Yan Guo

List of Publications by Year
in descending order

97 papers	3,062 citations	159585 30 h-index	182427 51 g-index
99 all docs	99 docs citations	99 times ranked	4700 citing authors

#	Article	IF	Citations
1	Improved Energy Storage Properties Achieved in (K, Na)NbO₃â€Based Relaxor Ferroelectric Ceramics via a Combinatorial Optimization Strategy. Advanced Functional Materials, 2022, 32, .	14.9	79
2	MetaDecoder: a novel method for clustering metagenomic contigs. Microbiome, 2022, 10, 46.	11.1	13
3	ExsgRNA: reduce off-target efficiency by on-target mismatched sgRNA. Briefings in Bioinformatics, 2022, 23, .	6.5	2
4	Detection of Haemophilus influenzae by loop-mediated isothermal amplification coupled with nanoparticle-based lateral flow biosensor assay. BMC Microbiology, 2022, 22, 123.	3.3	1
5	Individualized pathway activity algorithm identifies oncogenic pathways in pan-cancer analysis. EBioMedicine, 2022, 79, 104014.	6.1	7
6	Highâ€Temperature Flexible Nanocomposites with Ultraâ€High Energy Storage Density by Nanostructured MgO Fillers. Advanced Functional Materials, 2022, 32, .	14.9	41
7	LDBlockShow: a fast and convenient tool for visualizing linkage disequilibrium and haplotype blocks based on variant call format files. Briefings in Bioinformatics, 2021, 22, .	6.5	177
8	Transcriptome-wide association study identifies multiple genes associated with childhood body mass index. International Journal of Obesity, 2021, 45, 1105-1113.	3.4	11
9	Epigenetic Element-Based Transcriptome-Wide Association Study Identifies Novel Genes for Bipolar Disorder. Schizophrenia Bulletin, 2021, 47, 1642-1652.	4.3	8
10	Phenome-wide investigation of the causal associations between childhood BMI and adult trait outcomes: a two-sample Mendelian randomization study. Genome Medicine, 2021, 13, 48.	8.2	23
11	Enhancer-Gene Interaction Analyses Identified the Epidermal Growth Factor Receptor as a Susceptibility Gene for Type 2 Diabetes Mellitus. Diabetes and Metabolism Journal, 2021, 45, 241-250.	4.7	5
12	An Intronic Risk SNP rs12454712 for Central Obesity Acts As an Allele-Specific Enhancer To Regulate BCL2 Expression. Diabetes, 2021, 70, 1679-1688.	0.6	10
13	A transcriptome-wide association study identifies novel susceptibility genes for psoriasis. Human Molecular Genetics, 2021, 31, 300-308.	2.9	6
14	A Rapid Detection of Haemophilus influenzae Using Multiple Cross Displacement Amplification Linked With Nanoparticle-Based Lateral Flow Biosensor. Frontiers in Cellular and Infection Microbiology, 2021, 11, 721547.	3.9	4
15	A transcriptome-wide association study identifies susceptibility genes for Parkinsonâ€™s disease. Npj Parkinson's Disease, 2021, 7, 79.	5.3	32
16	Causal Associations Between Blood Lipids and COVID-19 Risk: A Two-Sample Mendelian Randomization Study. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 2802-2810.	2.4	15
17	DDRS: Detection of drug response SNPs specifically in patients receiving drug treatment. Computational and Structural Biotechnology Journal, 2021, 19, 3650-3657.	4.1	7
18	Transcriptome-wide association study identifies multiple genes and pathways associated with thyroid function. Human Molecular Genetics, 2021, , .	2.9	2

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19	An Allele-Specific Functional SNP Associated with Two Systemic Autoimmune Diseases Modulates IRF5 Expression by Long-Range Chromatin Loop Formation. Journal of Investigative Dermatology, 2020, 140, 348-360.e11.	0.7	25
20	Sexâ€specific SNPâ€SNP interaction analyses within topologically associated domains reveals ANGPT1 as a novel tumor suppressor gene for lung cancer. Genes Chromosomes and Cancer, 2020, 59, 13-22.	2.8	6
21	Transcription Factor Enrichment Analysis in Enhancers Identifies EZH2 as a Susceptibility Gene for Osteoporosis. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e1152-e1161.	3.6	3
22	Fibroblast growth factor receptor signaling as therapeutic targets in female reproductive system cancers. Journal of Cancer, 2020, 11, 7264-7275.	2.5	12
23	An integrative multi-omics network-based approach identifies key regulators for breast cancer. Computational and Structural Biotechnology Journal, 2020, 18, 2826-2835.	4.1	12
24	<scp>lncRNA</scp> Neat1 Stimulates Osteoclastogenesis Via Sponging <scp>miR</scp>â€. Journal of Bone and Mineral Research, 2020, 35, 1772-1781.	2.8	36
25	Multiomics dissection of molecular regulatory mechanisms underlying autoimmune-associated noncoding SNPs. JCI Insight, 2020, 5, .	5.0	13
26	An Osteoporosis Susceptibility Allele at 11p15 Regulates SOX6 Expression by Modulating TCF4 Chromatin Binding. Journal of Bone and Mineral Research, 2020, 37, 1147-1155.	2.8	4
27	The osteoporosis susceptible SNP rs4325274 remotely regulates the SOX6 gene through enhancers. Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji, 2020, 42, 889-897.	0.2	1
28	Addressing the Missing Heritability Problem With the Help of Regulatory Features. Evolutionary Bioinformatics, 2019, 15, 117693431986086.	1.2	0
29	Comprehensive functional annotation of susceptibility SNPs prioritized 10 genes for schizophrenia. Translational Psychiatry, 2019, 9, 56.	4.8	20
30	Comparative transcriptome analysis reveals potential evolutionary differences in adaptation of temperature and body shape among four Percidae species. PLoS ONE, 2019, 14, e0215933.	2.5	6
31	Integrating regulatory features data for prediction of functional disease-associated SNPs. Briefings in Bioinformatics, 2019, 20, 26-32.	6.5	11
32	Detecting epistasis within chromatin regulatory circuitry reveals CAND2 as a novel susceptibility gene for obesity. International Journal of Obesity, 2019, 43, 450-456.	3.4	4
33	Matrine suppresses cardiac fibrosis by inhibiting the TGFâ€Î²2/Smad pathway in experimental diabetic cardiomyopathy. Molecular Medicine Reports, 2018, 17, 1775-1781.	2.4	41
34	Association between fibroblast growth factor 21 and bone mineral density in adults. Endocrine, 2018, 59, 296-303.	2.3	21
35	An Osteoporosis Risk SNP at 1p36.12 Acts as an Allele-Specific Enhancer to Modulate LINC00339 Expression via Long-Range Loop Formation. American Journal of Human Genetics, 2018, 102, 776-793.	6.2	78
36	Multiple Functional Variants at 13q14 Risk Locus for Osteoporosis Regulate RANKL Expression Through Long-Range Super-Enhancer. Journal of Bone and Mineral Research, 2018, 33, 1335-1346.	2.8	38

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37	Runs of homozygosity associate with decreased risks of lung cancer in never-smoking East Asian females. Journal of Cancer, 2018, 9, 3858-3866.	2.5	1
38	Copy Number Variation. , 2018, , 43-54.		1
39	Matrine blocks AGEs- induced HCSMCs phenotypic conversion via suppressing Dll4-Notch pathway. European Journal of Pharmacology, 2018, 835, 126-131.	3.5	16
40	SNP-SNP interactions between WNT4 and WNT5A were associated with obesity related traits in Han Chinese Population. Scientific Reports, 2017, 7, 43939.	3.3	14
41	Regulatory element-based prediction identifies new susceptibility regulatory variants for osteoporosis. Human Genetics, 2017, 136, 963-974.	3.8	11
42	A functional SNP regulated by miR-196a-3p in the 3â€²UTR ofFGF2is associated with bone mineral density in the Chinese population. Human Mutation, 2017, 38, 725-735.	2.5	13
43	Matrineâ€Type Alkaloids Inhibit Advanced Glycation End Products Induced Reactive Oxygen Speciesâ€Mediated Apoptosis of Aortic Endothelial Cells In Vivo and In Vitro by Targeting MKK3 and p38MAPK Signaling. Journal of the American Heart Association, 2017, 6, .	3.7	26
44	Genetics association study and functional analysis on osteoporosis susceptibility gene BDNF. Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji, 2017, 39, 726-736.	0.2	5
45	Epigenomic data facilitate genetic studies for osteoporosis in post-GWAS era. Annals of Translational Medicine, 2017, 5, 93-93.	1.7	0
46	Replication of Caucasian Loci Associated with Osteoporosis-related Traits in East Asians. Journal of Bone Metabolism, 2016, 23, 233.	1.3	9
47	Identification of IDUA and WNT16 Phosphorylation-Related Non-Synonymous Polymorphisms for Bone Mineral Density in Meta-Analyses of Genome-Wide Association Studies. Journal of Bone and Mineral Research, 2016, 31, 358-368.	2.8	24
48	Associations of Plasma FGF2 Levels and Polymorphisms in the FGF2 Gene with Obesity Phenotypes in Han Chinese Population. Scientific Reports, 2016, 6, 19868.	3.3	19
49	Integrating Epigenomic Elements and GWASs Identifies BDNF Gene Affecting Bone Mineral Density and Osteoporotic Fracture Risk. Scientific Reports, 2016, 6, 30558.	3.3	29
50	FEN1 gene variants confer reduced risk of breast cancer in chinese women: A case-control study. Oncotarget, 2016, 7, 78110-78118.	1.8	12
51	Genome-Wide Survey of Runs of Homozygosity Identifies Recessive Loci for Bone Mineral Density in Caucasian and Chinese Populations. Journal of Bone and Mineral Research, 2015, 30, 2119-2126.	2.8	13
52	Genetic Analysis Identifies DDR2 as a Novel Gene Affecting Bone Mineral Density and Osteoporotic Fractures in Chinese Population. PLoS ONE, 2015, 10, e0117102.	2.5	6
53	Identification of a novelFGFRL1MicroRNA target site polymorphism for bone mineral density in meta-analyses of genome-wide association studies. Human Molecular Genetics, 2015, 24, 4710-4727.	2.9	22
54	DDR2 (discoidin domain receptor 2) suppresses osteoclastogenesis and is a potential therapeutic target in osteoporosis. Science Signaling, 2015, 8, ra31.	3.6	26

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55	Association analyses of FGFR2 gene polymorphisms with femoral neck bone mineral density in Chinese Han population. Molecular Genetics and Genomics, 2015, 290, 485-491.	2.1	5
56	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. Human Molecular Genetics, 2014, 23, 1923-1933.	2.9	130
57	Gene-gene interaction between RBMS3 and ZNF516 influences bone mineral density. Journal of Bone and Mineral Research, 2013, 28, 828-837.	2.8	21
58	Copy Number Variation on Chromosome 10q26.3 for Obesity Identified by a Genome-Wide Study. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E191-E195.	3.6	19
59	Suggestion of GLYAT gene underlying variation of bone size and body lean mass as revealed by a bivariate genome-wide association study. Human Genetics, 2013, 132, 189-199.	3.8	50
60	Comparative Study of Exome Copy Number Variation Estimation Tools Using Array Comparative Genomic Hybridization as Control. BioMed Research International, 2013, 2013, 1-7.	1.9	47
61	Meta-analysis identifies aMECOMgene as a novel predisposing factor of osteoporotic fracture. Journal of Medical Genetics, 2013, 50, 212-219.	3.2	30
62	Copy Number Variation. , 2013, , 123-132.		6
63	Genome-wide association study identifies HMGN3 locus for spine bone size variation in Chinese. Human Genetics, 2012, 131, 463-469.	3.8	6
64	Copy Number Variation in CNP267 Region May Be Associated with Hip Bone Size. PLoS ONE, 2011, 6, e22035.	2.5	5
65	The Fat Mass and Obesity Associated Gene, FTO, Is Also Associated with Osteoporosis Phenotypes. PLoS ONE, 2011, 6, e27312.	2.5	38
66	Mitochondria-Wide Association Study of Common Variants in Osteoporosis. Annals of Human Genetics, 2011, 75, 569-574.	0.8	33
67	Pathway-Based Association Analyses Identified TRAIL Pathway for Osteoporotic Fractures. PLoS ONE, 2011, 6, e21835.	2.5	14
68	IL21R and PTH may underlie variation of femoral neck bone mineral density as revealed by a genome-wide association study. Journal of Bone and Mineral Research, 2010, 25, 1042-1048.	2.8	36
69	Genome-wide association study for femoral neck bone geometry. Journal of Bone and Mineral Research, 2010, 25, 320-329.	2.8	43
70	Design and Interpretation of Linkage and Association Studies on Osteoporosis. Clinical Reviews in Bone and Mineral Metabolism, 2010, 8, 60-67.	0.8	0
71	Pathway-based genome-wide association analysis identified the importance of regulation-of-autophagy pathway for ultradistal radius BMD. Journal of Bone and Mineral Research, 2010, 25, 1572-1580.	2.8	103
72	HMGA2 Is Confirmed To Be Associated with Human Adult Height. Annals of Human Genetics, 2010, 74, 11-16.	0.8	32

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73	Molecular Genetic Studies of Gene Identification for Osteoporosis: The 2009 Update. Endocrine Reviews, 2010, 31, 447-505.	20.1	76
74	Genome-Wide Association Study Identifies ALDH7A1 as a Novel Susceptibility Gene for Osteoporosis. PLoS Genetics, 2010, 6, e1000806.	3.5	101
75	Runs of Homozygosity Identify a Recessive Locus 12q21.31 for Human Adult Height. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 3777-3782.	3.6	33
76	The regulation-of-autophagy pathway may influence Chinese stature variation: evidence from elder adults. Journal of Human Genetics, 2010, 55, 441-447.	2.3	20
77	Genome-wide association study identifies two novel loci containing FLNB and SBF2 genes underlying stature variation. Human Molecular Genetics, 2009, 18, 1661-1669.	2.9	27
78	Genome-wide association study suggested copy number variation may be associated with body mass index in the Chinese population. Journal of Human Genetics, 2009, 54, 199-202.	2.3	78
79	Powerful Bivariate Genome-Wide Association Analyses Suggest the SOX6 Gene Influencing Both Obesity and Osteoporosis Phenotypes in Males. PLoS ONE, 2009, 4, e6827.	2.5	87
80	Genome-wide association scan for stature in Chinese: evidence for ethnic specific loci. Human Genetics, 2009, 125, 1-9.	3.8	39
81	Association Analyses of RANKL/RANK/OPG Gene Polymorphisms with Femoral Neck Compression Strength Index Variation in Caucasians. Calcified Tissue International, 2009, 85, 104-112.	3.1	38
82	Genome-wide Association and Follow-Up Replication Studies Identified ADAMTS18 and TGFBR3 as Bone Mass Candidate Genes in Different Ethnic Groups. American Journal of Human Genetics, 2009, 84, 388-398.	6.2	187
83	Genome-wide Association and Replication Studies Identified TRHR as an Important Gene for Lean Body Mass. American Journal of Human Genetics, 2009, 84, 418-423.	6.2	103
84	Whole Genome Distribution and Ethnic Differentiation of Copy Number Variation in Caucasian and Asian Populations. PLoS ONE, 2009, 4, e7958.	2.5	51
85	Sex-Specific Association of the Glucocorticoid Receptor Gene With Extreme BMD. Journal of Bone and Mineral Research, 2008, 23, 247-252.	2.8	15
86	Chromosomal regions 22q13 and 3p25 may harbor quantitative trait loci influencing both age at menarche and bone mineral density. Human Genetics, 2008, 123, 419-427.	3.8	19
87	Genome-wide Copy-Number-Variation Study Identified a Susceptibility Gene, UGT2B17, for Osteoporosis. American Journal of Human Genetics, 2008, 83, 663-674.	6.2	209
88	Comprehensive association analyses of IGF1, ESR2, and CYP17 genes with adult height in Caucasians. European Journal of Human Genetics, 2008, 16, 1380-1387.	2.8	13
89	Molecular genetic studies of gene identification for osteoporosis. Expert Review of Endocrinology and Metabolism, 2008, 3, 223-267.	2.4	5
90	Polymorphisms in the estrogen receptor genes are associated with hip fractures in Chinese. Bone, 2008, 43, 910-914.	2.9	23

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91	Polymorphism in the insulin-like growth factor 1 gene is associated with age at menarche in caucasian females. Human Reproduction, 2007, 22, 1789-1794.	0.9	43
92	The chemokine (C-C-motif) receptor 3 (CCR3) gene is linked and associated with age at menarche in Caucasian females. Human Genetics, 2007, 121, 35-42.	3.8	16
93	Genomic Regions Identified for BMD in a Large Sample Including Epistatic Interactions and Gender-Specific Effects. Journal of Bone and Mineral Research, 2006, 21, 1536-1544.	2.8	49
94	Robust and Comprehensive Analysis of 20 Osteoporosis Candidate Genes by Very High-Density Single-Nucleotide Polymorphism Screen Among 405 White Nuclear Families Identified Significant Association and Geneâ€“Gene Interaction. Journal of Bone and Mineral Research, 2006, 21, 1678-1695.	2.8	85
95	Association analyses of CYP19 gene polymorphisms with height variation in a large sample of Caucasian nuclear families. Human Genetics, 2006, 120, 119-125.	3.8	9
96	Genomewide Linkage Scan for Quantitative Trait Loci Underlying Variation in Age at Menarche. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 1009-1014.	3.6	49
97	Polymorphisms of estrogen-biosynthesis genes CYP17 and CYP19 may influence age at menarche: a genetic association study in Caucasian females. Human Molecular Genetics, 2006, 15, 2401-2408.	2.9	47