Hui Guo

List of Publications by Year
in descending order

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32	2,181	566801 15	395343 33
papers	citations	h-index	g-index

34	34	34	5559
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Keratinocyte <scp>EGF</scp> signaling dominates in Atopic Dermatitis lesions: a comparative <scp>RNAseq</scp> analysis. Experimental Dermatology, 2022, , .	1.4	2
2	A suggested shared aetiology of dementia - a colocalization study. Neurobiology of Aging, 2022, 117, 71-82.	1.5	2
3	Comparison of clinical efficacy and safety of transvaginal natural endoscopic surgery and transumbilical single port laparoscopy surgery for endometrial cancer.. American Journal of Translational Research (discontinued), 2022, 14, 2647-2654.	0.0	0
4	Bayesian mendelian randomization with study heterogeneity and data partitioning for large studies. BMC Medical Research Methodology, 2022, 22, .	1.4	3
5	Trans-ancestral dissection of urate- and gout-associated major loci SLC2A9 and ABCG2 reveals primate-specific regulatory effects. Journal of Human Genetics, 2021, 66, 161-169.	1.1	6
6	Heritability and family-based GWAS analyses of the N-acyl ethanolamine and ceramide plasma lipidome. Human Molecular Genetics, 2021, 30, 500-513.	1.4	13
7	Quantitative evaluation of PTPN22 copy number variation by digital droplet PCR and association with type 2 diabetes risk. Endocrine Journal, 2021, 68, 153-162.	0.7	1
8	Uncovering genetic mechanisms of hypertension through multi-omic analysis of the kidney. Nature Genetics, 2021, 53, 630-637.	9.4	37
9	A Bayesian approach to Mendelian randomization with multiple pleiotropic variants. Biostatistics, 2020, 21, 86-101.	0.9	37
10	Overlapping-sample Mendelian randomisation with multiple exposures: a Bayesian approach. BMC Medical Research Methodology, 2020, 20, 295.	1.4	8
11	Higher BMI is linked to an increased risk of heart attacks in European adults: a Mendelian randomisation study. BMC Cardiovascular Disorders, 2020, 20, 258.	0.7	6
12	Integrative analysis of Mendelian randomization and Bayesian colocalization highlights four genes with putative BMI-mediated causal pathways to diabetes. Scientific Reports, 2020, 10, 7476.	1.6	7
13	Treating head and neck tumors during the <scp>SARSâ€CoV</scp>â€2 epidemic, 2019 to 2020: Sichuan Cancer Hospital. Head and Neck, 2020, 42, 1153-1158.	0.9	15
14	Association of congenital cardiovascular malformation and neuropsychiatric phenotypes with 15q11.2 (BP1â€“BP2) deletion in the UK Biobank. European Journal of Human Genetics, 2020, 28, 1265-1273.	1.4	14
15	The Inhibitory Effect of (â^')-Epigallocatechin-3-Gallate on Breast Cancer Progression via Reducing SCUBE2 Methylation and DNMT Activity. Molecules, 2019, 24, 2899.	1.7	66
16	Uncovering genetic mechanisms of kidney aging through transcriptomics, genomics, and epigenomics. Kidney International, 2019, 95, 624-635.	2.6	40
17	Long-term survival following on-pump and off-pump coronary artery bypass graft surgery: a propensity score-matched analysis. European Journal of Cardio-thoracic Surgery, 2019, 56, 1147-1153.	0.6	10
18	Investigating multiple sclerosis genetic susceptibility on the founder population of east-central Sardinia via association and linkage analysis of immune-related loci. Multiple Sclerosis Journal, 2018, 24, 1815-1824.	1.4	13

#	Article	IF	Citations
19	Molecular insights into genome-wide association studies of chronic kidney disease-defining traits. Nature Communications, 2018, 9, 4800.	5.8	52
20	Divergent patterns of genic copy number variation in <i>KCNIP1</i> gene reveal risk locus of type 2 diabetes in Chinese population. Endocrine Journal, 2018, 65, 537-545.	0.7	5
21	CREB1 functional polymorphisms modulating promoter transcriptional activity are associated with type 2 diabetes mellitus risk in Chinese population. Gene, 2018, 665, 133-140.	1.0	12
22	Dissection of a Complex Disease Susceptibility Region Using a Bayesian Stochastic Search Approach to Fine Mapping. PLoS Genetics, 2015, 11, e1005272.	1.5	55
23	Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers. Nature Genetics, 2015, 47, 381-386.	9.4	589
24	Detection and correction of artefacts in estimation of rare copy number variants and analysis of rare deletions in type 1 diabetes. Human Molecular Genetics, 2015, 24, 1774-1790.	1.4	20
25	Statistical colocalization of genetic risk variants for related autoimmune diseases in the context of common controls. Nature Genetics, 2015, 47, 839-846.	9.4	128
26	Integration of disease association and eQTL data using a Bayesian colocalisation approach highlights six candidate causal genes in immune-mediated diseases. Human Molecular Genetics, 2015, 24, 3305-3313.	1.4	134
27	Widespread seasonal gene expression reveals annual differences in human immunity and physiology. Nature Communications, 2015, 6, 7000.	5.8	367
28	VSEAMS: a pipeline for variant set enrichment analysis using summary GWAS data identifies IKZF3, BATF and ESRRA as key transcription factors in type 1 diabetes. Bioinformatics, 2014, 30, 3342-3348.	1.8	14
29	A Type I Interferon Transcriptional Signature Precedes Autoimmunity in Children Genetically at Risk for Type 1 Diabetes. Diabetes, 2014, 63, 2538-2550.	0.3	261
30	A Method for Geneâ€Based Pathway Analysis Using Genomewide Association Study Summary Statistics Reveals Nine New Type 1 Diabetes Associations. Genetic Epidemiology, 2014, 38, 661-670.	0.6	54
31	Postthymic Expansion in Human CD4 Naive T Cells Defined by Expression of Functional High-Affinity IL-2 Receptors. Journal of Immunology, 2013, 190, 2554-2566.	0.4	60
32	Seven newly identified loci for autoimmune thyroid disease. Human Molecular Genetics, 2012, 21, 5202-5208.	1.4	143