Hong-Wen Deng

List of Publications by Year
in descending order

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411 papers	13,594 citations	27035 58 h-index	49824 91 g-index
413 all docs	413 docs citations	413 times ranked	18104 citing authors

#	Article	IF	Citations
1	Relationship of Obesity with Osteoporosis. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 1640-1646.	1.8	494
2	Correlation of Obesity and Osteoporosis: Effect of Fat Mass on the Determination of Osteoporosis. Journal of Bone and Mineral Research, 2008, 23, 17-29.	3.1	408
3	Wnt/Î²-catenin signaling activates bone morphogenetic protein 2 expression in osteoblasts. Bone, 2013, 52, 145-156.	1.4	243
4	Genome-wide Copy-Number-Variation Study Identified a Susceptibility Gene, UGT2B17, for Osteoporosis. American Journal of Human Genetics, 2008, 83, 663-674.	2.6	209
5	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.	2.6	187
6	Genome-wide association scans identified CTNNBL1 as a novel gene for obesity. Human Molecular Genetics, 2008, 17, 1803-1813.	1.4	168
7	Genetic Determination of Colles' Fracture and Differential Bone Mass in Women With and Without Colles' Fracture. Journal of Bone and Mineral Research, 2000, 15, 1243-1252.	3.1	151
8	A Genomewide Linkage Scan for Quantitative-Trait Loci for Obesity Phenotypes. American Journal of Human Genetics, 2002, 70, 1138-1151.	2.6	151
9	Meta-Analysis of Genome-Wide Scans Provides Evidence for Sex- and Site-Specific Regulation of Bone Mass. Journal of Bone and Mineral Research, 2006, 22, 173-183.	3.1	144
10	Mutation Patterns at Dinucleotide Microsatellite Loci in Humans. American Journal of Human Genetics, 2002, 70, 625-634.	2.6	141
11	Metaâ€Analysis of Genomeâ€wide Linkage Studies in BMI and Obesity. Obesity, 2007, 15, 2263-2275.	1.5	138
12	Comparative Studies of Copy Number Variation Detection Methods for Next-Generation Sequencing Technologies. PLoS ONE, 2013, 8, e59128.	1.1	138
13	Genome Partitioning of Genetic Variation for Height from 11,214 Sibling Pairs. American Journal of Human Genetics, 2007, 81, 1104-1110.	2.6	135
14	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. Human Molecular Genetics, 2014, 23, 1923-1933.	1.4	130
15	A Whole-Genome Linkage Scan Suggests Several Genomic Regions Potentially Containing Quantitative Trait Loci for Osteoporosis. Journal of Clinical Endocrinology and Metabolism, 2002, 87, 5151-5159.	1.8	129
16	Relevance of the genes for bone mass variation to susceptibility to osteoporotic fractures and its implications to gene search for complex human diseases. Genetic Epidemiology, 2002, 22, 12-25.	0.6	121
17	A Novel Pathophysiological Mechanism for Osteoporosis Suggested by an in Vivo Gene Expression Study of Circulating Monocytes. Journal of Biological Chemistry, 2005, 280, 29011-29016.	1.6	118
18	Analyses and Comparison of Accuracy of Different Genotype Imputation Methods. PLoS ONE, 2008, 3, e3551.	1.1	117

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19	Mutant ZP1 in Familial Infertility. New England Journal of Medicine, 2014, 370, 1220-1226.	13.9	114
20	Population Admixture May Appear to Mask, Change or Reverse Genetic Effects of Genes Underlying Complex Traits. Genetics, 2001, 159, 1319-1323.	1.2	113
21	Tests of Linkage and/or Association of Genes for Vitamin D Receptor, Osteocalcin, and Parathyroid Hormone With Bone Mineral Density. Journal of Bone and Mineral Research, 2002, 17, 678-686.	3.1	109
22	Comparative studies of de novo assembly tools for next-generation sequencing technologies. Bioinformatics, 2011, 27, 2031-2037.	1.8	109
23	An Amplified Fragment Length Polymorphism Map of the Silkworm. Genetics, 2001, 157, 1277-1284.	1.2	108
24	Polymorphisms of the low-density lipoprotein receptor-related protein 5 (LRP5) gene are associated with obesity phenotypes in a large family-based association study. Journal of Medical Genetics, 2006, 43, 798-803.	1.5	106
25	Genome-Wide Association Study of Exercise Behavior in Dutch and American Adults. Medicine and Science in Sports and Exercise, 2009, 41, 1887-1895.	0.2	105
26	Population Admixture: Detection by Hardy-Weinberg Test and Its Quantitative Effects on Linkage-Disequilibrium Methods for Localizing Genes Underlying Complex Traits. Genetics, 2001, 157, 885-897.	1.2	105
27	Molecular Genetic Studies of Gene Identification for Osteoporosis: A 2004 Update. Journal of Bone and Mineral Research, 2005, 21, 1511-1535.	3.1	104
28	Genome-Wide Association Study of Alcohol Dependence Implicates KIAA0040 on Chromosome 1q. Neuropsychopharmacology, 2012, 37, 557-566.	2.8	104
29	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.	2.6	103
30	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.	3.1	103
31	Role of Genetics in Osteoporosis. Endocrine, 2002, 17, 55-66.	2.2	101
32	Genome-Wide Association Study Identifies ALDH7A1 as a Novel Susceptibility Gene for Osteoporosis. PLoS Genetics, 2010, 6, e1000806.	1.5	101
33	ALDH2 is associated to alcohol dependence and is the major genetic determinant of â€œdaily maximum drinksâ€• in a GWAS study of an isolated rural chinese sample. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 103-110.	1.1	101
34	Determination of bone mineral density of the hip and spine in human pedigrees by genetic and life-style factors. Genetic Epidemiology, 2000, 19, 160-177.	0.6	96
35	Meta-analysis suggests that smoking is associated with an increased risk of early natural menopause. Menopause, 2012, 19, 126-132.	0.8	96
36	A general and accurate approach for computing the statistical power of the transmission disequilibrium test for complex disease genes. Genetic Epidemiology, 2001, 21, 53-67.	0.6	91

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37	Group sparse canonical correlation analysis for genomic data integration. BMC Bioinformatics, 2013, 14, 245.	1.2	91
38	Bivariate association analyses for the mixture of continuous and binary traits with the use of extended generalized estimating equations. Genetic Epidemiology, 2009, 33, 217-227.	0.6	89
39	Molecular genetic studies of gene identification for sarcopenia. Human Genetics, 2012, 131, 1-31.	1.8	88
40	Association of VDR and Estrogen Receptor Genotypes with Bone Mass in Postmenopausal Caucasian Women: Different Conclusions with Different Analyses and the Implications. Osteoporosis International, 1999, 9, 499-507.	1.3	87
41	Hotelling's T2 multivariate profiling for detecting differential expression in microarrays. Bioinformatics, 2005, 21, 3105-3113.	1.8	87
42	Powerful Bivariate Genome-Wide Association Analyses Suggest the SOX6 Gene Influencing Both Obesity and Osteoporosis Phenotypes in Males. PLoS ONE, 2009, 4, e6827.	1.1	87
43	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 Gene-Gene Interaction. Journal of Bone and Mineral Research, 2006, 21, 1678-1695.	3.1	85
44	Association of Estrogen Receptor-Î± Genotypes with Body Mass Index in Normal Healthy Postmenopausal Caucasian Women1. Journal of Clinical Endocrinology and Metabolism, 2000, 85, 2748-2751.	1.8	84
45	Polymorphisms in predicted miRNA binding sites and osteoporosis. Journal of Bone and Mineral Research, 2011, 26, 72-78.	3.1	84
46	Searching for osteoporosis genes in the post-genome era: progress and challenges. Osteoporosis International, 2003, 14, 701-715.	1.3	81
47	Gene selection for classification of microarray data based on the Bayes error. BMC Bioinformatics, 2007, 8, 370.	1.2	79
48	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.	1.1	78
49	Differences in bone mineral density, bone mineral content, and bone areal size in fracturing and non-fracturing women, and their interrelationships at the spine and hip. Journal of Bone and Mineral Metabolism, 2002, 20, 358-366.	1.3	76
50	Molecular Genetic Studies of Gene Identification for Osteoporosis: The 2009 Update. Endocrine Reviews, 2010, 31, 447-505.	8.9	76
51	Meta-analysis of genome-wide association data identifies novel susceptibility loci for obesity. Human Molecular Genetics, 2014, 23, 820-830.	1.4	73
52	In Vivo Genome-Wide Expression Study on Human Circulating B Cells Suggests a Novel ESR1 and MAPK3 Network for Postmenopausal Osteoporosis. Journal of Bone and Mineral Research, 2008, 23, 644-654.	3.1	70
53	Transcriptional Regulation of BMP2 Expression by the PTH-CREB Signaling Pathway in Osteoblasts. PLoS ONE, 2011, 6, e20780.	1.1	67
54	DNA methylation levels of CYP2R1 and CYP24A1 predict vitamin D response variation. Journal of Steroid Biochemistry and Molecular Biology, 2014, 144, 207-214.	1.2	67

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55	Composition of gut microbiota in infants in China and global comparison. Scientific Reports, 2016, 6, 36666.	1.6	63
56	QTL Fine Mapping by Measuring and Testing for Hardy-Weinberg and Linkage Disequilibrium at a Series of Linked Marker Loci in Extreme Samples of Populations. American Journal of Human Genetics, 2000, 66, 1027-1045.	2.6	62
57	Nonreplication in Genetic Studies of Complex Diseases-Lessons Learned From Studies of Osteoporosis and Tentative Remedies. Journal of Bone and Mineral Research, 2004, 20, 365-376.	3.1	62
58	Biological Pathwayâ€Based Genomeâ€Wide Association Analysis Identified the Vasoactive Intestinal Peptide (VIP) Pathway Important for Obesity. Obesity, 2010, 18, 2339-2346.	1.5	62
59	Comprehensive Characterization of Human Genome Variation by High Coverage Whole-Genome Sequencing of Forty Four Caucasians. PLoS ONE, 2013, 8, e59494.	1.1	62
60	Toward High-Throughput Genotyping: Dynamic and Automatic Software for Manipulating Large-Scale Genotype Data Using Fluorescently Labeled Dinucleotide Markers. Genome Research, 2001, 11, 1304-1314.	2.4	61
61	A whole-genome linkage scan suggests several genomic regions potentially containing QTLs underlying the variation of stature. American Journal of Medical Genetics Part A, 2002, 113, 29-39.	2.4	60
62	The Imprinted Gene Neuronatin Is Regulated by Metabolic Status and Associated With Obesity. Obesity, 2010, 18, 1289-1296.	1.5	60
63	Genome-Wide Association Analyses Identify SPOCK as a Key Novel Gene Underlying Age at Menarche. PLoS Genetics, 2009, 5, e1000420.	1.5	59
64	Genome-wide Association Studies for Osteoporosis: A 2013 Update. Journal of Bone Metabolism, 2014, 21, 99.	0.5	57
65	A Review of Integrative Imputation for Multi-Omics Datasets. Frontiers in Genetics, 2020, 11, 570255.	1.1	57
66	Identification of PLCL1 Gene for Hip Bone Size Variation in Females in a Genome-Wide Association Study. PLoS ONE, 2008, 3, e3160.	1.1	57
67	Replication of 6 Obesity Genes in a Meta-Analysis of Genome-Wide Association Studies from Diverse Ancestries. PLoS ONE, 2014, 9, e96149.	1.1	56
68	NeuroPred-FRL: an interpretable prediction model for identifying neuropeptide using feature representation learning. Briefings in Bioinformatics, 2021, 22, .	3.2	56
69	Linkage and association analyses of the UCP3 gene with obesity phenotypes in Caucasian families. Physiological Genomics, 2005, 22, 197-203.	1.0	54
70	Peripheral Blood Monocyte-expressed ANXA2 Gene is Involved in Pathogenesis of Osteoporosis in Humans. Molecular and Cellular Proteomics, 2011, 10, M111.011700.	2.5	54
71	Involvement of the Skeletal Renin-Angiotensin System in Age-Related Osteoporosis of Ageing Mice. Bioscience, Biotechnology and Biochemistry, 2012, 76, 1367-1371.	0.6	54
72	Gene expression profiling in monocytes and SNP association suggest the importance of the STAT1 gene for osteoporosis in both Chinese and Caucasians. Journal of Bone and Mineral Research, 2010, 25, 339-355.	3.1	53

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73	Polymorphisms of four bone mineral density candidate genes in Chinese populations and comparison with other populations of different ethnicity. Journal of Bone and Mineral Metabolism, 2003, 21, 34-42.	1.3	51
74	Integrative Analysis of Genomics and Transcriptome Data to Identify Potential Functional Genes of BMDs in Females. Journal of Bone and Mineral Research, 2016, 31, 1041-1049.	3.1	51
75	Whole Genome Distribution and Ethnic Differentiation of Copy Number Variation in Caucasian and Asian Populations. PLoS ONE, 2009, 4, e7958.	1.1	51
76	Accurate recognition of colorectal cancer with semi-supervised deep learning on pathological images. Nature Communications, 2021, 12, 6311.	5.8	51
77	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.	1.8	50
78	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.	3.1	49
79	Genomewide Linkage Scan for Quantitative Trait Loci Underlying Variation in Age at Menarche. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 1009-1014.	1.8	49
80	Human gut microbiome impacts skeletal muscle mass via gut microbial synthesis of the shortâ€chain fatty acid butyrate among healthy menopausal women. Journal of Cachexia, Sarcopenia and Muscle, 2021, 12, 1860-1870.	2.9	48
81	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.	1.4	47
82	Genetics of Bone Mineral Density: Evidence for a Major Pleiotropic Effect From an Intercontinental Study. Journal of Bone and Mineral Research, 2004, 19, 914-923.	3.1	46
83	A Bivariate Whole-Genome Linkage Scan Suggests Several Shared Genomic Regions for Obesity and Osteoporosis. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 2751-2757.	1.8	46
84	Proteomic analysis of circulating monocytes in Chinese premenopausal females with extremely discordant bone mineral density. Proteomics, 2008, 8, 4259-4272.	1.3	46
85	Bayesian Mapping of Quantitative Trait Loci for Multiple Complex Traits with the Use of Variance Components. American Journal of Human Genetics, 2007, 81, 304-320.	2.6	45
86	Genetic determination and correlation of body mass index and bone mineral density at the spine and hip in Chinese Han ethnicity. Osteoporosis International, 2006, 17, 119-124.	1.3	44
87	Impaired osteoblast function in GPRC6A null mice. Journal of Bone and Mineral Research, 2010, 25, 1092-1102.	3.1	44
88	An in vivo genome wide gene expression study of circulating monocytes suggested GBP1, STAT1 and CXCL10 as novel risk genes for the differentiation of peak bone mass. Bone, 2009, 44, 1010-1014.	1.4	44
89	Evaluation of Compressive Strength Index of the Femoral Neck in Caucasians and Chinese. Calcified Tissue International, 2010, 87, 324-332.	1.5	44
90	Factors Predicting Vitamin D Response Variation in Non-Hispanic White Postmenopausal Women. Journal of Clinical Endocrinology and Metabolism, 2012, 97, 2699-2705.	1.8	44

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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.	0.4	43
92	Genome-wide association study for femoral neck bone geometry. Journal of Bone and Mineral Research, 2010, 25, 320-329.	3.1	43
93	Is Replication the Gold Standard for Validating Genome-Wide Association Findings?. PLoS ONE, 2008, 3, e4037.	1.1	43
94	Genome-wide copy number variation study and gene expression analysis identify ABI3BP as a susceptibility gene for Kashinâ€“Beck disease. Human Genetics, 2014, 133, 793-799.	1.8	42
95	Receiver-operating characteristic analyses of body mass index, waist circumference and waist-to-hip ratio for obesity: Screening in young adults in central south of China. Clinical Nutrition, 2006, 25, 1030-1039.	2.3	41
96	Genome-Wide Scan Identified QTLs Underlying Femoral Neck Cross-Sectional Geometry That Are Novel Studied Risk Factors of Osteoporosis. Journal of Bone and Mineral Research, 2005, 21, 424-437.	3.1	40
97	Networkâ€based proteomic analysis for postmenopausal osteoporosis in Caucasian females. Proteomics, 2016, 16, 12-28.	1.3	40
98	Novel common variants associated with body mass index and coronary artery disease detected using a pleiotropic cFDR method. Journal of Molecular and Cellular Cardiology, 2017, 112, 1-7.	0.9	40
99	Linking Alzheimer's disease and type 2 diabetes: Novel shared susceptibility genes detected by cFDR approach. Journal of the Neurological Sciences, 2017, 380, 262-272.	0.3	40
100	Deepm5C: A deep-learning-based hybrid framework for identifying human RNA N5-methylcytosine sites using a stacking strategy. Molecular Therapy, 2022, 30, 2856-2867.	3.7	40
101	Genome-wide association scan for stature in Chinese: evidence for ethnic specific loci. Human Genetics, 2009, 125, 1-9.	1.8	39
102	Genomeâ€Wide Significant Association Signals in <scp>IPO</scp>11â€<scp>HTR</scp>1<scp>A</scp> Region Specific for Alcohol and Nicotine Codependence. Alcoholism: Clinical and Experimental Research, 2013, 37, 730-739.	1.4	39
103	Effect of short-term room temperature storage on the microbial community in infant fecal samples. Scientific Reports, 2016, 6, 26648.	1.6	39
104	Identification of Novel Potentially Pleiotropic Variants Associated With Osteoporosis and Obesity Using the cFDR Method. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 125-138.	1.8	39
105	Age at menarche and osteoporosis: A Mendelian randomization study. Bone, 2018, 117, 91-97.	1.4	39
106	Single-cell RNA sequencing deconvolutes the in vivo heterogeneity of human bone marrow-derived mesenchymal stem cells. International Journal of Biological Sciences, 2021, 17, 4192-4206.	2.6	39
107	Predictive factors for age at menopause in Caucasian females. Maturitas, 2006, 54, 19-26.	1.0	38
108	Association Analyses of RANKL/RANK/OPG Gene Polymorphisms with Femoral Neck Compression Strength Index Variation in Caucasians. Calcified Tissue International, 2009, 85, 104-112.	1.5	38

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109	The Fat Mass and Obesity Associated Gene, FTO, Is Also Associated with Osteoporosis Phenotypes. PLoS ONE, 2011, 6, e27312.	1.1	38
110	CNV-TV: A robust method to discover copy number variation from short sequencing reads. BMC Bioinformatics, 2013, 14, 150.	1.2	38
111	Low-DensityLipoprotein Receptor-Related Protein 5(LRP5) Gene Polymorphisms Are Associated With Bone Mass in Both Chinese and Whites. Journal of Bone and Mineral Research, 2007, 22, 385-393.	3.1	37
112	Is Population Bone Mineral Density Variation Linked to the Marker D11S987 On Chromosome 11q12â€“13?. Journal of Clinical Endocrinology and Metabolism, 2001, 86, 3735-3741.	1.8	36
113	Estrogen Receptor Î± Gene Polymorphisms and Peak Bone Density in Chinese Nuclear Families. Journal of Bone and Mineral Research, 2003, 18, 1028-1035.	3.1	36
114	Several genomic regions potentially containing QTLs for bone size variation were identified in a whole-genome linkage scan. American Journal of Medical Genetics Part A, 2003, 119A, 121-131.	2.4	36
115	Genetic and Environmental Correlations between Bone Geometric Parameters and Body Compositions. Calcified Tissue International, 2006, 79, 43-49.	1.5	36
116	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.	3.1	36
117	Comparison of Population-Based Association Study Methods Correcting for Population Stratification. PLoS ONE, 2008, 3, e3392.	1.1	35
118	Tests of Association for Quantitative Traits in Nuclear Families Using Principal Components to Correct for Population Stratification. Annals of Human Genetics, 2009, 73, 601-613.	0.3	35
119	Effects of vibration therapy on muscle mass, muscle strength and physical function in older adults with sarcopenia: a systematic review and meta-analysis. European Review of Aging and Physical Activity, 2020, 17, 14.	1.3	35
120	Bone mineral density in elderly Chinese: effects of age, sex, weight, height, and body mass index. Journal of Bone and Mineral Metabolism, 2004, 22, 71-78.	1.3	34
121	SNPP: automating large-scale SNP genotype data management. Bioinformatics, 2005, 21, 266-268.	1.8	34
122	Analyses and Comparison of Imputation-Based Association Methods. PLoS ONE, 2010, 5, e10827.	1.1	34
123	Assessment of Genetic Linkage and Parent-of-Origin Effects on Obesity. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 4001-4005.	1.8	33
124	Runs of Homozygosity Identify a Recessive Locus 12q21.31 for Human Adult Height. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 3777-3782.	1.8	33
125	Mitochondria-Wide Association Study of Common Variants in Osteoporosis. Annals of Human Genetics, 2011, 75, 569-574.	0.3	33
126	Genomeâ€wide search for replicable risk gene regions in alcohol and nicotine coâ€dependence. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 437-444.	1.1	33

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127	Tests of linkage and/or association of the LEPR gene polymorphisms with obesity phenotypes in Caucasian nuclear families. Physiological Genomics, 2004, 17, 101-106.	1.0	32
128	A new permutation strategy of pathway-based approach for genome-wide association study. BMC Bioinformatics, 2009, 10, 429.	1.2	32
129	HMGA2 Is Confirmed To Be Associated with Human Adult Height. Annals of Human Genetics, 2010, 74, 11-16.	0.3	32
130	Quantitative trait loci, genes, and polymorphisms that regulate bone mineral density in mouse. Genomics, 2009, 93, 401-414.	1.3	31
131	Current limitations of SNP data from the public domain for studies of complex disorders: a test for ten candidate genes for obesity and osteoporosis. BMC Genetics, 2004, 5, 4.	2.7	30
132	Genetic Dissection of Human Stature in a Large Sample of Multiplex Pedigrees. Annals of Human Genetics, 2004, 68, 472-488.	0.3	30
133	A polymorphism of apolipoprotein E (APOE) gene is associated with age at natural menopause in Caucasian females. Maturitas, 2009, 62, 37-41.	1.0	30
134	Genetic Association Study of Common Mitochondrial Variants on Body Fat Mass. PLoS ONE, 2011, 6, e21595.	1.1	30
135	An integrative study ascertained SOD2 as a susceptibility gene for osteoporosis in Chinese. Journal of Bone and Mineral Research, 2011, 26, 2695-2701.	3.1	30
136	Genome-wide association study of copy number variation identified gremlin1 as a candidate gene for lean body mass. Journal of Human Genetics, 2012, 57, 33-37.	1.1	30
137	Rare ADH Variant Constellations are Specific for Alcohol Dependence. Alcohol and Alcoholism, 2013, 48, 9-14.	0.9	30
138	Meta-analysis identifies aMECOMgene as a novel predisposing factor of osteoporotic fracture. Journal of Medical Genetics, 2013, 50, 212-219.	1.5	30
139	On individual genome-wide association studies and their meta-analysis. Human Genetics, 2014, 133, 265-279.	1.8	30
140	A Follow-Up Linkage Study for Quantitative Trait Loci Contributing to Obesity-Related Phenotypes. Journal of Clinical Endocrinology and Metabolism, 2004, 89, 875-882.	1.8	29
141	Univariate/Multivariate Genome-Wide Association Scans Using Data from Families and Unrelated Samples. PLoS ONE, 2009, 4, e6502.	1.1	29
142	Brief Report: Genomeâ€Wide Association Study Identifies ITPR2 as a Susceptibility Gene for Kashinâ€Beck Disease in Han Chinese. Arthritis and Rheumatology, 2015, 67, 176-181.	2.9	29
143	Integrating Epigenomic Elements and GWASs Identifies BDNF Gene Affecting Bone Mineral Density and Osteoporotic Fracture Risk. Scientific Reports, 2016, 6, 30558.	1.6	29
144	An integrative imputation method based on multi-omics datasets. BMC Bioinformatics, 2016, 17, 247.	1.2	29

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145	Integration of summary data from GWAS and eQTL studies identified novel causal BMD genes with functional predictions. Bone, 2018, 113, 41-48.	1.4	29
146	Patterns of linkage disequilibrium and haplotype distribution in disease candidate genes. BMC Genetics, 2004, 5, 11.	2.7	28
147	Genetic linkage of human height is confirmed to 9q22 and Xq24. Human Genetics, 2006, 119, 295-304.	1.8	28
148	SNP rs6265 Regulates Protein Phosphorylation and Osteoblast Differentiation and Influences BMD in Humans. Journal of Bone and Mineral Research, 2013, 28, 2498-2507.	3.1	28
149	Genome-wide association study identifies two novel loci containing FLNB and SBF2 genes underlying stature variation. Human Molecular Genetics, 2009, 18, 1661-1669.	1.4	27
150	FISH: fast and accurate diploid genotype imputation via segmental hidden Markov model. Bioinformatics, 2014, 30, 1876-1883.	1.8	27
151	Causal Effects of Genetically Predicted Cardiovascular Risk Factors on Chronic Kidney Disease: A Two-Sample Mendelian Randomization Study. Frontiers in Genetics, 2019, 10, 415.	1.1	27
152	High heritability of bone size at the hip and spine in Chinese. Journal of Human Genetics, 2004, 49, 87-91.	1.1	26
153	Bivariate Whole Genome Linkage Analysis for Femoral Neck Geometric Parameters and Total Body Lean Mass. Journal of Bone and Mineral Research, 2007, 22, 808-816.	3.1	26
154	Attenuated Monocyte Apoptosis, a New Mechanism for Osteoporosis Suggested by a Transcriptome-Wide Expression Study of Monocytes. PLoS ONE, 2015, 10, e0116792.	1.1	26
155	Linkage and association of the CA repeat polymorphism of the IL6 gene, obesity-related phenotypes, and bone mineral density (BMD) in two independent Caucasian populations. Journal of Human Genetics, 2003, 48, 430-437.	1.1	25
156	Association and haplotype analyses of the COL1A2 and ER-Î± gene polymorphisms with bone size and height in Chinese. Bone, 2005, 36, 533-541.	1.4	25
157	The MTHFR gene polymorphism is associated with lean body mass but not fat body mass. Human Genetics, 2008, 123, 189-196.	1.8	25
158	Association analyses suggest multiple interaction effects of the methylenetetrahydrofolate reductase polymorphisms on timing of menarche and natural menopause in white women. Menopause, 2010, 17, 185-190.	0.8	25
159	Integrative Analysis of Transcriptomic and Epigenomic Data to Reveal Regulation Patterns for BMD Variation. PLoS ONE, 2015, 10, e0138524.	1.1	25
160	Structure and Molecular Phylogeny of sasA Genes in Cyanobacteria: Insights into Evolution of the Prokaryotic Circadian System. Molecular Biology and Evolution, 2004, 21, 1468-1476.	3.5	24
161	Association analysis of estrogen receptor Î± gene polymorphisms with cross-sectional geometry of the femoral neck in Caucasian nuclear families. Osteoporosis International, 2005, 16, 2113-2122.	1.3	24
162	Classification of Multicolor Fluorescence In Situ Hybridization (M-FISH) Images With Sparse Representation. IEEE Transactions on Nanobioscience, 2012, 11, 111-118.	2.2	24

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163	Bivariate Genome-Wide Association Study ImplicatesATP6V1G1as a Novel Pleiotropic Locus Underlying Osteoporosis and Age at Menarche. Journal of Clinical Endocrinology and Metabolism, 2015, 100, E1457-E1466.	1.8	24
164	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.	3.1	24
165	Multi-omics research in sarcopenia: Current progress and future prospects. Ageing Research Reviews, 2022, 76, 101576.	5.0	24
166	The power of the transmission disequilibrium test (TDT) with both caseâ€“parent and controlâ€“parent trios. Genetical Research, 2001, 78, 289-302.	0.3	23
167	A major gene model of adult height is suggested in Chinese. Journal of Human Genetics, 2004, 49, 148-153.	1.1	23
168	Mapping Quantitative Trait Loci for Cross-Sectional Geometry at the Femoral Neck. Journal of Bone and Mineral Research, 2005, 20, 1973-1982.	3.1	23
169	Polymorphisms in the estrogen receptor genes are associated with hip fractures in Chinese. Bone, 2008, 43, 910-914.	1.4	23
170	Identifying Gene Interaction Enrichment for Gene Expression Data. PLoS ONE, 2009, 4, e8064.	1.1	23
171	Early molecular responses of bone to obstructive nephropathy induced by unilateral ureteral obstruction in mice. Nephrology, 2012, 17, 767-773.	0.7	23
172	Significant association between body composition phenotypes and the osteocalcin genomic region in normative human population. Bone, 2012, 51, 688-694.	1.4	23
173	Genome-wide approaches for identifying genetic risk factors for osteoporosis. Genome Medicine, 2013, 5, 44.	3.6	23
174	Integrative analysis of multiple diverse omics datasets by sparse group multitask regression. Frontiers in Cell and Developmental Biology, 2014, 2, 62.	1.8	23
175	Genome-Wide Association Study of Copy Number Variants Suggests LTBP1 and FGD4 Are Important for Alcohol Drinking. PLoS ONE, 2012, 7, e30860.	1.1	23
176	BERT6mA: prediction of DNA N6-methyladenine site using deep learning-based approaches. Briefings in Bioinformatics, 2022, 23, .	3.2	23
177	TNFRSF11A and TNFSF11 are associated with age at menarche and natural menopause in white women. Menopause, 2010, 17, 1048-1054.	0.8	22
178	Copy Number Variations at the Praderâ€“Willi Syndrome Region on Chromosome 15 and associations with Obesity in Whites. Obesity, 2011, 19, 1229-1234.	1.5	22
179	Bivariate Genome-Wide Association Analyses of Femoral Neck Bone Geometry and Appendicular Lean Mass. PLoS ONE, 2011, 6, e27325.	1.1	22
180	Microtubule assembly affects bone mass by regulating both osteoblast and osteoclast functions: Stathmin deficiency produces an osteopenic phenotype in mice. Journal of Bone and Mineral Research, 2011, 26, 2052-2067.	3.1	22

#	Article	IF	Citations
181	Common Copy Number Variation Detection From Multiple Sequenced Samples. IEEE Transactions on Biomedical Engineering, 2014, 61, 928-937.	2.5	22
182	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.	1.4	22
183	Evidence for a major gene underlying bone size variation in the Chinese. American Journal of Human Biology, 2004, 16, 68-77.	0.8	21
184	The â^'1997 G/T Polymorphism in the COLIA1 Upstream Regulatory Region is Associated with Hip Bone Mineral Density (BMD) in Chinese Nuclear Families. Calcified Tissue International, 2005, 76, 107-112.	1.5	21
185	Establishment of peak bone mineral density in Southern Chinese males and its comparisons with other males from different regions of China. Journal of Bone and Mineral Metabolism, 2007, 25, 114-121.	1.3	21
186	Gene-gene interaction between RBMS3 and ZNF516 influences bone mineral density. Journal of Bone and Mineral Research, 2013, 28, 828-837.	3.1	21
187	Is GSN significant for hip BMD in female Caucasians?. Bone, 2014, 63, 69-75.	1.4	21
188	Critical assessment of coalescent simulators in modeling recombination hotspots in genomic sequences. BMC Bioinformatics, 2014, 15, 3.	1.2	21
189	Quantitative proteomics and integrative network analysis identified novel genes and pathways related to osteoporosis. Journal of Proteomics, 2016, 142, 45-52.	1.2	21
190	RNA-sequencing study of peripheral blood monocytes in chronic periodontitis. Gene, 2016, 581, 152-160.	1.0	21
191	Increased identification of novel variants in type 2 diabetes, birth weight and their pleiotropic loci. Journal of Diabetes, 2017, 9, 898-907.	0.8	21
192	Tissue-specific pathway association analysis using genome-wide association study summaries. Bioinformatics, 2017, 33, 243-247.	1.8	21
193	Genome scan for QTLs underlying bone size variation at 10 refined skeletal sites: genetic heterogeneity and the significance of phenotype refinement. Physiological Genomics, 2004, 17, 326-331.	1.0	20
194	APOE Haplotypes Influence Bone Mineral Density in Caucasian Males but Not Females. Calcified Tissue International, 2004, 75, 299-304.	1.5	20
195	Absence of linkage to 8q23.3â€“q24.1 and 2p11.1â€“q12.2 in a new BAFME pedigree in China: Indication of a third locus for BAFME. Epilepsy Research, 2005, 65, 147-152.	0.8	20
196	A genome-wide linkage scan for quantitative trait loci underlying obesity related phenotypes in 434 Caucasian families. Human Genetics, 2007, 121, 145-148.	1.8	20
197	ALOX12 gene is associated with the onset of natural menopause in white women. Menopause, 2010, 17, 152-156.	0.8	20
198	Impact of female cigarette smoking on circulating B cells in vivo: the suppressed ICOSLG, TCF3, and VCAM1 gene functional network may inhibit normal cell function. Immunogenetics, 2010, 62, 237-251.	1.2	20

#	Article	IF	Citations
199	The regulation-of-autophagy pathway may influence Chinese stature variation: evidence from elder adults. Journal of Human Genetics, 2010, 55, 441-447.	1.1	20
200	Low-, high-coverage, and two-stage DNA sequencing in the design of the genetic association study. Genetic Epidemiology, 2017, 41, 187-197.	0.6	20
201	Efficient Utilization of Rare Variants for Detection of Disease-Related Genomic Regions. PLoS ONE, 2010, 5, e14288.	1.1	20
202	The effects of selected sampling on the transmission disequilibrium test of a quantitative trait locus. Genetical Research, 2002, 79, 161-174.	0.3	19
203	Estrogen receptor Î± gene relationship with peak bone mass and body mass index in Chinese nuclear families. Journal of Human Genetics, 2005, 50, 477-482.	1.1	19
204	HDC gene polymorphisms are associated with age at natural menopause in Caucasian women. Biochemical and Biophysical Research Communications, 2006, 348, 1378-1382.	1.0	19
205	Paternal uniparental isodisomy of the entire chromosome 3 revealed in a person with no apparent phenotypic disorders. Human Mutation, 2006, 27, 133-137.	1.1	19
206	Bivariate Whole Genome Linkage Analyses for Total Body Lean Mass and BMD. Journal of Bone and Mineral Research, 2008, 23, 447-452.	3.1	19
207	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.	1.8	19
208	Pathway-based genome-wide association analysis identified the importance of EphrinAâ€“EphR pathway for femoral neck bone geometry. Bone, 2010, 46, 129-136.	1.4	19
209	Characterization of the DNA methylome and its interindividual variation in human peripheral blood monocytes. Epigenomics, 2013, 5, 255-269.	1.0	19
210	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.	1.8	19
211	Bivariate genome-wide association analyses identified genetic pleiotropic effects for bone mineral density and alcohol drinking in Caucasians. Journal of Bone and Mineral Metabolism, 2017, 35, 649-658.	1.3	19
212	Genetic sharing with coronary artery disease identifies potential novel loci for bone mineral density. Bone, 2017, 103, 70-77.	1.4	19
213	Assessing the Associations of Blood Metabolites With Osteoporosis: A Mendelian Randomization Study. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 1850-1855.	1.8	19
214	Identification of novel variants associated with osteoporosis, type 2 diabetes and potentially pleiotropic loci using pleiotropic cFDR method. Bone, 2018, 117, 6-14.	1.4	19
215	A systematic dissection of human primary osteoblasts in vivo at single-cell resolution. Aging, 2021, 13, 20629-20650.	1.4	19
216	Association between COL1A1 gene polymorphisms and bone size in Caucasians. European Journal of Human Genetics, 2004, 12, 383-388.	1.4	18

#	Article	IF	Citations
217	Race and sex differences and contribution of height: A study on bone size in healthy Caucasians and Chinese. American Journal of Human Biology, 2005, 17, 568-575.	0.8	18
218	A multilocus linkage disequilibrium measure based on mutual information theory and its applications. Genetica, 2009, 137, 355-364.	0.5	18
219	On Genome-Wide Association Studies and Their Meta-Analyses: Lessons Learned From Osteoporosis Studies. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E1278-E1282.	1.8	18
220	Bivariate Genome-Wide Association Analyses Identified Genes with Pleiotropic Effects for Femoral Neck Bone Geometry and Age at Menarche. PLoS ONE, 2013, 8, e60362.	1.1	18
221	Incorporating Single-Locus Tests into Haplotype Cladistic Analysis in Case-Control Studies. PLoS Genetics, 2007, 3, e46.	1.5	18
222	Choice of study phenotype in osteoporosis genetic research. Journal of Bone and Mineral Metabolism, 2009, 27, 121-126.	1.3	17
223	Drug Repurposing for COVID-19 Treatment by Integrating Network Pharmacology and Transcriptomics. Pharmaceutics, 2021, 13, 545.	2.0	17
224	Genome-Wide Pathway Association Studies of Multiple Correlated Quantitative Phenotypes Using Principle Component Analyses. PLoS ONE, 2012, 7, e53320.	1.1	17
225	Genetic determination of variation and covariation of bone mineral density at the hip and spine in a Chinese population. Journal of Bone and Mineral Metabolism, 2005, 23, 181-185.	1.3	16
226	No major effect of the insulin-like growth factor I gene on bone mineral density in premenopausal Chinese women. Bone, 2005, 36, 694-699.	1.4	16
227	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.	1.8	16
228	Is the EFNB2 locus associated with schizophrenia? Single nucleotide polymorphisms and haplotypes analysis. Psychiatry Research, 2010, 180, 5-9.	1.7	16
229	Integrated Analysis of Gene Expression and Copy Number Data on Gene Shaving Using Independent Component Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1568-1579.	1.9	16
230	Genome-wide association study identified UQCC locus for spine bone size in humans. Bone, 2013, 53, 129-133.	1.4	16
231	Sarcopenia-related traits and coronary artery disease: a bi-directional Mendelian randomization study. Aging, 2020, 12, 3340-3353.	1.4	16
232	The (GT)n polymorphism and haplotype of the COL1A2 gene, but not the (AAAG)n polymorphism of the PTHR1 gene, are associated with bone mineral density in Chinese. Human Genetics, 2005, 116, 200-207.	1.8	15
233	Linkage exclusion analysis of two candidate regions on chromosomes 7 and 11: Leptin and UCP2/UCP3 are not QTLs for obesity in US Caucasians. Biochemical and Biophysical Research Communications, 2005, 332, 602-608.	1.0	15
234	Is a gene important for bone resorption a candidate for obesity? An association and linkage study on the RANK (receptor activator of nuclear factor-Î²B) gene in a large Caucasian sample. Human Genetics, 2006, 120, 561-570.	1.8	15

#	Article	IF	Citations
235	Association and linkage analysis of COL1A1 and AHSG gene polymorphisms with femoral neck bone geometric parameters in both Caucasian and Chinese nuclear families. Acta Pharmacologica Sinica, 2007, 28, 375-381.	2.8	15
236	Sex-Specific Association of the Glucocorticoid Receptor Gene With Extreme BMD. Journal of Bone and Mineral Research, 2008, 23, 247-252.	3.1	15
237	Identification of Genes for Complex Diseases Using Integrated Analysis of Multiple Types of Genomic Data. PLoS ONE, 2012, 7, e42755.	1.1	15
238	Systemic analysis of osteoblast-specific DNA methylation marks reveals novel epigenetic basis of osteoblast differentiation. Bone Reports, 2017, 6, 109-119.	0.2	15
239	Malnutrition and its associated factors among elderly Chinese with physical functional dependency. Public Health Nutrition, 2021, 24, 1404-1414.	1.1	15
240	Interaction effects between estrogen receptor Î± gene, vitamin D receptor gene, age, and sex on bone mineral density in Chinese. Journal of Human Genetics, 2003, 48, 514-519.	1.1	14
241	Interaction effects between estrogen receptor alpha and vitamin D receptor genes on age at menarche in Chinese women. Acta Pharmacologica Sinica, 2005, 26, 860-864.	2.8	14
242	Multivariate Association Test Using Haplotype Trend Regression. Annals of Human Genetics, 2009, 73, 456-464.	0.3	14
243	Genome-wide association study in East Asians suggests UHMK1 as a novel bone mineral density susceptibility gene. Bone, 2016, 91, 113-121.	1.4	14
244	Genome-wide association meta-analyses identified 1q43 and 2q32.2 for hip Ward's triangle areal bone mineral density. Bone, 2016, 91, 1-10.	1.4	14
245	SNP-SNP interactions between WNT4 and WNT5A were associated with obesity related traits in Han Chinese Population. Scientific Reports, 2017, 7, 43939.	1.6	14
246	Identification and Functional Characterization of Metabolites for Bone Mass in Peri- and Postmenopausal Chinese Women. Journal of Clinical Endocrinology and Metabolism, 2021, 106, e3159-e3177.	1.8	14
247	Pathway-Based Association Analyses Identified TRAIL Pathway for Osteoporotic Fractures. PLoS ONE, 2011, 6, e21835.	1.1	14
248	Lack of association between the Hind III RFLP of the osteocalcin (BGP) gene and bone mineral density (BMD) in healthy pre- and postmenopausal Chinese women. Journal of Bone and Mineral Metabolism, 2004, 22, 264-269.	1.3	13
249	Genetic and environmental correlations between bone phenotypes and anthropometric indices in Chinese. Osteoporosis International, 2005, 16, 1134-1140.	1.3	13
250	The contributions of lean tissue mass and fat mass to bone geometric adaptation at the femoral neck in Chinese overweight adults. Annals of Human Biology, 2007, 34, 344-353.	0.4	13
251	A Bivariate Whole Genome Linkage Study Identified Genomic Regions Influencing Both BMD and Bone Structure. Journal of Bone and Mineral Research, 2008, 23, 1806-1814.	3.1	13
252	Comprehensive association analyses of IGF1, ESR2, and CYP17 genes with adult height in Caucasians. European Journal of Human Genetics, 2008, 16, 1380-1387.	1.4	13

#	Article	IF	Citations
253	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.	3.1	13
254	Functional relevance for associations between osteoporosis and genetic variants. PLoS ONE, 2017, 12, e0174808.	1.1	13
255	Influence of mouse defective zona pellucida in folliculogenesis on apoptosis of granulosa cells and developmental competence of oocytesâ€. Biology of Reproduction, 2019, 101, 457-465.	1.2	13
256	Single-cell RNA sequencing of human femoral head in vivo. Aging, 2021, 13, 15595-15619.	1.4	13
257	Effect of polygenes on Xiong?s transmission disequilibrium test of a QTL in nuclear families with multiple children. Genetic Epidemiology, 2001, 21, 243-265.	0.6	12
258	Tests of linkage and/or association of TGF-?1 and COL1A1 genes with bone mass. Osteoporosis International, 2005, 16, 86-92.	1.3	12
259	Bone mineral density and five prominent candidate genes in Chinese men: associations, interaction effects and their implications. Maturitas, 2005, 51, 199-206.	1.0	12
260	Perspective: On Genetic Studies of Bone Loss. Journal of Bone and Mineral Research, 2006, 21, 1676-1677.	3.1	12
261	Genetic determination and correlation of body weight and body mass index (BMI) and cross-sectional geometric parameters of the femoral neck. Osteoporosis International, 2006, 17, 1602-1607.	1.3	12
262	Genome-Wide Association Study Identified Copy Number Variants Important for Appendicular Lean Mass. PLoS ONE, 2014, 9, e89776.	1.1	12
263	Genome-wide pathway-based association study implicates complement system in the development of Kashin-Beck disease in Han Chinese. Bone, 2015, 71, 36-41.	1.4	12
264	A novel computational strategy for DNA methylation imputation using mixture regression model (MRM). BMC Bioinformatics, 2020, 21, 552.	1.2	12
265	GWA-based pleiotropic analysis identified potential SNPs and genes related to type 2 diabetes and obesity. Journal of Human Genetics, 2021, 66, 297-306.	1.1	12
266	Multilocus Association Testing of Quantitative Traits Based on Partial Least-Squares Analysis. PLoS ONE, 2011, 6, e16739.	1.1	12
267	Network-Based Meta-Analyses of Associations of Multiple Gene Expression Profiles with Bone Mineral Density Variations in Women. PLoS ONE, 2016, 11, e0147475.	1.1	12
268	Identification of novel genetic loci for osteoporosis and/or rheumatoid arthritis using cFDR approach. PLoS ONE, 2017, 12, e0183842.	1.1	12
269	QTL Fine Mapping, in Extreme Samples of Finite Populations, for Complex Traits with Familial Correlation Due to Polygenes. American Journal of Human Genetics, 2000, 67, 259-261.	2.6	11
270	The VDR, COL1A1, PTH, and PTHR1 gene polymorphisms are not associated with bone size and height in Chinese nuclear families. Journal of Bone and Mineral Metabolism, 2005, 23, 501-505.	1.3	11

#	Article	IF	Citations
271	Anthropometric indices as the predictors of trunk obesity in Chinese young adults: Receiver operating characteristic analyses. Annals of Human Biology, 2008, 35, 342-348.	0.4	11
272	Regulatory element-based prediction identifies new susceptibility regulatory variants for osteoporosis. Human Genetics, 2017, 136, 963-974.	1.8	11
273	Identifying potentially common genes between dyslipidemia and osteoporosis using novel analytical approaches. Molecular Genetics and Genomics, 2018, 293, 711-723.	1.0	11
274	Assessing the Genetic Correlations Between Blood Plasma Proteins and Osteoporosis: A Polygenic Risk Score Analysis. Calcified Tissue International, 2019, 104, 171-181.	1.5	11
275	System network analysis of genomics and transcriptomics data identified type 1 diabetes-associated pathway and genes. Genes and Immunity, 2019, 20, 500-508.	2.2	11
276	Identification of novel functional CpG-SNPs associated with type 2 diabetes and coronary artery disease. Molecular Genetics and Genomics, 2020, 295, 607-619.	1.0	11
277	Osteoporosis- and obesity-risk interrelationships: an epigenetic analysis of GWAS-derived SNPs at the developmental gene TBX15. Epigenetics, 2020, 15, 728-749.	1.3	11
278	Searching for obesity genes: Progress and prospects. Drugs of Today, 2005, 41, 345.	2.4	11
279	Test of linkage and/or association between the estrogen receptor Î± gene with bone mineral density in Caucasian nuclear families. Bone, 2004, 35, 395-402.	1.4	10
280	A follow-up linkage study for bone size variation in an extended sample. Bone, 2004, 35, 777-784.	1.4	10
281	Tests of linkage and association of PTH/PTHrP receptor type 1 gene with bone mineral density and height in Caucasians. Journal of Bone and Mineral Metabolism, 2005, 24, 36-41.	1.3	10
282	Association of rare PTP4A1-PHF3-EYS variants with alcohol dependence. Journal of Human Genetics, 2013, 58, 178-179.	1.1	10
283	Integrative Analysis of GWASs, Human Protein Interaction, and Gene Expression Identified Gene Modules Associated With BMDs. Journal of Clinical Endocrinology and Metabolism, 2014, 99, E2392-E2399.	1.8	10
284	MicroRNAâ€“mRNA interaction analysis to detect potential dysregulation in complex diseases. Network Modeling Analysis in Health Informatics and Bioinformatics, 2015, 4, 1.	1.2	10
285	A systematic review of association studies of common variants associated with idiopathic congenital talipes equinovarus (ICTEV) in humans in the past 30Âyears. SpringerPlus, 2016, 5, 896.	1.2	10
286	Exome sequencing identified FGF12 as a novel candidate gene for Kashin-Beck disease. Functional and Integrative Genomics, 2016, 16, 13-17.	1.4	10
287	Genomic variants at 20p11 associated with body fat mass in the European population. Obesity, 2017, 25, 757-764.	1.5	10
288	Genomeâ€wide association study of lncRNA polymorphisms with bone mineral density. Annals of Human Genetics, 2018, 82, 244-253.	0.3	10

#	Article	IF	Citations
289	Examining the causal role of leptin in bone mineral density: A Mendelian randomization study. Bone, 2019, 125, 25-29.	1.4	10
290	Genome-wide meta-analysis of alcohol use disorder in East Asians. Neuropsychopharmacology, 2022, 47, 1791-1797.	2.8	10
291	Associations of physical activity with sarcopenia and sarcopenic obesity in middle-aged and older adults: the Louisiana osteoporosis study. BMC Public Health, 2022, 22, 896.	1.2	10
292	Association tests of interleukin-6 (IL-6) and type II tumor necrosis factor receptor (TNFR2) genes with bone mineral density in Caucasians using a re-sampling approach. Human Genetics, 2005, 117, 340-348.	1.8	9
293	Association analyses of CYP19 gene polymorphisms with height variation in a large sample of Caucasian nuclear families. Human Genetics, 2006, 120, 119-125.	1.8	9
294	Accurate Haplotype Inference for Multiple Linked Single-Nucleotide Polymorphisms Using Sibship Data. Genetics, 2006, 174, 499-509.	1.2	9
295	Differences of height and body mass index of youths in urban vs rural areas in Hunan province of China. Annals of Human Biology, 2009, 36, 750-755.	0.4	9
296	A Unified Sparse Representation for Sequence Variant Identification for Complex Traits. Genetic Epidemiology, 2014, 38, 671-679.	0.6	9
297	Replication of Caucasian Loci Associated with Osteoporosis-related Traits in East Asians. Journal of Bone Metabolism, 2016, 23, 233.	0.5	9
298	A bivariate genome-wide association study identifies ADAM12 as a novel susceptibility gene for Kashin-Beck disease. Scientific Reports, 2016, 6, 31792.	1.6	9
299	Exploring the Major Sources and Extent of Heterogeneity in a Genomeâ€Wide Association Metaâ€Analysis. Annals of Human Genetics, 2016, 80, 113-122.	0.3	9
300	Assessing the genetic correlations between early growth parameters and bone mineral density: A polygenic risk score analysis. Bone, 2018, 116, 301-306.	1.4	9
301	Mendelian Randomization Identifies CpG Methylation Sites With Mediation Effects for Genetic Influences on BMD in Peripheral Blood Monocytes. Frontiers in Genetics, 2020, 11, 60.	1.1	9
302	Integration of the Human Gut Microbiome and Serum Metabolome Reveals Novel Biological Factors Involved in the Regulation of Bone Mineral Density. Frontiers in Cellular and Infection Microbiology, 2022, 12, 853499.	1.8	9
303	The (CA)n polymorphism of the TNFR2 gene is associated with peak bone density in Chinese nuclear families. Journal of Human Genetics, 2005, 50, 301-304.	1.1	8
304	Improvement of Mapping Accuracy by Unifying Linkage and Association Analysis. Genetics, 2006, 172, 647-661.	1.2	8
305	AHSG gene polymorphisms are associated with bone mineral density in Caucasian nuclear families. European Journal of Epidemiology, 2007, 22, 527-532.	2.5	8
306	HAPSIMU: a genetic simulation platform for population-based association studies. BMC Bioinformatics, 2008, 9, 331.	1.2	8

#	Article	IF	Citations
307	Bivariate genome-wide linkage analysis for traits BMD and AAM: Effect of menopause on linkage signals. Maturitas, 2009, 62, 16-20.	1.0	8
308	Correcting for Cryptic Relatedness in Population-Based Association Studies of Continuous Traits. Human Heredity, 2010, 69, 28-33.	0.4	8
309	Identification of genes for bone mineral density variation by computational disease gene identification strategy. Journal of Bone and Mineral Metabolism, 2011, 29, 709-716.	1.3	8
310	The rs1142345 in TPMT Affects the Therapeutic Effect of Traditional Hypoglycemic Herbs in Prediabetes. Evidence-based Complementary and Alternative Medicine, 2013, 2013, 1-8.	0.5	8
311	On Combining Reference Data to Improve Imputation Accuracy. PLoS ONE, 2013, 8, e55600.	1.1	8
312	Inferring causal relationships between phenotypes using summary statistics from genome-wide association studies. Human Genetics, 2018, 137, 247-255.	1.8	8
313	Combining artificial intelligence: deep learning with Hi-C data to predict the functional effects of non-coding variants. Bioinformatics, 2021, 37, 1339-1344.	1.8	8
314	Network-based Transcriptome-wide Expression Study for Postmenopausal Osteoporosis. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 2678-2691.	1.8	8
315	Two novel pleiotropic loci associated with osteoporosis and abdominal obesity. Human Genetics, 2020, 139, 1023-1035.	1.8	8
316	Cellâ€specific network analysis of human folliculogenesis reveals network rewiring in antral stage oocytes. Journal of Cellular and Molecular Medicine, 2021, 25, 2851-2860.	1.6	8
317	ST-V-Net: incorporating shape prior into convolutional neural networks for proximal femur segmentation. Complex & Intelligent Systems, 2023, 9, 2747-2758.	4.0	8
318	A multiethnic whole genome sequencing study to identify novel loci for bone mineral density. Human Molecular Genetics, 2022, 31, 1067-1081.	1.4	8
319	Lack of Evidence for a Major Gene in the Mendelian Transmission of BMI in Chinese. Obesity, 2004, 12, 1967-1973.	4.0	7
320	Association and linkage analyses of interleukin-6 gene 634C/G polymorphism and bone phenotypes in Chinese. Journal of Bone and Mineral Metabolism, 2005, 23, 323-328.	1.3	7
321	Epistasis between Loci on Chromosomes 2 and 6 Influences Human Height. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 3821-3825.	1.8	7
322	Polymorphisms of the vitamin D receptor gene predict the onset of surgical menopause in Caucasian females. Gynecological Endocrinology, 2006, 22, 552-556.	0.7	7
323	Genetic Determination of Osteoporosis: Lessons Learned from a Large Genome-Wide Linkage Study. Human Biology, 2007, 79, 593-608.	0.4	7
324	Evaluating the correlation and prediction of trunk fat mass with five anthropometric indices in Chinese females aged 20â€“40years. Nutrition, Metabolism and Cardiovascular Diseases, 2007, 17, 676-683.	1.1	7

#	Article	IF	Citations
325	The Impact of Imputation on Meta-Analysis of Genome-Wide Association Studies. PLoS ONE, 2012, 7, e34486.	1.1	7
326	Zp4 is completely dispensable for fertility in female rats. Biology of Reproduction, 2021, 104, 1282-1291.	1.2	7
327	Family-Based Bivariate Association Tests for Quantitative Traits. PLoS ONE, 2009, 4, e8133.	1.1	7
328	A bi-directional Mendelian randomization study of the sarcopenia-related traits and osteoporosis. Aging, 2022, , 5681-5698.	1.4	7
329	Variations in RANK gene are associated with adult height in Caucasians. American Journal of Human Biology, 2007, 19, 559-565.	0.8	6
330	Evidence for major pleiotropic effects on bone size variation from a principal component analysis of 451 Caucasian families. Acta Pharmacologica Sinica, 2008, 29, 745-751.	2.8	6
331	Bivariate genome linkage analysis suggests pleiotropic effects on chromosomes 20p and 3p for body fat mass and lean mass. Genetical Research, 2008, 90, 259-268.	0.3	6
332	A PCA-based method for ancestral informative markers selection in structured populations. Science in China Series C: Life Sciences, 2009, 52, 972-976.	1.3	6
333	Testing Rare Variants for Association with Diseases: A Bayesian Marker Selection Approach. Annals of Human Genetics, 2012, 76, 74-85.	0.3	6
334	Genome-wide association study identifies HMGN3 locus for spine bone size variation in Chinese. Human Genetics, 2012, 131, 463-469.	1.8	6
335	Trans-omics pathway analysis suggests that eQTLs contribute to chondrocyte apoptosis of Kashinâ€“Beck disease through regulating apoptosis pathway expression. Gene, 2014, 553, 166-169.	1.0	6
336	Genetic Analysis Identifies DDR2 as a Novel Gene Affecting Bone Mineral Density and Osteoporotic Fractures in Chinese Population. PLoS ONE, 2015, 10, e0117102.	1.1	6
337	Mass spectrometry based proteomics profiling of human monocytes. Protein and Cell, 2017, 8, 123-133.	4.8	6
338	Geographical differences in osteoporosis, obesity, and sarcopenia related traits in white American cohorts. Scientific Reports, 2019, 9, 12311.	1.6	6
339	PCA-based GRS analysis enhances the effectiveness for genetic correlation detection. Briefings in Bioinformatics, 2019, 20, 2291-2298.	3.2	6
340	Integrative analysis of multi-omics data to detect the underlying molecular mechanisms for obesity in vivo in humans. Human Genomics, 2022, 16, 15.	1.4	6
341	Robust Indices of Hardy-Weinberg Disequilibrium for QTL Fine Mapping. Human Heredity, 2003, 56, 160-165.	0.4	5
342	Quantifying the Relationship Between Gene Expressions and Trait Values in General Pedigrees. Genetics, 2004, 168, 2395-2405.	1.2	5

#	Article	IF	Citations
343	Upper limit of the rate and per generation effects of deleterious genomic mutations. Genetical Research, 2006, 88, 57-65.	0.3	5
344	The Human Calcium-Sensing Receptor and Interleukin-6 Genes are Associated with Bone Mineral Density in Chinese. Journal of Genetics and Genomics, 2006, 33, 870-880.	0.3	5
345	Chromosome 2q32 May Harbor a QTL Affecting BMD Variation at Different Skeletal Sites. Journal of Bone and Mineral Research, 2007, 22, 1672-1678.	3.1	5
346	Copy Number Variation in CNP267 Region May Be Associated with Hip Bone Size. PLoS ONE, 2011, 6, e22035.	1.1	5
347	Nuclear receptor NR5A2 and bone: gene expression and association with bone mineral density. European Journal of Endocrinology, 2012, 166, 69-75.	1.9	5
348	Unified tests for fine-scale mapping and identifying sparse high-dimensional sequence associations. Bioinformatics, 2016, 32, 330-337.	1.8	5
349	A Sparse Model Based Detection of Copy Number Variations From Exome Sequencing Data. IEEE Transactions on Biomedical Engineering, 2016, 63, 496-505.	2.5	5
350	Additional common variants associated with type 2 diabetes and coronary artery disease detected using a pleiotropic cFDR method. Journal of Diabetes and Its Complications, 2018, 32, 1105-1112.	1.2	5
351	Identification of a 1p21 independent functional variant for abdominal obesity. International Journal of Obesity, 2019, 43, 2480-2490.	1.6	5
352	Identification of pleiotropic genes between risk factors of stroke by multivariate metaCCA analysis. Molecular Genetics and Genomics, 2020, 295, 1173-1185.	1.0	5
353	Mutant Zp1 impedes incorporation of ZP3 and ZP4 in the zona pellucida, resulting in zona absence and female infertility in rats. Biology of Reproduction, 2021, 104, 1262-1270.	1.2	5
354	Identification of Novel Pleiotropic SNPs Associated with Osteoporosis and Rheumatoid Arthritis. Calcified Tissue International, 2021, 109, 17-31.	1.5	5
355	Estimation of Parameters of Deleterious Mutations in Partial Selfing or Partial Outcrossing Populations and in Nonequilibrium Populations. Genetics, 2000, 154, 1893-1906.	1.2	5
356	Improved Detection of Rare Genetic Variants for Diseases. PLoS ONE, 2010, 5, e13857.	1.1	5
357	Epigenomic and Transcriptomic Prioritization of Candidate Obesity-Risk Regulatory GWAS SNPs. International Journal of Molecular Sciences, 2022, 23, 1271.	1.8	5
358	Pathway-based metabolomics study of sarcopenia-related traits in two US cohorts. Aging, 2022, 14, 2101-2112.	1.4	5
359	DeepDNAbP: A deep learning-based hybrid approach to improve the identification of deoxyribonucleic acid-binding proteins. Computers in Biology and Medicine, 2022, 145, 105433.	3.9	5
360	Discovery and functional assessment of a novel adipocyte population driven by intracellular Wnt/Î²-catenin signaling in mammals. ELife, 2022, 11, .	2.8	5

#	Article	IF	Citations
361	Transmission disequilibrium test with discordant sib pairs when parents are available. Human Genetics, 2002, 110, 451-461.	1.8	4
362	LOD Score Exclusion Analyses for Candidate QTLs using Random Population Samples. Genetica, 2003, 119, 303-315.	0.5	4
363	The genetic, environmental and phenotypic correlations of bone phenotypes at the spine and hip in Chinese. Annals of Human Biology, 2006, 33, 500-509.	0.4	4
364	Epistatic Interactions between Genomic Regions Containing the COL1A1 Gene and Genes Regulating Osteoclast Differentiation may Influence Femoral Neck Bone Mineral Density. Annals of Human Genetics, 2007, 71, 152-159.	0.3	4
365	Polymorphisms of the tumor necrosis factor-alpha receptor 2 gene are associated with obesity phenotypes among 405 Caucasian nuclear families. Human Genetics, 2008, 124, 171-177.	1.8	4
366	Detecting epistasis within chromatin regulatory circuitry reveals CAND2 as a novel susceptibility gene for obesity. International Journal of Obesity, 2019, 43, 450-456.	1.6	4
367	Identifying Pleiotropic SNPs Associated With Femoral Neck and Heel Bone Mineral Density. Frontiers in Genetics, 2020, 11, 772.	1.1	4
368	Three pleiotropic loci associated with bone mineral density and lean body mass. Molecular Genetics and Genomics, 2021, 296, 55-65.	1.0	4
369	The genetics of osteoporosis. Drugs of Today, 2005, 41, 205.	2.4	4
370	Interpretation of Genetic Linkage Findings. Journal of Bone and Mineral Research, 2003, 18, 2077-2078.	3.1	3
371	Linkage exclusion analysis of two important chromosomal regions for height. Biochemical and Biophysical Research Communications, 2005, 335, 1287-1292.	1.0	3
372	Exclusion mapping of chromosomes 1, 4, 6 and 14 with bone mineral density in 79 Caucasian pedigrees. Bone, 2006, 38, 450-455.	1.4	3
373	Genetic and Environmental Correlations Between Bone Mineral Density and Bone Size in Caucasians. Human Biology, 2007, 79, 15-24.	0.4	3
374	Detection of common copy number variation with application to population clustering from next generation sequencing data. , 2012, 2012, 1246-9.		3
375	Novel QTL at chromosome 6p22 for alcohol consumption: Implications for the genetic liability of alcohol use disorders. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 294-302.	1.1	3
376	Pleiotropic genomic variants at 17q21.31 associated with bone mineral density and body fat mass: a bivariate genome-wide association analysis. European Journal of Human Genetics, 2021, 29, 553-563.	1.4	3
377	Identification of pleiotropic loci underlying hip bone mineral density and trunk lean mass. Journal of Human Genetics, 2021, 66, 251-260.	1.1	3
378	A transcriptome-wide association study to detect novel genes for volumetric bone mineral density. Bone, 2021, 153, 116106.	1.4	3

#	Article	IF	Citations
379	Identification of PDXDC1 as a novel pleiotropic susceptibility locus shared between lumbar spine bone mineral density and birth weight. Journal of Molecular Medicine, 2022, 100, 723-734.	1.7	3
380	CA repeat polymorphism of the TNFR2 gene is not associated with bone mineral density in two independent Caucasian populations. Journal of Bone and Mineral Metabolism, 2006, 24, 132-137.	1.3	2
381	Linkage exclusion mapping with bone size in 79 Caucasian pedigrees. Journal of Bone and Mineral Metabolism, 2006, 24, 337-343.	1.3	2
382	Genetic determination in onset age of wrist fracture. Journal of Human Genetics, 2007, 52, 481-484.	1.1	2
383	A bootstrap-based regression method for comprehensive discovery of differential gene expressions: An application to the osteoporosis study. European Journal of Medical Genetics, 2011, 54, e560-e564.	0.7	2
384	Genome-Wide Copy Number Variation Association Analyses for Age at Menarche. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E2133-E2139.	1.8	2
385	Characterization of Human Chromosomal Material Exchange with Regard to the Chromosome Translocations Using Next-Generation Sequencing Data. Genome Biology and Evolution, 2014, 6, 3015-3024.	1.1	2
386	Multiple analyses indicate the specific association of NR1I3, C6 and TNN with low hip BMD risk. Journal of Genetics and Genomics, 2017, 44, 327-330.	1.7	2
387	Medium-coverage DNA sequencing in the design of the genetic association study. European Journal of Human Genetics, 2020, 28, 1459-1466.	1.4	2
388	A transâ€ethnic twoâ€stage polygenetic scoring analysis detects genetic correlation between osteoporosis and schizophrenia. Clinical and Translational Medicine, 2020, 9, 21.	1.7	2
389	Integrated metagenome and metabolome analyses of blood pressure studies in early postmenopausal Chinese women. Journal of Hypertension, 2021, 39, 1800-1809.	0.3	2
390	Identification of novel pleiotropic gene for bone mineral density and lean mass using the cFDR method. Annals of Human Genetics, 2021, 85, 201-212.	0.3	2
391	A generalized kernel machine approach to identify higher-order composite effects in multi-view datasets, with application to adolescent brain development and osteoporosis. Journal of Biomedical Informatics, 2021, 120, 103854.	2.5	2
392	Quantitative Trait Loci Mapping. Methods in Molecular Biology, 2008, 455, 203-235.	0.4	2
393	Genome-Wide Association Study Identified CNP12587 Region Underlying Height Variation in Chinese Females. PLoS ONE, 2012, 7, e44292.	1.1	2
394	Hypothetical SisterKiller. Nature, 1994, 369, 26-26.	13.7	1
395	Inferring deleterious-mutation parameters in natural daphnia populations. Biological Procedures Online, 1998, 1, 1-9.	1.4	1
396	Linkage and Association Between CA Repeat Polymorphism of the TNFR2 Gene and Obesity Phenotypes in Two Independent Caucasian Populations. Journal of Genetics and Genomics, 2006, 33, 775-781.	0.3	1

#	Article	IF	Citations
397	A Bayesian Analysis for Identifying DNA Copy Number Variations Using a Compound Poisson Process. Eurasip Journal on Bioinformatics and Systems Biology, 2010, 2010, 1-10.	1.4	1
398	SWGDT: A sliding window-based genotype dependence testing tool for genome-wide susceptibility gene scan. Journal of Biomedical Informatics, 2015, 57, 38-41.	2.5	1
399	PPARGC1B gene is associated with Kashin-Beck disease in Han Chinese. Functional and Integrative Genomics, 2016, 16, 459-463.	1.4	1
400	Bivariate genomeâ€wide association analysis identified three pleiotropic loci underlying osteoporosis and obesity. Clinical Genetics, 2020, 97, 785-786.	1.0	1
401	The mediating effect of skeletal muscle index on the relationship between menarcheal age and bone mineral density in premenopausal women by race/ethnicity. Menopause, 2021, 28, 1143-1149.	0.8	1
402	Determination of bone mineral density of the hip and spine in human pedigrees by genetic and life-style factors. , 0, .		1
403	Fusing Gene Interaction to Improve Disease Discrimination on Classification Analysis. Advancements in Genetic Engineering, 2012, 01, 1000102.	0.1	1
404	RECENT ADVANCES IN BONE BIOLOGY RESEARCH. , 2005, , 497-511.		0
405	The Vital Role of ORWH. Science, 2009, 323, 1009-1010.	6.0	0
406	Design and Interpretation of Linkage and Association Studies on Osteoporosis. Clinical Reviews in Bone and Mineral Metabolism, 2010, 8, 60-67.	1.3	0
407	Identification of genes for complex diseases by integrating multiple types of genomic data. , 2012, 2012, 5541-4.		0
408	Population clustering based on copy number variations detected from next generation sequencing data. Journal of Bioinformatics and Computational Biology, 2014, 12, 1450021.	0.3	0
409	Polymorphisms of the TNF, LTA, and TNFRSF1B genes are associated with onsets of menarche and menopause in US women of European ancestry. Annals of Human Biology, 2021, 48, 400-405.	0.4	0
410	STUDYING OSTEOPOROSIS AT THE WHOLE-GENOME LEVEL: PROBLEMS AND PROSPECTS. , 2005, , 464-498.		0
411	GENETICS OF OSTEOPOROSIS. , 2005, , 415-444.		0