Hui Guo

List of Publications by Year
in descending order

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Version: 2024-02-01

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	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
2	Widespread seasonal gene expression reveals annual differences in human immunity and physiology. Nature Communications, 2015, 6, 7000.	5.8	367
3	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
4	Seven newly identified loci for autoimmune thyroid disease. Human Molecular Genetics, 2012, 21, 5202-5208.	1.4	143
5	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
6	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
7	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
8	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
9	Dissection of a Complex Disease Susceptibility Region Using a Bayesian Stochastic Search Approach to Fine Mapping. PLoS Genetics, 2015, 11, e1005272.	1.5	55
10	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
11	Molecular insights into genome-wide association studies of chronic kidney disease-defining traits. Nature Communications, 2018, 9, 4800.	5.8	52
12	Uncovering genetic mechanisms of kidney aging through transcriptomics, genomics, and epigenomics. Kidney International, 2019, 95, 624-635.	2.6	40
13	A Bayesian approach to Mendelian randomization with multiple pleiotropic variants. Biostatistics, 2020, 21, 86-101.	0.9	37
14	Uncovering genetic mechanisms of hypertension through multi-omic analysis of the kidney. Nature Genetics, 2021, 53, 630-637.	9.4	37
15	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
16	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
17	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
18	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

#	Article	IF	Citations
19	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
20	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
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	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
23	Overlapping-sample Mendelian randomisation with multiple exposures: a Bayesian approach. BMC Medical Research Methodology, 2020, 20, 295.	1.4	8
24	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
25	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
26	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
27	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
28	Bayesian mendelian randomization with study heterogeneity and data partitioning for large studies. BMC Medical Research Methodology, 2022, 22, .	1.4	3
29	Keratinocyte <scp>EGF</scp> signaling dominates in Atopic Dermatitis lesions: a comparative <scp>RNAseq</scp> analysis. Experimental Dermatology, 2022, , .	1.4	2
30	A suggested shared aetiology of dementia - a colocalization study. Neurobiology of Aging, 2022, 117, 71-82.	1.5	2
31	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
32	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