

Xing-bo Mo

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

1,356
citations

430754

18
h-index

360920

35
g-index

54
all docs

54
docs citations

54
times ranked

3085
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association study in Han Chinese identifies four new susceptibility loci for coronary artery disease. <i>Nature Genetics</i> , 2012, 44, 890-894.	9.4	295
2	Genome-wide association study in Chinese identifies novel loci for blood pressure and hypertension. <i>Human Molecular Genetics</i> , 2015, 24, 865-874.	1.4	157
3	Rheumatoid arthritis-associated DNA methylation sites in peripheral blood mononuclear cells. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 36-42.	0.5	75
4	A polygenic risk score improves risk stratification of coronary artery disease: a large-scale prospective Chinese cohort study. <i>European Heart Journal</i> , 2022, 43, 1702-1711.	1.0	58
5	Pharmacogenetics and pharmacogenomics for rheumatoid arthritis responsiveness to methotrexate treatment: the 2013 update. <i>Pharmacogenomics</i> , 2014, 15, 551-566.	0.6	53
6	Adiponectin Levels and Risk of Coronary Heart Disease: A Meta-analysis of Prospective Studies. <i>American Journal of the Medical Sciences</i> , 2013, 345, 455-461.	0.4	50
7	Examination of the associations between m6A-associated single-nucleotide polymorphisms and blood pressure. <i>Hypertension Research</i> , 2019, 42, 1582-1589.	1.5	47
8	Gene-Based Genome-Wide Association Analysis in European and Asian Populations Identified Novel Genes for Rheumatoid Arthritis. <i>PLoS ONE</i> , 2016, 11, e0167212.	1.1	45
9	Detection of m ⁶ A-associated SNPs as potential functional variants for coronary artery disease. <i>Epigenomics</i> , 2018, 10, 1279-1287.	1.0	41
10	Genome-Wide Identification of N6-Methyladenosine (m6A) SNPs Associated With Rheumatoid Arthritis. <i>Frontiers in Genetics</i> , 2018, 9, 299.	1.1	39
11	Association between polymorphisms in the adiponectin gene and cardiovascular disease: a meta-analysis. <i>BMC Medical Genetics</i> , 2012, 13, 40.	2.1	35
12	Association of peroxisome proliferator-activated receptor gamma coactivator 1 alpha (<i>PPARGC1A</i>) gene polymorphisms and type 2 diabetes mellitus: a meta-analysis. <i>Diabetes/Metabolism Research and Reviews</i> , 2011, 27, 177-184.	1.7	34
13	Integrative analysis revealed potential causal genetic and epigenetic factors for multiple sclerosis. <i>Journal of Neurology</i> , 2019, 266, 2699-2709.	1.8	34
14	Gene-Based Association Analysis Identified Novel Genes Associated with Bone Mineral Density. <i>PLoS ONE</i> , 2015, 10, e0121811.	1.1	27
15	Identification of novel rheumatoid arthritis-associated MiRNA-204-5p from plasma exosomes. <i>Experimental and Molecular Medicine</i> , 2022, 54, 334-345.	3.2	27
16	PLA2G7 gene polymorphisms and coronary heart disease risk: A meta-analysis. <i>Thrombosis Research</i> , 2010, 126, 498-503.	0.8	24
17	Association of Plasma Irisin with Bone Mineral Density in a Large Chinese Population Using an Extreme Sampling Design. <i>Calcified Tissue International</i> , 2018, 103, 246-251.	1.5	23
18	Association between polymorphisms in the coagulation factor VII gene and coronary heart disease risk in different ethnicities: a meta-analysis. <i>BMC Medical Genetics</i> , 2011, 12, 107.	2.1	22

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19	Relative abundance of mature myostatin rather than total myostatin is negatively associated with bone mineral density in Chinese. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 1329-1336.	1.6	21
20	Novel Genes Affecting Blood Pressure Detected Via Gene-Based Association Analysis. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1035-1042.	0.8	19
21	Integrated Analyses of Gene Expression Profiles Digs out Common Markers for Rheumatic Diseases. <i>PLoS ONE</i> , 2015, 10, e0137522.	1.1	18
22	Mendelian randomization analysis revealed potential causal factors for systemic lupus erythematosus. <i>Immunology</i> , 2020, 159, 279-288.	2.0	18
23	Identification of PBMC-expressed miRNAs for rheumatoid arthritis. <i>Epigenetics</i> , 2020, 15, 386-397.	1.3	16
24	Integrative Analysis Identified IRF6 and NDST1 as Potential Causal Genes for Ischemic Stroke. <i>Frontiers in Neurology</i> , 2019, 10, 517.	1.1	13
25	Multiple correlation analyses revealed complex relationship between DNA methylation and mRNA expression in human peripheral blood mononuclear cells. <i>Functional and Integrative Genomics</i> , 2018, 18, 1-10.	1.4	12
26	Correlation analyses revealed global microRNA-mRNA expression associations in human peripheral blood mononuclear cells. <i>Molecular Genetics and Genomics</i> , 2018, 293, 95-105.	1.0	12
27	Lipoprotein lipase gene polymorphism rs1059611 functionally influences serum lipid concentrations. <i>Atherosclerosis</i> , 2013, 229, 511-516.	0.4	11
28	Identification and evaluation of lncRNA and mRNA integrative modules in human peripheral blood mononuclear cells. <i>Epigenomics</i> , 2017, 9, 943-954.	1.0	11
29	Integrative analysis identifies the association between CASZ1 methylation and ischemic stroke. <i>Neurology: Genetics</i> , 2020, 6, e509.	0.9	11
30	Multi-omics integrative analysis identified SNP-methylation-mRNA: Interaction in peripheral blood mononuclear cells. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 4601-4610.	1.6	10
31	Functional relevance for multiple sclerosis-associated genetic variants. <i>Immunogenetics</i> , 2015, 67, 7-14.	1.2	9
32	Detection of lncRNA-mRNA interaction modules by integrating eQTL with weighted gene co-expression network analysis. <i>Functional and Integrative Genomics</i> , 2019, 19, 217-225.	1.4	9
33	Integrative analysis highlighted susceptibility genes for rheumatoid arthritis. <i>International Immunopharmacology</i> , 2020, 86, 106716.	1.7	8
34	Epigenetically regulated co-expression network of genes significant for rheumatoid arthritis. <i>Epigenomics</i> , 2019, 11, 1601-1612.	1.0	7
35	Integrative lncRNA-mRNA co-expression network analysis identifies novel lncRNA E2F3-IT1 for rheumatoid arthritis. <i>Clinical and Translational Medicine</i> , 2021, 11, e325.	1.7	7
36	Associations between potentially functional CORIN SNPs and serum corin levels in the Chinese Han population. <i>BMC Genetics</i> , 2019, 20, 99.	2.7	6

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37	Integrative analysis identifies potential causal methylation-mRNA regulation chains for rheumatoid arthritis. <i>Molecular Immunology</i> , 2021, 131, 89-96.	1.0	6
38	Association of DNA Methylation in Blood Pressure-Related Genes With Ischemic Stroke Risk and Prognosis. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 796245.	1.1	6
39	Association of lipoprotein lipase polymorphism rs2197089 with serum lipid concentrations and LPL gene expression. <i>Journal of Human Genetics</i> , 2013, 58, 160-164.	1.1	5
40	Alteration of circulating microbiome and its associated regulation role in rheumatoid arthritis: Evidence from integration of multiomics data. <i>Clinical and Translational Medicine</i> , 2020, 10, e229.	1.7	5
41	Detecting novel genes for low-density lipoprotein cholesterol in European population using bioinformatics analysis. <i>Personalized Medicine</i> , 2016, 13, 225-231.	0.8	4
42	Plasma gelsolin is associated with hip BMD in Chinese postmenopausal women. <i>PLoS ONE</i> , 2018, 13, e0197732.	1.1	4
43	Functional Analysis of Single-Nucleotide Polymorphisms in the Regulation of Coactivator-Associated Arginine Methyltransferase 1 Expression and Plasma Homocysteine Levels. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 642-649.	5.1	3
44	Smoking modifies the effect of two independent SNPs rs5063 and rs198358 of NPPA on central obesity in the Chinese Han population. <i>Journal of Genetics</i> , 2018, 97, 987-994.	0.4	3
45	Integrative Analysis Confirmed the Association between Osteoprotegerin and Osteoporosis. <i>Chinese Medical Sciences Journal</i> , 2019, 34, 55.	0.2	3
46	Identification of important genes associated with total cholesterol using bioinformatics analysis. <i>Pharmacogenomics</i> , 2016, 17, 219-230.	0.6	2
47	The distribution and functional relevance analysis of runs of homozygosity (ROHs) in Chinese Han female population. <i>Molecular Genetics and Genomics</i> , 2018, 293, 197-206.	1.0	2
48	Putative functional SNPs in SLC22A3 and H3F3B might influence the development of CAD by regulating the lipid levels. <i>Thrombosis Research</i> , 2018, 168, 37-39.	0.8	2
49	SNPs rs10224002 in PRKAG2 may disturb gene expression and consequently affect hypertension. <i>Molecular Biology Reports</i> , 2019, 46, 1617-1624.	1.0	2
50	Protein array test detected three osteoporosis related plasma inflammatory cytokines in Chinese postmenopausal women. <i>Cytokine</i> , 2020, 133, 155166.	1.4	2
51	Promoter DNA Methylation in GWAS-Identified Genes as Potential Functional Elements for Blood Pressure: An Observational and Mendelian Randomization Study. <i>Frontiers in Genetics</i> , 2021, 12, 791146.	1.1	2
52	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. <i>Journal of Cardiovascular Pharmacology</i> , 2019, 73, 48-55.	0.8	1
53	Integrative analysis identified mediation effects of lncRNAs on the correlations between methylation and mRNA. <i>International Journal of Biochemistry and Cell Biology</i> , 2018, 104, 66-72.	1.2	0