# Xueya Zhou

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8306116/publications.pdf

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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 | 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 |
| 2 | Polygenic scores via penalized regression on summary statistics. Genetic Epidemiology, 2017, 41, 469-480. | 1.3 | 297 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | Identification of long non-protein coding RNAs in chicken skeletal muscle using next generation sequencing. Genomics, 2012, 99, 292-298. | 2.9 | 173 |
| 7 | Exome sequencing of 457 autism families recruited online provides evidence for autism risk genes. Npj Genomic Medicine, 2019, 4, 19. | 3.8 | 163 |
| 8 | Cell Culture System for Analysis of Genetic Heterogeneity WithinÂHepatocellular Carcinomas and Response to Pharmacologic Agents. Gastroenterology, 2017, 152, 232-242.e4. | 1.3 | 107 |
| 9 | Large-scale targeted sequencing identifies risk genes for neurodevelopmental disorders. Nature Communications, 2020, 11, 4932. | 12.8 | 105 |
| 10 | 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 |
| 11 | Recent ultra-rare inherited variants implicate new autism candidate risk genes. Nature Genetics, 2021, 53, 1125-1134. | 21.4 | 68 |
| 12 | 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 |
| 13 | Systematic Characterization and Prediction of Post-Translational Modification Cross-Talk *. Molecular and Cellular Proteomics, 2015, 14, 761-770. | 3.8 | 30 |
| 14 | 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 |
| 15 | 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 |
| 16 | Co-occurring protein phosphorylation are functionally associated. PLoS Computational Biology, 2017, 13, e1005502. | 3.2 | 26 |
| 17 | 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 |
| 18 | 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | 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 |
| 20 | 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 |
| 21 | 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 |
| 22 | Identification and Characterization of Human snoRNA Core Promoters. Genomics, 2010, 96, 50-56. | 2.9 | 18 |
| 23 | Polymorphisms at 16p13 are associated with systemic lupus erythematosus in the Chinese population. Journal of Medical Genetics, 2011, 48, 69-72. | 3.2 | 17 |
| 24 | 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 |
| 25 | 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 |
| 26 | 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 |
| 27 | 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 |
| 28 | 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 |
| 29 | Exome Sequencing and Gene Prioritization Correct Misdiagnosis in a Chinese Kindred with Familial Amyloid Polyneuropathy. Scientific Reports, 2016, 6, 26362. | 3.3 | 8 |
| 30 | 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 |
| 31 | 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 |
| 32 | <b><i>MYH9</i></b>-Related Disease: Description of a Large Chinese Pedigree and a Survey of Reported Mutations. Acta Haematologica, 2014, 132, 193-198. | 1.4 | 5 |
| 33 | Basics for Bioinformatics. , 2013, , 1-25. | | 4 |
| 34 | Prioritizing genes responsible for host resistance to influenza using network approaches. BMC Genomics, 2013, 14, 816. | 2.8 | 3 |
| 35 | Short Read Mapping for Exome Sequencing. Methods in Molecular Biology, 2013, 1038, 93-111. | 0.9 | 0 |