

Xianyong Yin

List of Publications by Year in descending order

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49
papers

3,033
citations

279798

23
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182427

51
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63
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docs citations

63
times ranked

5918
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. <i>Nature Communications</i> , 2022, 13, 1644.	12.8	63
2	Biological insights into systemic lupus erythematosus through an immune cell-specific transcriptome-wide association study. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, 1273-1280.	0.9	9
3	Whole Exome Sequencing Enhanced Imputation Identifies 85 Metabolite Associations in the Alpine CHRIS Cohort. <i>Metabolites</i> , 2022, 12, 604.	2.9	6
4	Meta-analysis of 208370 East Asians identifies 113 susceptibility loci for systemic lupus erythematosus. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 632-640.	0.9	103
5	Identification of 38 novel loci for systemic lupus erythematosus and genetic heterogeneity between ancestral groups. <i>Nature Communications</i> , 2021, 12, 772.	12.8	128
6	Causal Relationship and Shared Genetic Loci between Psoriasis and Type 2 Diabetes through Trans-Disease Meta-Analysis. <i>Journal of Investigative Dermatology</i> , 2021, 141, 1493-1502.	0.7	29
7	Discovery of Novel Genetic Risk Loci for Acute Central Serous Chorioretinopathy and Genetic Pleiotropic Effect With Age-Related Macular Degeneration. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 696885.	3.7	2
8	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	27.8	353
9	JAK2 and PTPRC mRNA expression in peripheral blood mononuclear cells from patients with systemic lupus erythematosus. <i>Clinical Rheumatology</i> , 2020, 39, 443-448.	2.2	8
10	Association of the Polymorphism rs13259960 in <i>SLEAR</i> With Predisposition to Systemic Lupus Erythematosus. <i>Arthritis and Rheumatology</i> , 2020, 72, 985-996.	5.6	22
11	Exome sequencing of Finnish isolates enhances rare-variant association power. <i>Nature</i> , 2019, 572, 323-328.	27.8	161
12	Fine mapping and subphenotyping implicates <i>ADRA1B</i> gene variants in psoriasis susceptibility in a Chinese population. <i>Epigenomics</i> , 2019, 11, 455-467.	2.1	10
13	Identification of seven novel loci associated with amino acid levels using single-variant and gene-based tests in 8545 Finnish men from the METSIM study. <i>Human Molecular Genetics</i> , 2018, 27, 1664-1674.	2.9	30
14	Exome-wide association study identifies four novel loci for systemic lupus erythematosus in Han Chinese population. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 417-417.	0.9	50
15	Genotype imputation for Han Chinese population using Haplotype Reference Consortium as reference. <i>Human Genetics</i> , 2018, 137, 431-436.	3.8	15
16	A catalog of potential putative functional variants in psoriasis genome-wide association regions. <i>PLoS ONE</i> , 2018, 13, e0196635.	2.5	5
17	Genome-wide meta-analysis identifies a novel susceptibility signal at <i>CACNA2D3</i> for nicotine dependence. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 557-567.	1.7	15
18	Integration of expression quantitative trait loci and pleiotropy identifies a novel psoriasis susceptibility gene, <i>PTPN1</i> . <i>Journal of Gene Medicine</i> , 2017, 19, e2939.	2.8	5

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19	Common susceptibility variants are shared between schizophrenia and psoriasis in the Han Chinese population. <i>Journal of Psychiatry and Neuroscience</i> , 2016, 41, 413-421.	2.4	19
20	Genetic Susceptibility to Vitiligo: GWAS Approaches for Identifying Vitiligo Susceptibility Genes and Loci. <i>Frontiers in Genetics</i> , 2016, 7, 3.	2.3	69
21	Genome-wide association meta-analysis in Chinese and European individuals identifies ten new loci associated with systemic lupus erythematosus. <i>Nature Genetics</i> , 2016, 48, 940-946.	21.4	283
22	Epigenome-wide association data implicates DNA methylation-mediated genetic risk in psoriasis. <i>Clinical Epigenetics</i> , 2016, 8, 131.	4.1	31
23	Several Critical Cell Types, Tissues, and Pathways Are Implicated in Genome-Wide Association Studies for Systemic Lupus Erythematosus. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1503-1511.	1.8	12
24	Deep sequencing of the MHC region in the Chinese population contributes to studies of complex disease. <i>Nature Genetics</i> , 2016, 48, 740-746.	21.4	188
25	Epigenome-Wide Association Analysis Identified Nine Skin DNA Methylation Loci for Psoriasis. <i>Journal of Investigative Dermatology</i> , 2016, 136, 779-787.	0.7	75
26	A rare variant in COL11A1 is strongly associated with adult height in Chinese Han population. <i>Journal of Genetics and Genomics</i> , 2016, 43, 549-554.	3.9	2
27	Identification of cell types, tissues and pathways affected by risk loci in psoriasis. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1005-1012.	2.1	3
28	Discovery of a novel genetic susceptibility locus on X chromosome for systemic lupus erythematosus. <i>Arthritis Research and Therapy</i> , 2015, 17, 349.	3.5	26
29	Rs4948496 within <i>ARID5B</i> gene is associated with clinical features of systemic lupus erythematosus in the Chinese Han population. <i>Journal of Dermatology</i> , 2015, 42, 608-612.	1.2	2
30	A Weighted Polygenic Risk Score Using 14 Known Susceptibility Variants to Estimate Risk and Age Onset of Psoriasis in Han Chinese. <i>PLoS ONE</i> , 2015, 10, e0125369.	2.5	22
31	Whole-exome SNP array identifies 15 new susceptibility loci for psoriasis. <i>Nature Communications</i> , 2015, 6, 6793.	12.8	118
32	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. <i>Nature Communications</i> , 2015, 6, 6916.	12.8	154
33	Association of the Late Cornified Envelope-3 Genes with Psoriasis and Psoriatic Arthritis: A Systematic Review. <i>Journal of Genetics and Genomics</i> , 2015, 42, 49-56.	3.9	19
34	More heritability probably captured by psoriasis genome-wide association study in Han Chinese. <i>Gene</i> , 2015, 573, 46-49.	2.2	6
35	The Contribution of Meta-Analysis of Genome-Wide Association Studies in Investigating the Genetic Susceptibility to Lupus. <i>Journal of Investigative Dermatology Symposium Proceedings</i> , 2015, 17, 51-52.	0.8	0
36	Four genetic variants interact to confer susceptibility to atopic dermatitis in Chinese Han population. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1493-1498.	2.1	9

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37	Introduction of the Institute of Dermatology, Anhui Medical University. Journal of Investigative Dermatology Symposium Proceedings, 2015, 17, 8.	0.8	0
38	Combined effect of five single nucleotide polymorphisms related to IL23/Th17 pathway in the risk of psoriasis. Immunogenetics, 2014, 66, 215-218.	2.4	8
39	Common variants explain a large fraction of the variability in the liability to psoriasis in a Han Chinese population. BMC Genomics, 2014, 15, 87.	2.8	16
40	A large-scale screen for coding variants predisposing to psoriasis. Nature Genetics, 2014, 46, 45-50.	21.4	183
41	Exome sequencing identifies SLC17A9 pathogenic gene in two Chinese pedigrees with disseminated superficial actinic porokeratosis. Journal of Medical Genetics, 2014, 51, 699-704.	3.2	32
42	Five regulatory genes detected by matching signatures of eQTL and GWAS in psoriasis. Journal of Dermatological Science, 2014, 76, 139-142.	1.9	7
43	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
44	Genome-wide association analyses in Han Chinese identify two new susceptibility loci for amyotrophic lateral sclerosis. Nature Genetics, 2013, 45, 697-700.	21.4	67
45	Confirmation of C4 gene copy number variation and the association with systemic lupus erythematosus in Chinese Han population. Rheumatology International, 2012, 32, 3047-3053.	3.0	28
46	Meta-analysis of NOD2/CARD15 polymorphisms with psoriasis and psoriatic arthritis. Rheumatology International, 2012, 32, 1893-1900.	3.0	21
47	Down-regulated expression of IKZF1 mRNA in peripheral blood mononuclear cells from patients with systemic lupus erythematosus. Rheumatology International, 2011, 31, 819-822.	3.0	25
48	Platelet-derived Growth Factor Receptor Alpha Gene Mutations in Vitiligo Vulgaris. Acta Dermato-Venereologica, 2010, 90, 131-135.	1.3	15
49	Genomic Dissection of Population Substructure of Han Chinese and Its Implication in Association Studies. American Journal of Human Genetics, 2009, 85, 762-774.	6.2	338