76.	12.4	100
15	Comparison of multiple single-nucleotide variant association tests in a meta-analysis of Genetic Analysis Workshop 19 family and unrelated data. <i>BMC Proceedings</i> , 2016, 10, 187-191.	1.6	0
16	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015, 6, 5897.	12.8	173
17	Association of Levels of Fasting Glucose and Insulin With Rare Variants at the Chromosome 11p11.2- <i>MADD</i> Locus. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 374-382.	5.1	12
18	Comparing baseline and longitudinal measures in association studies. <i>BMC Proceedings</i> , 2014, 8, S84.	1.6	2