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	ST-V-Net: incorporating shape prior into convolutional neural networks for proximal femur segmentation. Complex & Intelligent Systems, 2023, 9, 2747-2758.	4.0	8
2	A multiethnic whole genome sequencing study to identify novel loci for bone mineral density. Human Molecular Genetics, 2022, 31, 1067-1081.	1.4	8
3	Genome-wide meta-analysis of alcohol use disorder in East Asians. Neuropsychopharmacology, 2022, 47, 1791-1797.	2.8	10
4	Epigenomic and Transcriptomic Prioritization of Candidate Obesity-Risk Regulatory GWAS SNPs. International Journal of Molecular Sciences, 2022, 23, 1271.	1.8	5
5	BERT6mA: prediction of DNA N6-methyladenine site using deep learning-based approaches. Briefings in Bioinformatics, 2022, 23, .	3.2	23
6	Multi-omics research in sarcopenia: Current progress and future prospects. Ageing Research Reviews, 2022, 76, 101576.	5.0	24
7	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
8	Pathway-based metabolomics study of sarcopenia-related traits in two US cohorts. Aging, 2022, 14, 2101-2112.	1.4	5
9	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
10	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
11	Discovery and functional assessment of a novel adipocyte population driven by intracellular Wnt/β-catenin signaling in mammals. ELife, 2022, 11, .	2.8	5
12	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
13	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
14	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
15	A bi-directional Mendelian randomization study of the sarcopenia-related traits and osteoporosis. Aging, 2022, , 5681-5698.	1.4	7
16	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
17	Malnutrition and its associated factors among elderly Chinese with physical functional dependency. Public Health Nutrition, 2021, 24, 1404-1414.	1.1	15
18	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

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19	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
20	Three pleiotropic loci associated with bone mineral density and lean body mass. Molecular Genetics and Genomics, 2021, 296, 55-65.	1.0	4
21	Identification of pleiotropic loci underlying hip bone mineral density and trunk lean mass. Journal of Human Genetics, 2021, 66, 251-260.	1.1	3
22	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
23	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
24	Zp4 is completely dispensable for fertility in female rats. Biology of Reproduction, 2021, 104, 1282-1291.	1.2	7
25	Integrated metagenome and metabolome analyses of blood pressure studies in early postmenopausal Chinese women. Journal of Hypertension, 2021, 39, 1800-1809.	0.3	2
26	Identification of Novel Pleiotropic SNPs Associated with Osteoporosis and Rheumatoid Arthritis. Calcified Tissue International, 2021, 109, 17-31.	1.5	5
27	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
28	Drug Repurposing for COVID-19 Treatment by Integrating Network Pharmacology and Transcriptomics. Pharmaceutics, 2021, 13, 545.	2.0	17
29	NeuroPred-FRL: an interpretable prediction model for identifying neuropeptide using feature representation learning. Briefings in Bioinformatics, 2021, 22, .	3.2	56
30	Single-cell RNA sequencing of human femoral head in vivo. Aging, 2021, 13, 15595-15619.	1.4	13
31	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
32	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
33	A systematic dissection of human primary osteoblasts in vivo at single-cell resolution. Aging, 2021, 13, 20629-20650.	1.4	19
34	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
35	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
36	A transcriptome-wide association study to detect novel genes for volumetric bone mineral density. Bone, 2021, 153, 116106.	1.4	3

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37	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
38	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
39	Accurate recognition of colorectal cancer with semi-supervised deep learning on pathological images. Nature Communications, 2021, 12, 6311.	5.8	51
40	Bivariate genomeâ€wide association analysis identified three pleiotropic loci underlying osteoporosis and obesity. Clinical Genetics, 2020, 97, 785-786.	1.0	1
41	A novel computational strategy for DNA methylation imputation using mixture regression model (MRM). BMC Bioinformatics, 2020, 21, 552.	1.2	12
42	Identifying Pleiotropic SNPs Associated With Femoral Neck and Heel Bone Mineral Density. Frontiers in Genetics, 2020, 11, 772.	1.1	4
43	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
44	A Review of Integrative Imputation for Multi-Omics Datasets. Frontiers in Genetics, 2020, 11, 570255.	1.1	57
45	Identification of pleiotropic genes between risk factors of stroke by multivariate metaCCA analysis. Molecular Genetics and Genomics, 2020, 295, 1173-1185.	1.0	5
46	Network-based Transcriptome-wide Expression Study for Postmenopausal Osteoporosis. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 2678-2691.	1.8	8
47	Medium-coverage DNA sequencing in the design of the genetic association study. European Journal of Human Genetics, 2020, 28, 1459-1466.	1.4	2
48	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
49	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
50	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
51	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
52	Two novel pleiotropic loci associated with osteoporosis and abdominal obesity. Human Genetics, 2020, 139, 1023-1035.	1.8	8
53	Sarcopenia-related traits and coronary artery disease: a bi-directional Mendelian randomization study. Aging, 2020, 12, 3340-3353.	1.4	16
54	Geographical differences in osteoporosis, obesity, and sarcopenia related traits in white American cohorts. Scientific Reports, 2019, 9, 12311.	1.6	6

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55	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
56	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
57	Examining the causal role of leptin in bone mineral density: A Mendelian randomization study. Bone, 2019, 125, 25-29.	1.4	10
58	Identification of a 1p21 independent functional variant for abdominal obesity. International Journal of Obesity, 2019, 43, 2480-2490.	1.6	5
59	PCA-based GRS analysis enhances the effectiveness for genetic correlation detection. Briefings in Bioinformatics, 2019, 20, 2291-2298.	3.2	6
60	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
61	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
62	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
63	Inferring causal relationships between phenotypes using summary statistics from genome-wide association studies. Human Genetics, 2018, 137, 247-255.	1.8	8
64	Genomeâ€wide association study of lncRNA polymorphisms with bone mineral density. Annals of Human Genetics, 2018, 82, 244-253.	0.3	10
65	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
66	Identifying potentially common genes between dyslipidemia and osteoporosis using novel analytical approaches. Molecular Genetics and Genomics, 2018, 293, 711-723.	1.0	11
67	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
68	Age at menarche and osteoporosis: A Mendelian randomization study. Bone, 2018, 117, 91-97.	1.4	39
69	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
70	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
71	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
72	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

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73	Genomic variants at 20p11 associated with body fat mass in the European population. Obesity, 2017, 25, 757-764.	1.5	10
74	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
75	Systemic analysis of osteoblast-specific DNA methylation marks reveals novel epigenetic basis of osteoblast differentiation. Bone Reports, 2017, 6, 109-119.	0.2	15
76	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
77	Mass spectrometry based proteomics profiling of human monocytes. Protein and Cell, 2017, 8, 123-133.	4.8	6
78	Regulatory element-based prediction identifies new susceptibility regulatory variants for osteoporosis. Human Genetics, 2017, 136, 963-974.	1.8	11
79	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
80	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
81	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
82	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
83	Genetic sharing with coronary artery disease identifies potential novel loci for bone mineral density. Bone, 2017, 103, 70-77.	1.4	19
84	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
85	Tissue-specific pathway association analysis using genome-wide association study summaries. Bioinformatics, 2017, 33, 243-247.	1.8	21
86	Functional relevance for associations between osteoporosis and genetic variants. PLoS ONE, 2017, 12, e0174808.	1.1	13
87	Identification of novel genetic loci for osteoporosis and/or rheumatoid arthritis using cFDR approach. PLoS ONE, 2017, 12, e0183842.	1.1	12
88	Replication of Caucasian Loci Associated with Osteoporosis-related Traits in East Asians. Journal of Bone Metabolism, 2016, 23, 233.	0.5	9
89	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
90	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

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91	Effect of short-term room temperature storage on the microbial community in infant fecal samples. Scientific Reports, 2016, 6, 26648.	1.6	39
92	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
93	Quantitative proteomics and integrative network analysis identified novel genes and pathways related to osteoporosis. Journal of Proteomics, 2016, 142, 45-52.	1.2	21
94	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
95	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
96	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
97	Composition of gut microbiota in infants in China and global comparison. Scientific Reports, 2016, 6, 36666.	1.6	63
98	Integrating Epigenomic Elements and GWASs Identifies BDNF Gene Affecting Bone Mineral Density and Osteoporotic Fracture Risk. Scientific Reports, 2016, 6, 30558.	1.6	29
99	An integrative imputation method based on multi-omics datasets. BMC Bioinformatics, 2016, 17, 247.	1.2	29
100	Networkâ€based proteomic analysis for postmenopausal osteoporosis in Caucasian females. Proteomics, 2016, 16, 12-28.	1.3	40
101	PPARGC1B gene is associated with Kashin-Beck disease in Han Chinese. Functional and Integrative Genomics, 2016, 16, 459-463.	1.4	1
102	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
103	Unified tests for fine-scale mapping and identifying sparse high-dimensional sequence associations. Bioinformatics, 2016, 32, 330-337.	1.8	5
104	RNA-sequencing study of peripheral blood monocytes in chronic periodontitis. Gene, 2016, 581, 152-160.	1.0	21
105	Exome sequencing identified FGF12 as a novel candidate gene for Kashin-Beck disease. Functional and Integrative Genomics, 2016, 16, 13-17.	1.4	10
106	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
107	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
108	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

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109	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
110	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
111	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
112	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
113	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
114	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
115	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
116	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
117	Integrative Analysis of Transcriptomic and Epigenomic Data to Reveal Regulation Patterns for BMD Variation. PLoS ONE, 2015, 10, e0138524.	1.1	25
118	Genome-Wide Association Study Identified Copy Number Variants Important for Appendicular Lean Mass. PLoS ONE, 2014, 9, e89776.	1.1	12
119	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
120	Integrative analysis of multiple diverse omics datasets by sparse group multitask regression. Frontiers in Cell and Developmental Biology, 2014, 2, 62.	1.8	23
121	Genome-wide Association Studies for Osteoporosis: A 2013 Update. Journal of Bone Metabolism, 2014, 21, 99.	0.5	57
122	Mutant ZP1 in Familial Infertility. New England Journal of Medicine, 2014, 370, 1220-1226.	13.9	114
123	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
124	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
125	FISH: fast and accurate diploid genotype imputation via segmental hidden Markov model. Bioinformatics, 2014, 30, 1876-1883.	1.8	27
126	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

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127	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
128	Is GSN significant for hip BMD in female Caucasians?. Bone, 2014, 63, 69-75.	1.4	21
129	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
130	Critical assessment of coalescent simulators in modeling recombination hotspots in genomic sequences. BMC Bioinformatics, 2014, 15, 3.	1.2	21
131	Meta-analysis of genome-wide association data identifies novel susceptibility loci for obesity. Human Molecular Genetics, 2014, 23, 820-830.	1.4	73
132	On individual genome-wide association studies and their meta-analysis. Human Genetics, 2014, 133, 265-279.	1.8	30
133	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
134	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. Human Molecular Genetics, 2014, 23, 1923-1933.	1.4	130
135	Common Copy Number Variation Detection From Multiple Sequenced Samples. IEEE Transactions on Biomedical Engineering, 2014, 61, 928-937.	2.5	22
136	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
137	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
138	A Unified Sparse Representation for Sequence Variant Identification for Complex Traits. Genetic Epidemiology, 2014, 38, 671-679.	0.6	9
139	CNV-TV: A robust method to discover copy number variation from short sequencing reads. BMC Bioinformatics, 2013, 14, 150.	1.2	38
140	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
141	Characterization of the DNA methylome and its interindividual variation in human peripheral blood monocytes. Epigenomics, 2013, 5, 255-269.	1.0	19
142	Group sparse canonical correlation analysis for genomic data integration. BMC Bioinformatics, 2013, 14, 245.	1.2	91
143	Gene-gene interaction between RBMS3 and ZNF516 influences bone mineral density. Journal of Bone and Mineral Research, 2013, 28, 828-837.	3.1	21
144	Genome-wide approaches for identifying genetic risk factors for osteoporosis. Genome Medicine, 2013, 5, 44.	3.6	23

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145	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
146	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
147	Genome-wide association study identified UQCC locus for spine bone size in humans. Bone, 2013, 53, 129-133.	1.4	16
148	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
149	Wnt/Î²-catenin signaling activates bone morphogenetic protein 2 expression in osteoblasts. Bone, 2013, 52, 145-156.	1.4	243
150	Rare ADH Variant Constellations are Specific for Alcohol Dependence. Alcohol and Alcoholism, 2013, 48, 9-14.	0.9	30
151	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
152	Meta-analysis identifies aMECOMgene as a novel predisposing factor of osteoporotic fracture. Journal of Medical Genetics, 2013, 50, 212-219.	1.5	30
153	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
154	Association of rare PTP4A1-PHF3-EYS variants with alcohol dependence. Journal of Human Genetics, 2013, 58, 178-179.	1.1	10
155	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
156	On Combining Reference Data to Improve Imputation Accuracy. PLoS ONE, 2013, 8, e55600.	1.1	8
157	Comparative Studies of Copy Number Variation Detection Methods for Next-Generation Sequencing Technologies. PLoS ONE, 2013, 8, e59128.	1.1	138
158	Comprehensive Characterization of Human Genome Variation by High Coverage Whole-Genome Sequencing of Forty Four Caucasians. PLoS ONE, 2013, 8, e59494.	1.1	62
159	Nuclear receptor NR5A2 and bone: gene expression and association with bone mineral density. European Journal of Endocrinology, 2012, 166, 69-75.	1.9	5
160	Genome-Wide Association Study of Alcohol Dependence Implicates KIAA0040 on Chromosome 1q. Neuropsychopharmacology, 2012, 37, 557-566.	2.8	104
161	Genome-Wide Copy Number Variation Association Analyses for Age at Menarche. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E2133-E2139.	1.8	2
162	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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163	Identification of genes for complex diseases by integrating multiple types of genomic data. , 2012, 2012, 5541-4.		0
164	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
165	Detection of common copy number variation with application to population clustering from next generation sequencing data. , 2012, 2012, 1246-9.		3
166	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
167	Meta-analysis suggests that smoking is associated with an increased risk of early natural menopause. Menopause, 2012, 19, 126-132.	0.8	96
168	Identification of Genes for Complex Diseases Using Integrated Analysis of Multiple Types of Genomic Data. PLoS ONE, 2012, 7, e42755.	1.1	15
169	Classification of Multicolor Fluorescence In Situ Hybridization (M-FISH) Images With Sparse Representation. IEEE Transactions on Nanobioscience, 2012, 11, 111-118.	2.2	24
170	Early molecular responses of bone to obstructive nephropathy induced by unilateral ureteral obstruction in mice. Nephrology, 2012, 17, 767-773.	0.7	23
171	Significant association between body composition phenotypes and the osteocalcin genomic region in normative human population. Bone, 2012, 51, 688-694.	1.4	23
172	The Impact of Imputation on Meta-Analysis of Genome-Wide Association Studies. PLoS ONE, 2012, 7, e34486.	1.1	7
173	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
174	Testing Rare Variants for Association with Diseases: A Bayesian Marker Selection Approach. Annals of Human Genetics, 2012, 76, 74-85.	0.3	6
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