# Yan Zhang

List of Publications by Year
in descending order



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|---|---|---|---|
| 22 papers | 1,263 citations | 933447 10 h-index | 677142 22 g-index |
| 23 all docs | 23 docs citations | 23 times ranked | 2121 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Genome-Wide Association Study in Asian Populations Identifies Variants in ETS1 and WDFY4 Associated with Systemic Lupus Erythematosus. PLoS Genetics, 2010, 6, e1000841. | 3.5 | 378 |
| 2 | Genome-wide association meta-analysis in Chinese and European individuals identifies ten new loci associated with systemic lupus erythematosus. Nature Genetics, 2016, 48, 940-946. | 21.4 | 283 |
| 3 | Meta-analysis Followed by Replication Identifies Loci in or near CDKN1B, TET3, CD80, DRAM1, and ARID5B as Associated with Systemic Lupus Erythematosus in Asians. American Journal of Human Genetics, 2013, 92, 41-51. | 6.2 | 184 |
| 4 | Identification of 38 novel loci for systemic lupus erythematosus and genetic heterogeneity between ancestral groups. Nature Communications, 2021, 12, 772. | 12.8 | 128 |
| 5 | ELF1 is associated with systemic lupus erythematosus in Asian populations. Human Molecular Genetics, 2011, 20, 601-607. | 2.9 | 78 |
| 6 | Meta-analysis of GWAS on two Chinese populations followed by replication identifies novel genetic variants on the X chromosome associated with systemic lupus erythematosus. Human Molecular Genetics, 2015, 24, 274-284. | 2.9 | 35 |
| 7 | Identification of ST3AGL4, MFHAS1, CSNK2A2 and CD226 as loci associated with systemic lupus erythematosus (SLE) and evaluation of SLE genetics in drug repositioning. Annals of the Rheumatic Diseases, 2018, 77, 1078-1084. | 0.9 | 34 |
| 8 | Meta-analysis of GWASÂonÂboth Chinese and European populations identifies GPR173 as a novel X chromosome susceptibility gene for SLE. Arthritis Research and Therapy, 2018, 20, 92. | 3.5 | 19 |
| 9 | Epistatic Interaction between Genetic Variants in Susceptibility Gene ETS1 Correlates with ILâ€17 Levels in SLE Patients. Annals of Human Genetics, 2013, 77, 344-350. | 0.8 | 16 |
| 10 | Genome-wide association study on Northern Chinese identifies KLF2, DOT1L and STAB2 associated with systemic lupus erythematosus. Rheumatology, 2021, 60, 4407-4417. | 1.9 | 16 |
| 11 | Association of polymorphism in the <scp>VEGFA</scp> gene 3â€²â€<scp>UTR</scp> +936T/C with susceptibility to biliary atresia in a Southern Chinese Han population. Journal of Clinical Laboratory Analysis, 2018, 32, e22342. | 2.1 | 12 |
| 12 | Epistatic Association of CD14 and NOTCH2 Genetic Polymorphisms with Biliary Atresia in a Southern Chinese Population. Molecular Therapy - Nucleic Acids, 2018, 13, 590-595. | 5.1 | 10 |
| 13 | Identification of Regulatory Modules That Stratify Lupus Disease Mechanism through Integrating Multi-Omics Data. Molecular Therapy - Nucleic Acids, 2020, 19, 318-329. | 5.1 | 10 |
| 14 | PDGFA gene rs9690350 polymorphism increases biliary atresia risk in Chinese children. Bioscience Reports, 2020, 40, . | 2.4 | 10 |
| 15 | Association of IL18 genetic polymorphisms with increased risk of Biliary atresia susceptibility in Southern Chinese children. Gene, 2018, 677, 228-231. | 2.2 | 9 |
| 16 | Independent Replication on Genome-Wide Association Study Signals Identifies IRF3 as a Novel Locus for Systemic Lupus Erythematosus. Frontiers in Genetics, 2020, 11, 600. | 2.3 | 9 |
| 17 | Associations of SLC6A20 genetic polymorphisms with Hirschsprungâ€™s disease in a Southern Chinese population. Bioscience Reports, 2019, 39, . | 2.4 | 9 |
| 18 | Meta-analysis of two Chinese populations identifies an autoimmune disease risk allele in 22q11.21 as associated with systemic lupus erythematosus. Arthritis Research and Therapy, 2015, 17, 67. | 3.5 | 6 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 19 | Associations between common genetic variants in microRNAs and Hirschsprung disease susceptibility in Southern Chinese children. Journal of Gene Medicine, 2021, 23, e3301. | 2.8 | 6 |
| 20 | Down-regulation of STAT3 enhanced chemokine expression and neutrophil recruitment in biliary atresia. Clinical Science, 2021, 135, 865-884. | 4.3 | 5 |
| 21 | Association between DSCAM polymorphisms and non-syndromic Hirschsprung disease in Chinese population. BMC Medical Genetics, 2018, 19, 116. | 2.1 | 4 |
| 22 | Significant Association of rs2147555 Genetic Polymorphism in the EDNRB Gene with Hirschsprung Disease in Southern Chinese Children. BioMed Research International, 2020, 2020, 1-6. | 1.9 | 1 |