Xueya Zhou

List of Publications by Year
in descending order

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35 papers	2,593 citations	430874 18 h-index	377865 34 g-index
41 all docs	41 docs citations	41 times ranked	6591 citing authors

#	Article	IF	Citations
1	Rare variant analysis of 4241 pulmonary arterial hypertension cases from an international consortium implicates FBLN2, PDGFD, and rare de novo variants in PAH. Genome Medicine, 2021, 13, 80.	8.2	43
2	Recent ultra-rare inherited variants implicate new autism candidate risk genes. Nature Genetics, 2021, 53, 1125-1134.	21.4	68
3	Rare and de novo variants in 827 congenital diaphragmatic hernia probands implicate LONP1 as candidate risk gene. American Journal of Human Genetics, 2021, 108, 1964-1980.	6.2	22
4	Likely damaging de novo variants in congenital diaphragmatic hernia patients are associated with worse clinical outcomes. Genetics in Medicine, 2020, 22, 2020-2028.	2.4	21
5	Large-scale targeted sequencing identifies risk genes for neurodevelopmental disorders. Nature Communications, 2020, 11, 4932.	12.8	105
6	Exome sequencing of 457 autism families recruited online provides evidence for autism risk genes. Npj Genomic Medicine, 2019, 4, 19.	3.8	163
7	A rare variant in MLKL confers susceptibility to ApoE É›4-negative Alzheimer's disease in Hong Kong Chinese population. Neurobiology of Aging, 2018, 68, 160.e1-160.e7.	3.1	23
8	Integrated analysis of mRNA-seq and miRNA-seq for host susceptibilities to influenza A (H7N9) infection in inbred mouse lines. Functional and Integrative Genomics, 2018, 18, 411-424.	3.5	6
9	De novo variants in congenital diaphragmatic hernia identify MYRF as a new syndrome and reveal genetic overlaps with other developmental disorders. PLoS Genetics, 2018, 14, e1007822.	3.5	79
10	Trans-Ethnic Polygenic Analysis Supports Genetic Overlaps of Lumbar Disc Degeneration With Height, Body Mass Index, and Bone Mineral Density. Frontiers in Genetics, 2018, 9, 267.	2.3	8
11	Polygenic scores via penalized regression on summary statistics. Genetic Epidemiology, 2017, 41, 469-480.	1.3	297
12	Cell Culture System for Analysis of Genetic Heterogeneity WithinÂHepatocellular Carcinomas and Response to Pharmacologic Agents. Gastroenterology, 2017, 152, 232-242.e4.	1.3	107
13	Co-occurring protein phosphorylation are functionally associated. PLoS Computational Biology, 2017, 13, e1005502.	3.2	26
14	Identification and functional analysis of a novel LHX1 mutation associated with congenital absence of the uterus and vagina. Oncotarget, 2017, 8, 8785-8790.	1.8	11
15	CNV analysis in Chinese children of mental retardation highlights a sex differentiation in parental contribution to de novo and inherited mutational burdens. Scientific Reports, 2016, 6, 25954.	3.3	19
16	Exome Sequencing and Gene Prioritization Correct Misdiagnosis in a Chinese Kindred with Familial Amyloid Polyneuropathy. Scientific Reports, 2016, 6, 26362.	3.3	8
17	A dominant negative mutation at the ATP binding domain ofAMHR2is associated with a defective anti-MÃ¼llerian hormone signaling pathway. Molecular Human Reproduction, 2016, 22, 669-678.	2.8	28
18	Systematic Characterization and Prediction of Post-Translational Modification Cross-Talk *. Molecular and Cellular Proteomics, 2015, 14, 761-770.	3.8	30

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19	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	21.4	294
20	Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. Human Molecular Genetics, 2014, 23, 5492-5504.	2.9	192
21	<i>MYH9</i>-Related Disease: Description of a Large Chinese Pedigree and a Survey of Reported Mutations. Acta Haematologica, 2014, 132, 193-198.	1.4	5
22	Resolving the genetic heterogeneity of prelingual hearing loss within one family: Performance comparison and application of two targeted next generation sequencing approaches. Journal of Human Genetics, 2014, 59, 599-607.	2.3	16
23	Exome Sequencing Identifies a Novel Frameshift Mutation ofMYO6as the Cause of Autosomal Dominant Nonsyndromic Hearing Loss in a Chinese Family. Annals of Human Genetics, 2014, 78, 410-423.	0.8	10
24	Common variants in the ATP2B1 gene are associated with hypertension and arterial stiffness in Chinese population. Molecular Biology Reports, 2013, 40, 1867-1873.	2.3	20
25	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	6.2	189
26	Prioritizing genes responsible for host resistance to influenza using network approaches. BMC Genomics, 2013, 14, 816.	2.8	3
27	Basics for Bioinformatics. , 2013, , 1-25.		4
28	Short Read Mapping for Exome Sequencing. Methods in Molecular Biology, 2013, 1038, 93-111.	0.9	0
29	Identification of long non-protein coding RNAs in chicken skeletal muscle using next generation sequencing. Genomics, 2012, 99, 292-298.	2.9	173
30	A novel non-synonymous mutation in the homeodomain of HOXD13 causes synpolydactyly in a Chinese family. Clinica Chimica Acta, 2012, 413, 1049-1052.	1.1	13
31	Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians. Nature Genetics, 2011, 43, 531-538.	21.4	516
32	Fine mapping of the awn gene on chromosome 4 in rice by association and linkage analyses. Science Bulletin, 2011, 56, 835-839.	1.7	26
33	A Rare Variant at theKYNUGene Is Associated With Kynureninase Activity and Essential Hypertension in the Han Chinese Population. Circulation: Cardiovascular Genetics, 2011, 4, 687-694.	5.1	14
34	Polymorphisms at 16p13 are associated with systemic lupus erythematosus in the Chinese population. Journal of Medical Genetics, 2011, 48, 69-72.	3.2	17
35	Identification and Characterization of Human snoRNA Core Promoters. Genomics, 2010, 96, 50-56.	2.9	18