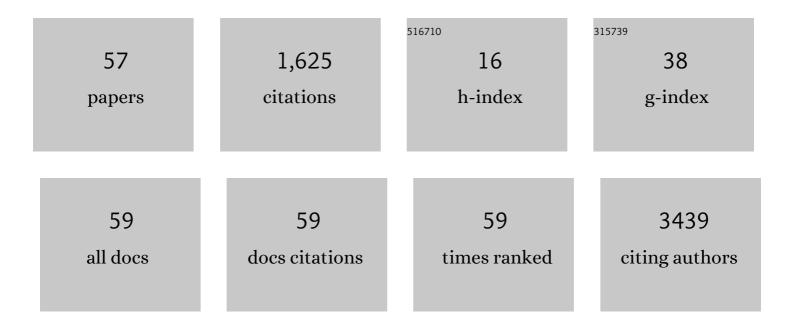
## Xiaodong Zheng

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genome-wide analyses of non-syndromic cleft lip with palate identify 14 novel loci and genetic heterogeneity. Nature Communications, 2017, 8, 14364.	12.8	207
2	Deep sequencing of the MHC region in the Chinese population contributes to studies of complex disease. Nature Genetics, 2016, 48, 740-746.	21.4	188
3	A large-scale screen for coding variants predisposing to psoriasis. Nature Genetics, 2014, 46, 45-50.	21.4	183
4	Whole-exome SNP array identifies 15 new susceptibility loci for psoriasis. Nature Communications, 2015, 6, 6793.	12.8	118
5	Meta-analysis of 208370 East Asians identifies 113 susceptibility loci for systemic lupus erythematosus. Annals of the Rheumatic Diseases, 2021, 80, 632-640.	0.9	103
6	A genome-wide association study identifies six novel risk loci for primary biliary cholangitis. Nature Communications, 2017, 8, 14828.	12.8	102
7	A new magnetorheological elastomer isolator in shear–compression mixed mode. Journal of Intelligent Material Systems and Structures, 2015, 26, 1290-1300.	2.5	79
8	Epigenome-Wide Association Analysis Identified Nine Skin DNA Methylation LociÂfor Psoriasis. Journal of Investigative Dermatology, 2016, 136, 779-787.	0.7	75
9	Genetic Susceptibility to Vitiligo: GWAS Approaches for Identifying Vitiligo Susceptibility Genes and Loci. Frontiers in Genetics, 2016, 7, 3.	2.3	69
10	Sequencing-based approach identified three new susceptibility loci for psoriasis. Nature Communications, 2014, 5, 4331.	12.8	67
11	Exome-wide association study identifies four novel loci for systemic lupus erythematosus in Han Chinese population. Annals of the Rheumatic Diseases, 2018, 77, 417-417.	0.9	50
12	Exome sequencing identifiesSLC17A9pathogenic gene in two Chinese pedigrees with disseminated superficial actinic porokeratosis. Journal of Medical Genetics, 2014, 51, 699-704.	3.2	32
13	Epigenome-wide association data implicates DNA methylation-mediated genetic risk in psoriasis. Clinical Epigenetics, 2016, 8, 131.	4.1	31
14	Integrative analyses reveal biological pathways and key genes in psoriasis. British Journal of Dermatology, 2017, 177, 1349-1357.	1.5	30
15	Discovery of a novel genetic susceptibility locus on X chromosome for systemic lupus erythematosus. Arthritis Research and Therapy, 2015, 17, 349.	3.5	26
16	Rapid diagnosis of Fusarium root rot in soybean caused by Fusarium equiseti or Fusarium graminearum using loop-mediated isothermal amplification (LAMP) assays. Australasian Plant Pathology, 2015, 44, 437-443.	1.0	23
17	Quantitative proteomics analysis of young and elderly skin with DIA mass spectrometry reveals new skin aging-related proteins. Aging, 2020, 12, 13529-13554.	3.1	21
18	Common susceptibility variants are shared between schizophrenia and psoriasis in the Han Chinese population. Journal of Psychiatry and Neuroscience, 2016, 41, 413-421.	2.4	19

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19	Downregulated expression of <i>LBH</i> mRNA in peripheral blood mononuclear cells from patients with systemic lupus erythematosus. Journal of Dermatology, 2016, 43, 99-102.	1.2	14
20	Effects of laying breeder hens dietary β-carotene, curcumin, allicin, and sodium butyrate supplementation on the jejunal microbiota and immune response of their offspring chicks. Poultry Science, 2020, 99, 3807-3816.	3.4	13
21	Bach2 overexpression represses Th9 cell differentiation by suppressing IRF4 expression in systemic lupus erythematosus. FEBS Open Bio, 2021, 11, 395-403.	2.3	12
22	Association Study Reveals One Susceptibility Locus with Vitiligo in the Chinese Han Population. Genetic Testing and Molecular Biomarkers, 2019, 23, 791-796.	0.7	11
23	Fine mapping and subphenotyping implicates <i>ADRA1B</i> gene variants in psoriasis susceptibility in a Chinese population. Epigenomics, 2019, 11, 455-467.	2.1	10
24	Identification of a Novel Mutation in SASH1 Gene in a Chinese Family With Dyschromatosis Universalis Hereditaria and Genotype-Phenotype Correlation Analysis. Frontiers in Genetics, 2020, 11, 841.	2.3	9
25	First Report of Elm Yellows Phytoplasma Infecting Clover in China. Plant Disease, 2009, 93, 321-321.	1.4	9
26	A genetic coding variant rs72474224 in GJB2 is associated with clinical features of psoriasis vulgaris in a Chinese Han population. Tissue Antigens, 2015, 86, 134-138.	1.0	8
27	DNA methylation-based subclassification of psoriasis in the Chinese Han population. Frontiers of Medicine, 2018, 12, 717-725.	3.4	8
28	HLA-C*01:02 and HLA-A*02:07 Confer Risk Specific for Psoriatic Patients in Southern China. Journal of Investigative Dermatology, 2019, 139, 2045-2048.e4.	0.7	8
29	Assay for Transposase-Accessible Chromatin Using Sequencing Analysis Reveals a Widespread Increase in Chromatin Accessibility in Psoriasis. Journal of Investigative Dermatology, 2021, 141, 1745-1753.	0.7	8
30	AURKA facilitates the psoriasis-related inflammation by impeding autophagy-mediated AIM2 inflammasome suppression. Immunology Letters, 2021, 240, 98-105.	2.5	8
31	<i>CYP2S1</i> might regulate proliferation and immune response of keratinocyte in psoriasis. Epigenetics, 2021, 16, 618-628.	2.7	7
32	Exome-Wide Rare Loss-of-Function Variant Enrichment Study of 21,347 Han Chinese Individuals Identifies Four Susceptibility Genes for Psoriasis. Journal of Investigative Dermatology, 2020, 140, 799-805.e1.	0.7	6
33	A Genetic Variant rs1020760at <i>NFKB1</i> is Associated with Clinical Features of Psoriasis Vulgaris in a Han Chinese Population. Annals of Human Genetics, 2016, 80, 197-202.	0.8	5
34	Integration of expression quantitative trait loci and pleiotropy identifies a novel psoriasis susceptibility gene, <i>PTPN1</i> . Journal of Gene Medicine, 2017, 19, e2939.	2.8	5
35	Genotype combination contributes to psoriasis: An exhaustive algorithm perspective. PLoS ONE, 2017, 12, e0186067.	2.5	5
36	<scp>HLA</scp> â€ <scp>DQ</scp> β1 amino acid position 87 and <scp>DQB</scp> 1*0301 are associated with Chinese Han <scp>SLE</scp> . Molecular Genetics & Genomic Medicine, 2018, 6, 541-546.	1.2	5

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37	A catalog of potential putative functional variants in psoriasis genome-wide association regions. PLoS ONE, 2018, 13, e0196635.	2.5	5
38	A Genomeâ€wide association study identified <i>HLAâ€C</i> associated with the effectiveness of methotrexate for psoriasis treatment. Journal of the European Academy of Dermatology and Venereology, 2021, 35, e898-e900.	2.4	5
39	Genomeâ€wide association study of 7661 Chinese Han individuals and fineâ€mapping major histocompatibility complex identifies HLAâ€DRB1 as associated with IgA vasculitis. Journal of Clinical Laboratory Analysis, 2022, 36, e24457.	2.1	5
40	Correlation analysis of the <i>HLAâ€ÐPB1*05:01</i> and <i>BTNL2</i> genes within the histocompatibility complex region with a clinical phenotype of psoriasis vulgaris in the Chinese Han population. Journal of Gene Medicine, 2017, 19, e2961.	2.8	4
41	A KRT16 mutation in the first Chinese pedigree with Pachyonychia congenita and review of the literatures. Journal of Cosmetic Dermatology, 2019, 18, 1930-1934.	1.6	4
42	Identification of cell types, tissues and pathways affected by risk loci in psoriasis. Molecular Genetics and Genomics, 2016, 291, 1005-1012.	2.1	3
43	A novel insertion mutation of <i>CDSN</i> responsible for hypotrichosis simplex of scalp in a Chinese family. Clinical and Experimental Dermatology, 2018, 43, 722-723.	1.3	3
44	DNA methylation profile of psoriatic skins from different body locations. Epigenomics, 2019, 11, 1613-1625.	2.1	3
45	Physical origin of the expansion of polymer coils in a binary solvent in the vicinity of its demixing critical point. Molecular Physics, 2019, 117, 3806-3811.	1.7	3
46	Loss-of-function variants in FSIP1 identified by targeted sequencing are associated with one particular subtype of mucosal melanoma. Gene, 2020, 759, 144964.	2.2	3
47	Rs4948496 within <i><scp>ARID5B</scp></i> gene is associated with clinical features of systemic lupus erythematosus in the <scp>C</scp> hinese <scp>H</scp> an population. Journal of Dermatology, 2015, 42, 608-612.	1.2	2
48	Changes in the hepatitis B surface antibody in childhood acute lymphocytic leukaemia survivors after treatment with the CCLG-ALL 2008 protocol. Clinical and Experimental Immunology, 2020, 203, 80-86.	2.6	2
49	Molecular Characterization and Tissue-specific Expression of a Novel FKBP38 Gene in the Cashmere Goat (Capra hircus). Asian-Australasian Journal of Animal Sciences, 2012, 25, 758-763.	2.4	2
50	Case Report: Challenges in the Diagnosis of a Case of Mal de Meleda and a Therapeutic Attempt of Ixekizumab and Adalimumab. Frontiers in Medicine, 2022, 9, 821301.	2.6	2
51	Association analysis of allergic sensitization susceptibility loci with atopic dermatitis in Chinese population. Journal of Dermatological Science, 2015, 80, 217-220.	1.9	1
52	Association of the novel susceptible locus rs9266150 with clinical features of psoriasis vulgaris in the Chinese Han population. Experimental Dermatology, 2018, 27, 748-753.	2.9	1
53	A high stem to leaf ratio reduced rainfall use efficiency under altered rainfall patterns in a semiâ€arid grassland in northeast China. Plant Biology, 2021, 23, 760-769.	3.8	1
54	An in-depth analysis reveals two new genetic variants on 22q11.2 associated with vitiligo in the Chinese Han population. Molecular Biology Reports, 2021, 48, 5955-5964.	2.3	1

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55	Gene interaction analysis of psoriasis in Chinese Han population. Molecular Genetics & Genomic Medicine, 2022, , e1858.	1.2	1
56	Association analysis of the major histocompatibility complex region in psoriasis vulgaris. British Journal of Dermatology, 2019, 180, 1553-1554.	1.5	0
57	Appropriate Osmotic Balance Duration for Different Volumes of Ovarian Tissue in Vitrification Solution: a Study of Ovary Tissue Vitrification and Transplantation in Sheep. Cryo-Letters, 2016, 37, 365-378.	0.3	0