Xing-bo Mo

List of Publications by Year
in descending order

53	1,356	430874	361022
papers	citations	18	35
		h-index	g-index

54	54	54	3085
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A polygenic risk score improves risk stratification of coronary artery disease: a large-scale prospective Chinese cohort study. European Heart Journal, 2022, 43, 1702-1711.	2.2	58
2	Association of DNA Methylation in Blood Pressure-Related Genes With Ischemic Stroke Risk and Prognosis. Frontiers in Cardiovascular Medicine, 2022, 9, 796245.	2.4	6
3	Identification of novel rheumatoid arthritis-associated MiRNA-204-5p from plasma exosomes. Experimental and Molecular Medicine, 2022, 54, 334-345.	7.7	27
4	Integrative lncRNA–mRNA co‐expression network analysis identifies novel lncRNA E2F3–IT1 for rheumatoid arthritis. Clinical and Translational Medicine, 2021, 11, e325.	4.0	7
5	Integrative analysis identifies potential causal methylation-mRNA regulation chains for rheumatoid arthritis. Molecular Immunology, 2021, 131, 89-96.	2.2	6
6	Promoter DNA Methylation in GWAS-Identified Genes as Potential Functional Elements for Blood Pressure: An Observational and Mendelian Randomization Study. Frontiers in Genetics, 2021, 12, 791146.	2.3	2
7	Identification of PBMC-expressed miRNAs for rheumatoid arthritis. Epigenetics, 2020, 15, 386-397.	2.7	16
8	Mendelian randomization analysis revealed potential causal factors for systemic lupus erythematosus. Immunology, 2020, 159, 279-288.	4.4	18
9	Alteration of circulating microbiome and its associated regulation role in rheumatoid arthritis: Evidence from integration of multiomics data. Clinical and Translational Medicine, 2020, 10, e229.	4.0	5
10	Integrative analysis identifies the association between CASZ1 methylation and ischemic stroke. Neurology: Genetics, 2020, 6, e509.	1.9	11
11	Protein array test detected three osteoporosis related plasma inflammatory cytokines in Chinese postmenopausal women. Cytokine, 2020, 133, 155166.	3.2	2
12	Integrative analysis highlighted susceptibility genes for rheumatoid arthritis. International Immunopharmacology, 2020, 86, 106716.	3.8	8
13	Integrative analysis revealed potential causal genetic and epigenetic factors for multiple sclerosis. Journal of Neurology, 2019, 266, 2699-2709.	3.6	34
14	Epigenetically regulated co-expression network of genes significant for rheumatoid arthritis. Epigenomics, 2019, 11, 1601-1612.	2.1	7
15	SNPs rs10224002 in PRKAG2 may disturb gene expression and consequently affect hypertension. Molecular Biology Reports, 2019, 46, 1617-1624.	2.3	2
16	Multi‐omics integrative analysis identified SNP‐methylation‐mRNA: Interaction in peripheral blood mononuclear cells. Journal of Cellular and Molecular Medicine, 2019, 23, 4601-4610.	3.6	10
17	Examination of the associations between m6A-associated single-nucleotide polymorphisms and blood pressure. Hypertension Research, 2019, 42, 1582-1589.	2.7	47
18	Integrative Analysis Identified IRF6 and NDST1 as Potential Causal Genes for Ischemic Stroke. Frontiers in Neurology, 2019, 10, 517.	2.4	13

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19	Associations between potentially functional CORIN SNPs and serum corin levels in the Chinese Han population. BMC Genetics, 2019, 20, 99.	2.7	6
20	Detection of Putative Functional Single Nucleotide Polymorphisms in Blood Pressure Loci and Validation of Association Between Single Nucleotide Polymorphism in WBP1L and Hypertension in the Chinese Han Population. Journal of Cardiovascular Pharmacology, 2019, 73, 48-55.	1.9	1
21	Rheumatoid arthritisâ€"associated DNA methylation sites in peripheral blood mononuclear cells. Annals of the Rheumatic Diseases, 2019, 78, 36-42.	0.9	75
22	Detection of lncRNA-mRNA interaction modules by integrating eQTL with weighted gene co-expression network analysis. Functional and Integrative Genomics, 2019, 19, 217-225.	3.5	9
23	Integrative Analysis Confirmed the Association between Osteoprotegerin and Osteoporosis. Chinese Medical Sciences Journal, 2019, 34, 55.	0.4	3
24	Relative abundance of mature myostatin rather than total myostatin is negatively associated with bone mineral density in Chinese. Journal of Cellular and Molecular Medicine, 2018, 22, 1329-1336.	3.6	21
25	Association of Plasma Irisin with Bone Mineral Density in a Large Chinese Population Using an Extreme Sampling Design. Calcified Tissue International, 2018, 103, 246-251.	3.1	23
26	Multiple correlation analyses revealed complex relationship between DNA methylation and mRNA expression in human peripheral blood mononuclear cells. Functional and Integrative Genomics, 2018, 18, 1-10.	3.5	12
27	The distribution and functional relevance analysis of runs of homozygosity (ROHs) in Chinese Han female population. Molecular Genetics and Genomics, 2018, 293, 197-206.	2.1	2
28	Correlation analyses revealed global microRNAâ€"mRNA expression associations in human peripheral blood mononuclear cells. Molecular Genetics and Genomics, 2018, 293, 95-105.	2.1	12
29	Integrative analysis identified mediation effects of lncRNAs on the correlations between methylation and mRNA. International Journal of Biochemistry and Cell Biology, 2018, 104, 66-72.	2.8	0
30	Detection of m^{6}A-associated SNPs as potential functional variants for coronary artery disease. Epigenomics, 2018, 10, 1279-1287.	2.1	41
31	Smoking modifies the effect of two independent SNPs rs5063 and rs198358 of NPPA on central obesity in the Chinese Han population. Journal of Genetics, 2018, 97, 987-994.	0.7	3
32	Plasma gelsolin is associated with hip BMD in Chinese postmenopausal women. PLoS ONE, 2018, 13, e0197732.	2.5	4
33	Genome-Wide Identification of N6-Methyladenosine (m6A) SNPs Associated With Rheumatoid Arthritis. Frontiers in Genetics, 2018, 9, 299.	2.3	39
34	Putative functional SNPs in SLC22A3 and H3F3B might influence the development of CAD by regulating the lipid levels. Thrombosis Research, 2018, 168, 37-39.	1.7	2
35	Identification and evaluation of lncRNA and mRNA integrative modules in human peripheral blood mononuclear cells. Epigenomics, 2017, 9, 943-954.	2.1	11
36	Detecting novel genes for low-density lipoprotein cholesterol in European population using bioinformatics analysis. Personalized Medicine, 2016, 13, 225-231.	1.5	4

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37	Identification of important genes associated with total cholesterol using bioinformatics analysis. Pharmacogenomics, 2016, 17, 219-230.	1.3	2
38	Gene-Based Genome-Wide Association Analysis in European and Asian Populations Identified Novel Genes for Rheumatoid Arthritis. PLoS ONE, 2016, 11, e0167212.	2.5	45
39	Integrated Analyses of Gene Expression Profiles Digs out Common Markers for Rheumatic Diseases. PLoS ONE, 2015, 10, e0137522.	2.5	18
40	Novel Genes Affecting Blood Pressure Detected Via Gene-Based Association Analysis. G3: Genes, Genomes, Genetics, 2015, 5, 1035-1042.	1.8	19
41	Functional relevance for multiple sclerosis-associated genetic variants. Immunogenetics, 2015, 67, 7-14.	2.4	9
42	Genome-wide association study in Chinese identifies novel loci for blood pressure and hypertension. Human Molecular Genetics, 2015, 24, 865-874.	2.9	157
43	Gene-Based Association Analysis Identified Novel Genes Associated with Bone Mineral Density. PLoS ONE, 2015, 10, e0121811.	2.5	27
44	Functional Analysis of Single-Nucleotide Polymorphisms in the Regulation of Coactivator-Associated Arginine Methyltransferase 1 Expression and Plasma Homocysteine Levels. Circulation: Cardiovascular Genetics, 2014, 7, 642-649.	5.1	3
45	Pharmacogenetics and pharmacogenomics for rheumatoid arthritis responsiveness to methotrexate treatment: the 2013 update. Pharmacogenomics, 2014, 15, 551-566.	1.3	53
46	Association of lipoprotein lipase polymorphism rs2197089 with serum lipid concentrations and LPL gene expression. Journal of Human Genetics, 2013, 58, 160-164.	2.3	5
47	Lipoprotein lipase gene polymorphism rs1059611 functionally influences serum lipid concentrations. Atherosclerosis, 2013, 229, 511-516.	0.8	11
48	Adiponectin Levels and Risk of Coronary Heart Disease: A Meta-analysis of Prospective Studies. American Journal of the Medical Sciences, 2013, 345, 455-461.	1.1	50
49	Association between polymorphisms in the adiponectin gene and cardiovascular disease: a meta-analysis. BMC Medical Genetics, 2012, 13, 40.	2.1	35
50	Genome-wide association study in Han Chinese identifies four new susceptibility loci for coronary artery disease. Nature Genetics, 2012, 44, 890-894.	21.4	295
51	Association between polymorphisms in the coagulation factor VII gene and coronary heart disease risk in different ethnicities: a meta-analysis. BMC Medical Genetics, 2011, 12, 107.	2.1	22
52	Association of peroxisome proliferatorâ€activated receptor gamma coactivator 1 alpha (<i>PPARGC1A</i>) gene polymorphisms and type 2 diabetes mellitus: a metaâ€analysis. Diabetes/Metabolism Research and Reviews, 2011, 27, 177-184.	4.0	34
53	PLA2G7 gene polymorphisms and coronary heart disease risk: A meta-analysis. Thrombosis Research, 2010, 126, 498-503.	1.7	24