Hong-Wen Deng

List of Publications by Year
in descending order

411 papers	13,594 citations	22153 59 h-index	43889 91 g-index
413 all docs	413 docs citations	413 times ranked	16480 citing authors

#	Article	IF	Citations
1	Relationship of Obesity with Osteoporosis. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 1640-1646.	3.6	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.	2.8	408
3	Wnt/Î²-catenin signaling activates bone morphogenetic protein 2 expression in osteoblasts. Bone, 2013, 52, 145-156.	2.9	243
4	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
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.	6.2	187
6	Genome-wide association scans identified CTNNBL1 as a novel gene for obesity. Human Molecular Genetics, 2008, 17, 1803-1813.	2.9	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.	2.8	151
8	A Genomewide Linkage Scan for Quantitative-Trait Loci for Obesity Phenotypes. American Journal of Human Genetics, 2002, 70, 1138-1151.	6.2	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, 2007, 22, 173-183.	2.8	144
10	Mutation Patterns at Dinucleotide Microsatellite Loci in Humans. American Journal of Human Genetics, 2002, 70, 625-634.	6.2	141
11	Metaâ€Analysis of Genomeâ€wide Linkage Studies in BMI and Obesity. Obesity, 2007, 15, 2263-2275.	3.0	138
12	Comparative Studies of Copy Number Variation Detection Methods for Next-Generation Sequencing Technologies. PLoS ONE, 2013, 8, e59128.	2.5	138
13	Genome Partitioning of Genetic Variation for Height from 11,214 Sibling Pairs. American Journal of Human Genetics, 2007, 81, 1104-1110.	6.2	135
14	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. Human Molecular Genetics, 2014, 23, 1923-1933.	2.9	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.	3.6	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.	1.3	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.	3.4	118
18	Analyses and Comparison of Accuracy of Different Genotype Imputation Methods. PLoS ONE, 2008, 3, e3551.	2.5	117

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19	Mutant ZP1 in Familial Infertility. New England Journal of Medicine, 2014, 370, 1220-1226.	27.0	114
20	Population Admixture May Appear to Mask, Change or Reverse Genetic Effects of Genes Underlying Complex Traits. Genetics, 2001, 159, 1319-1323.	2.9	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.	2.8	109
22	Comparative studies of de novo assembly tools for next-generation sequencing technologies. Bioinformatics, 2011, 27, 2031-2037.	4.1	109
23	An Amplified Fragment Length Polymorphism Map of the Silkworm. Genetics, 2001, 157, 1277-1284.	2.9	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.	3.2	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.	0.4	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.	2.9	105
27	Molecular Genetic Studies of Gene Identification for Osteoporosis: A 2004 Update. Journal of Bone and Mineral Research, 2005, 21, 1511-1535.	2.8	104
28	Genome-Wide Association Study of Alcohol Dependence Implicates KIAA0040 on Chromosome 1q. Neuropsychopharmacology, 2012, 37, 557-566.	5.4	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.	6.2	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.	2.8	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.	3.5	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.	1.7	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.	1.3	96
35	Meta-analysis suggests that smoking is associated with an increased risk of early natural menopause. Menopause, 2012, 19, 126-132.	2.0	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.	1.3	91

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37	Group sparse canonical correlation analysis for genomic data integration. BMC Bioinformatics, 2013, 14, 245.	2.6	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.	1.3	89
39	Molecular genetic studies of gene identification for sarcopenia. Human Genetics, 2012, 131, 1-31.	3.8	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.	3.1	87
41	Hotelling's T2 multivariate profiling for detecting differential expression in microarrays. Bioinformatics, 2005, 21, 3105-3113.	4.1	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.	2.5	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 Geneâ€“Gene Interaction. Journal of Bone and Mineral Research, 2006, 21, 1678-1695.	2.8	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.	3.6	84
45	Polymorphisms in predicted miRNA binding sites and osteoporosis. Journal of Bone and Mineral Research, 2011, 26, 72-78.	2.8	84
46	Searching for osteoporosis genes in the post-genome era: progress and challenges. Osteoporosis International, 2003, 14, 701-715.	3.1	81
47	Gene selection for classification of microarray data based on the Bayes error. BMC Bioinformatics, 2007, 8, 370.	2.6	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.	2.3	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.	2.7	76
50	Molecular Genetic Studies of Gene Identification for Osteoporosis: The 2009 Update. Endocrine Reviews, 2010, 31, 447-505.	20.1	76
51	Meta-analysis of genome-wide association data identifies novel susceptibility loci for obesity. Human Molecular Genetics, 2014, 23, 820-830.	2.9	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.	2.8	70
53	Transcriptional Regulation of BMP2 Expression by the PTH-CREB Signaling Pathway in Osteoblasts. PLoS ONE, 2011, 6, e20780.	2.5	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.	2.5	67

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55	Composition of gut microbiota in infants in China and global comparison. Scientific Reports, 2016, 6, 36666.	3.3	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.	6.2	62
57	Nonreplication in Genetic Studies of Complex Diseasesâ€"Lessons Learned From Studies of Osteoporosis and Tentative Remedies. Journal of Bone and Mineral Research, 2005, 20, 365-376.	2.8	62
58	Biological Pathwayâ€Based Genomeâ€Wide Association Analysis Identified the Vasoactive Intestinal Peptide (VIP) Pathway Important for Obesity. Obesity, 2010, 18, 2339-2346.	3.0	62
59	Comprehensive Characterization of Human Genome Variation by High Coverage Whole-Genome Sequencing of Forty Four Caucasians. PLoS ONE, 2013, 8, e59494.	2.5	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.	5.5	61
61	A wholeâ€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.	3.0	60
63	Genome-Wide Association Analyses Identify SPOCK as a Key Novel Gene Underlying Age at Menarche. PLoS Genetics, 2009, 5, e1000420.	3.5	59
64	Genome-wide Association Studies for Osteoporosis: A 2013 Update. Journal of Bone Metabolism, 2014, 21, 99.	1.3	57
65	A Review of Integrative Imputation for Multi-Omics Datasets. Frontiers in Genetics, 2020, 11, 570255.	2.3	57
66	Identification of PLCL1 Gene for Hip Bone Size Variation in Females in a Genome-Wide Association Study. PLoS ONE, 2008, 3, e3160.	2.5	57
67	Replication of 6 Obesity Genes in a Meta-Analysis of Genome-Wide Association Studies from Diverse Ancestries. PLoS ONE, 2014, 9, e96149.	2.5	56
68	NeuroPred-FRL: an interpretable prediction model for identifying neuropeptide using feature representation learning. Briefings in Bioinformatics, 2021, 22, .	6.5	56
69	Linkage and association analyses of the UCP3 gene with obesity phenotypes in Caucasian families. Physiological Genomics, 2005, 22, 197-203.	2.3	54
70	Peripheral Blood Monocyte-expressed ANXA2 Gene is Involved in Pathogenesis of Osteoporosis in Humans. Molecular and Cellular Proteomics, 2011, 10, M111.011700.	3.8	54
71	Involvement of the Skeletal Renin-Angiotensin System in Age-Related Osteoporosis of Ageing Mice. Bioscience, Biotechnology and Biochemistry, 2012, 76, 1367-1371.	1.3	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.	2.8	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.	2.7	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.	2.8	51
75	Whole Genome Distribution and Ethnic Differentiation of Copy Number Variation in Caucasian and Asian Populations. PLoS ONE, 2009, 4, e7958.	2.5	51
76	Accurate recognition of colorectal cancer with semi-supervised deep learning on pathological images. Nature Communications, 2021, 12, 6311.	12.8	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.	3.8	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.	2.8	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.	3.6	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.	7.3	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.	2.9	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.	2.8	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.	3.6	46
84	Proteomic analysis of circulating monocytes in Chinese premenopausal females with extremely discordant bone mineral density. Proteomics, 2008, 8, 4259-4272.	2.2	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.	6.2	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.	3.1	44
87	Impaired osteoblast function in GPRC6A null mice. Journal of Bone and Mineral Research, 2010, 25, 1092-1102.	2.8	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.	2.9	44
89	Evaluation of Compressive Strength Index of the Femoral Neck in Caucasians and Chinese. Calcified Tissue International, 2010, 87, 324-332.	3.1	44
90	Factors Predicting Vitamin D Response Variation in Non-Hispanic White Postmenopausal Women. Journal of Clinical Endocrinology and Metabolism, 2012, 97, 2699-2705.	3.6	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.	0.9	43
92	Genome-wide association study for femoral neck bone geometry. Journal of Bone and Mineral Research, 2010, 25, 320-329.	2.8	43
93	Is Replication the Gold Standard for Validating Genome-Wide Association Findings?. PLoS ONE, 2008, 3, e4037.	2.5	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.	3.8	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.	5.0	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.	2.8	40
97	Networkâ€based proteomic analysis for postmenopausal osteoporosis in Caucasian females. Proteomics, 2016, 16, 12-28.	2.2	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.	1.9	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.	0.6	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.	8.2	40
101	Genome-wide association scan for stature in Chinese: evidence for ethnic specific loci. Human Genetics, 2009, 125, 1-9.	3.8	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.	2.4	39
103	Effect of short-term room temperature storage on the microbial community in infant fecal samples. Scientific Reports, 2016, 6, 26648.	3.3	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.	3.6	39
105	Age at menarche and osteoporosis: A Mendelian randomization study. Bone, 2018, 117, 91-97.	2.9	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.	6.4	39
107	Predictive factors for age at menopause in Caucasian females. Maturitas, 2006, 54, 19-26.	2.4	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.	3.1	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.	2.5	38
110	CNV-TV: A robust method to discover copy number variation from short sequencing reads. BMC Bioinformatics, 2013, 14, 150.	2.6	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.	2.8	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.	3.6	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.	2.8	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.	3.1	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.	2.8	36
117	Comparison of Population-Based Association Study Methods Correcting for Population Stratification. PLoS ONE, 2008, 3, e3392.	2.5	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.	0.8	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.	2.9	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.	2.7	34
121	SNPP: automating large-scale SNP genotype data management. Bioinformatics, 2005, 21, 266-268.	4.1	34
122	Analyses and Comparison of Imputation-Based Association Methods. PLoS ONE, 2010, 5, e10827.	2.5	34
123	Assessment of Genetic Linkage and Parent-of-Origin Effects on Obesity. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 4001-4005.	3.6	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.	3.6	33
125	Mitochondria-Wide Association Study of Common Variants in Osteoporosis. Annals of Human Genetics, 2011, 75, 569-574.	0.8	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.	1.7	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.	2.3	32
128	A new permutation strategy of pathway-based approach for genome-wide association study. BMC Bioinformatics, 2009, 10, 429.	2.6	32
129	HMGA2 Is Confirmed To Be Associated with Human Adult Height. Annals of Human Genetics, 2010, 74, 11-16.	0.8	32
130	Quantitative trait loci, genes, and polymorphisms that regulate bone mineral density in mouse. Genomics, 2009, 93, 401-414.	2.9	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.	0.8	30
133	A polymorphism of apolipoprotein E (APOE) gene is associated with age at natural menopause in Caucasian females. Maturitas, 2009, 62, 37-41.	2.4	30
134	Genetic Association Study of Common Mitochondrial Variants on Body Fat Mass. PLoS ONE, 2011, 6, e21595.	2.5	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.	2.8	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.	2.3	30
137	Rare ADH Variant Constellations are Specific for Alcohol Dependence. Alcohol and Alcoholism, 2013, 48, 9-14.	1.6	30
138	Meta-analysis identifies aMECOMgene as a novel predisposing factor of osteoporotic fracture. Journal of Medical Genetics, 2013, 50, 212-219.	3.2	30
139	On individual genome-wide association studies and their meta-analysis. Human Genetics, 2014, 133, 265-279.	3.8	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.	3.6	29
141	Univariate/Multivariate Genome-Wide Association Scans Using Data from Families and Unrelated Samples. PLoS ONE, 2009, 4, e6502.	2.5	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.	5.6	29
143	Integrating Epigenomic Elements and GWASs Identifies BDNF Gene Affecting Bone Mineral Density and Osteoporotic Fracture Risk. Scientific Reports, 2016, 6, 30558.	3.3	29
144	An integrative imputation method based on multi-omics datasets. BMC Bioinformatics, 2016, 17, 247.	2.6	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.	2.9	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.	3.8	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.	2.8	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.	2.9	27
150	FISH: fast and accurate diploid genotype imputation via segmental hidden Markov model. Bioinformatics, 2014, 30, 1876-1883.	4.1	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.	2.3	27
152	High heritability of bone size at the hip and spine in Chinese. Journal of Human Genetics, 2004, 49, 87-91.	2.3	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.	2.8	26
154	Attenuated Monocyte Apoptosis, a New Mechanism for Osteoporosis Suggested by a Transcriptome-Wide Expression Study of Monocytes. PLoS ONE, 2015, 10, e0116792.	2.5	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.	2.3	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.	2.9	25
157	The MTHFR gene polymorphism is associated with lean body mass but not fat body mass. Human Genetics, 2008, 123, 189-196.	3.8	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.	2.0	25
159	Integrative Analysis of Transcriptomic and Epigenomic Data to Reveal Regulation Patterns for BMD Variation. PLoS ONE, 2015, 10, e0138524.	2.5	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.	8.9	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.	3.1	24
162	Classification of Multicolor Fluorescence In Situ Hybridization (M-FISH) Images With Sparse Representation. IEEE Transactions on Nanobioscience, 2012, 11, 111-118.	3.3	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.	3.6	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.	2.8	24
165	Multi-omics research in sarcopenia: Current progress and future prospects. Ageing Research Reviews, 2022, 76, 101576.	10.9	24
166	The power of the transmission disequilibrium test (TDT) with both caseâ€“parent and controlâ€“parent trios. Genetical Research, 2001, 78, 289-302.	0.9	23
167	A major gene model of adult height is suggested in Chinese. Journal of Human Genetics, 2004, 49, 148-153.	2.3	23
168	Mapping Quantitative Trait Loci for Cross-Sectional Geometry at the Femoral Neck. Journal of Bone and Mineral Research, 2005, 20, 1973-1982.	2.8	23
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