Yan Zhang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	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
2	Genome-wide association study on Northern Chinese identifies <i>KLF2</i> , <i>DOT1L</i> and <i>STAB2</i> associated with systemic lupus erythematosus. Rheumatology, 2021, 60, 4407-4417.	1.9	16
3	Identification of 38 novel loci for systemic lupus erythematosus and genetic heterogeneity between ancestral groups. Nature Communications, 2021, 12, 772.	12.8	128
4	Down-regulation of STAT3 enhanced chemokine expression and neutrophil recruitment in biliary atresia. Clinical Science, 2021, 135, 865-884.	4.3	5
5	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
6	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
7	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
8	<i>PDGFA</i> gene rs9690350 polymorphism increases biliary atresia risk in Chinese children. Bioscience Reports, 2020, 40, .	2.4	10
9	Associations of <i>SLC6A20</i> genetic polymorphisms with Hirschsprung's disease in a Southern Chinese population. Bioscience Reports, 2019, 39, .	2.4	9
10	ldentification of <i>ST3AGL4</i> , <i>MFHAS1, CSNK2A2</i> and <i>CD226</i> 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
11	Association of polymorphism in the <scp>VEGFA</scp> gene 3′â€ <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	Association of IL18 genetic polymorphisms with increased risk of Biliary atresia susceptibility in Southern Chinese children. Gene, 2018, 677, 228-231.	2.2	9
14	Association between DSCAM polymorphisms and non-syndromic Hirschsprung disease in Chinese population. BMC Medical Genetics, 2018, 19, 116.	2.1	4
15	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
16	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
17	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
18	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

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19	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
20	Epistatic Interaction between Genetic Variants in Susceptibility Gene <i>ETS1</i> Correlates with ILâ€17 Levels in SLE Patients. Annals of Human Genetics, 2013, 77, 344-350.	0.8	16
21	ELF1 is associated with systemic lupus erythematosus in Asian populations. Human Molecular Genetics, 2011, 20, 601-607.	2.9	78
22	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