List of Publications by Year in descending order

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454 papers	14,863 citations	20817 60 h-index	39675 94 g-index
463 all docs	463 docs citations	463 times ranked	17438 citing authors

#	Article	IF	Citations
1	A multiethnic whole genome sequencing study to identify novel loci for bone mineral density. Human Molecular Genetics, 2022, 31, 1067-1081.	2.9	8
2	Genome-wide meta-analysis of alcohol use disorder in East Asians. Neuropsychopharmacology, 2022, 47, 1791-1797.	5.4	10
3	Epigenomic and Transcriptomic Prioritization of Candidate Obesity-Risk Regulatory GWAS SNPs. International Journal of Molecular Sciences, 2022, 23, 1271.	4.1	5
4	Multi-omics research in sarcopenia: Current progress and future prospects. Ageing Research Reviews, 2022, 76, 101576.	10.9	24
5	Network-Based Approach to Repurpose Approved Drugs for COVID-19 by Integrating GWAS and Text Mining Data. Processes, 2022, 10, 326.	2.8	1
6	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.	3.9	3
7	A deep learning-based approach to automatic proximal femur segmentation in quantitative CT images. Medical and Biological Engineering and Computing, 2022, 60, 1417-1429.	2.8	15
8	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.	3.9	9
9	DeepDNAbP: A deep learning-based hybrid approach to improve the identification of deoxyribonucleic acid-binding proteins. Computers in Biology and Medicine, 2022, 145, 105433.	7.0	5
10	Integrative analysis of multi-omics data to detect the underlying molecular mechanisms for obesity in vivo in humans. Human Genomics, 2022, 16, 15.	2.9	6
11	Combining artificial intelligence: deep learning with Hi-C data to predict the functional effects of non-coding variants. Bioinformatics, 2021, 37, 1339-1344.	4.1	8
12	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.	2.8	3
13	GWA-based pleiotropic analysis identified potential SNPs and genes related to type 2 diabetes and obesity. Journal of Human Genetics, 2021, 66, 297-306.	2.3	12
14	Three pleiotropic loci associated with bone mineral density and lean body mass. Molecular Genetics and Genomics, 2021, 296, 55-65.	2.1	4
15	Identification of pleiotropic loci underlying hip bone mineral density and trunk lean mass. Journal of Human Genetics, 2021, 66, 251-260.	2.3	3
16	A gene-level methylome-wide association analysis identifies novel Alzheimerâ€™s disease genes. Bioinformatics, 2021, 37, 1933-1940.	4.1	7
17	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.	2.7	5
18	Zp4 is completely dispensable for fertility in female rats. Biology of Reproduction, 2021, 104, 1282-1291.	2.7	7

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19	Identification of Novel Pleiotropic SNPs Associated with Osteoporosis and Rheumatoid Arthritis. Calcified Tissue International, 2021, 109, 17-31.	3.1	5
20	Prioritization of Osteoporosisâ€Associated Genomeâ€wide Association Study (<scp>GWAS)</scp> Singleâ€Nucleotide Polymorphisms (<scp>SNPs)</scp> Using Epigenomics and Transcriptomics. JBMR Plus, 2021, 5, e10481.	2.7	14
21	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.	3.6	14
22	Identification of novel functional CpG-SNPs associated with Type 2 diabetes and birth weight. Aging, 2021, 13, 10619-10658.	3.1	5
23	Enhanced Identification of Novel Potential Variants for Appendicular Lean Mass by Leveraging Pleiotropy With Bone Mineral Density. Frontiers in Immunology, 2021, 12, 643894.	4.8	3
24	NeuroPred-FRL: an interpretable prediction model for identifying neuropeptide using feature representation learning. Briefings in Bioinformatics, 2021, 22, .	6.5	56
25	Identification of novel pleiotropic gene for bone mineral density and lean mass using the cFDR method. Annals of Human Genetics, 2021, 85, 201-212.	0.8	2
26	A systematic dissection of human primary osteoblasts in vivo at single-cell resolution. Aging, 2021, 13, 20629-20650.	3.1	19
27	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
28	A transcriptome-wide association study to detect novel genes for volumetric bone mineral density. Bone, 2021, 153, 116106.	2.9	3
29	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.	1.0	0
30	Bivariate genomeâ€wide association analysis identified three pleiotropic loci underlying osteoporosis and obesity. Clinical Genetics, 2020, 97, 785-786.	2.0	1
31	A road map for understanding molecular and genetic determinants of osteoporosis. Nature Reviews Endocrinology, 2020, 16, 91-103.	9.6	200
32	A novel computational strategy for DNA methylation imputation using mixture regression model (MRM). BMC Bioinformatics, 2020, 21, 552.	2.6	12
33	Identifying Pleiotropic SNPs Associated With Femoral Neck and Heel Bone Mineral Density. Frontiers in Genetics, 2020, 11, 772.	2.3	4
34	Four pleiotropic loci associated with fat mass and lean mass. International Journal of Obesity, 2020, 44, 2113-2123.	3.4	2
35	Gene Expression and RNA Splicing Imputation Identifies Novel Candidate Genes Associated with Osteoporosis. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e4742-e4757.	3.6	12
36	A Review of Integrative Imputation for Multi-Omics Datasets. Frontiers in Genetics, 2020, 11, 570255.	2.3	57

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37	Identification of pleiotropic genes between risk factors of stroke by multivariate metaCCA analysis. Molecular Genetics and Genomics, 2020, 295, 1173-1185.	2.1	5
38	Wholeâ€exome sequencing and genomeâ€wide association studies identify novel sarcopenia risk genes in Han Chinese. Molecular Genetics & Genomic Medicine, 2020, 8, e1267.	1.2	6
39	Network-based Transcriptome-wide Expression Study for Postmenopausal Osteoporosis. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 2678-2691.	3.6	8
40	Medium-coverage DNA sequencing in the design of the genetic association study. European Journal of Human Genetics, 2020, 28, 1459-1466.	2.8	2
41	Mendelian Randomization Identifies CpG Methylation Sites With Mediation Effects for Genetic Influences on BMD in Peripheral Blood Monocytes. Frontiers in Genetics, 2020, 11, 60.	2.3	9
42	Association of 3p27.1 Variants with Whole Body Lean Mass Identified by a Genome-wide Association Study. Scientific Reports, 2020, 10, 4293.	3.3	2
43	Identification of novel functional CpG-SNPs associated with type 2 diabetes and coronary artery disease. Molecular Genetics and Genomics, 2020, 295, 607-619.	2.1	11
44	Replication of FTO Gene associated with lean mass in a Meta-Analysis of Genome-Wide Association Studies. Scientific Reports, 2020, 10, 5057.	3.3	12
45	A transâ€ethnic twoâ€stage polygenetic scoring analysis detects genetic correlation between osteoporosis and schizophrenia. Clinical and Translational Medicine, 2020, 9, 21.	4.0	2
46	Osteoporosis- and obesity-risk interrelationships: an epigenetic analysis of GWAS-derived SNPs at the developmental gene TBX15. Epigenetics, 2020, 15, 728-749.	2.7	11
47	Quantification of aminobutyric acids and their clinical applications as biomarkers for osteoporosis. Communications Biology, 2020, 3, 39.	4.4	39
48	Two novel pleiotropic loci associated with osteoporosis and abdominal obesity. Human Genetics, 2020, 139, 1023-1035.	3.8	8
49	Detecting potential causal relationship between multiple risk factors and Alzheimerâ€™s disease using multivariable Mendelian randomization. Aging, 2020, 12, 21747-21757.	3.1	6
50	A Statistical Test for Differential Network Analysis Based on Inference of Gaussian Graphical Model. Scientific Reports, 2019, 9, 10863.	3.3	12
51	Geographical differences in osteoporosis, obesity, and sarcopenia related traits in white American cohorts. Scientific Reports, 2019, 9, 12311.	3.3	6
52	Gene shaving using a sensitivity analysis of kernel based machine learning approach, with applications to cancer data. PLoS ONE, 2019, 14, e0217027.	2.5	2
53	A statistical approach to fine-mapping for the identification of potential causal variants related to human intelligence. Journal of Human Genetics, 2019, 64, 781-787.	2.3	11
54	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.	2.7	13

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55	Long Noncoding RNA Analyses for Osteoporosis Risk in Caucasian Women. Calcified Tissue International, 2019, 105, 183-192.	3.1	20
56	Genetic risk factors identified in populations of European descent do not improve the prediction of osteoporotic fracture and bone mineral density in Chinese populations. Scientific Reports, 2019, 9, 6086.	3.3	6
57	Identification of a 1p21 independent functional variant for abdominal obesity. International Journal of Obesity, 2019, 43, 2480-2490.	3.4	5
58	Identification of novel genetic variants for type 2 diabetes, childhood obesity, and their pleiotropic loci. Journal of Human Genetics, 2019, 64, 369-377.	2.3	6
59	Two functional variants at 6p21.1 were associated with lean mass. Skeletal Muscle, 2019, 9, 28.	4.2	7
60	Assessing the Genetic Correlations Between Blood Plasma Proteins and Osteoporosis: A Polygenic Risk Score Analysis. Calcified Tissue International, 2019, 104, 171-181.	3.1	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.	4.1	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.	3.4	4
63	Joint study of two genome-wide association meta-analyses identified 20p12.1 and 20q13.33 for bone mineral density. Bone, 2018, 110, 378-385.	2.9	22
64	Genomeâ€wide association study of lncRNA polymorphisms with bone mineral density. Annals of Human Genetics, 2018, 82, 244-253.	0.8	10
65	A Sparse Regression Method for Group-Wise Feature Selection with False Discovery Rate Control. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1066-1078.	3.0	5
66	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
67	EPS-LASSO: test for high-dimensional regression under extreme phenotype sampling of continuous traits. Bioinformatics, 2018, 34, 1996-2003.	4.1	11
68	A novel approach for correction of crosstalk effects in pathway analysis and its application in osteoporosis research. Scientific Reports, 2018, 8, 668.	3.3	37
69	Identifying potentially common genes between dyslipidemia and osteoporosis using novel analytical approaches. Molecular Genetics and Genomics, 2018, 293, 711-723.	2.1	11
70	Fast and Accurate Detection of Complex Imaging Genetics Associations Based on Greedy Projected Distance Correlation. IEEE Transactions on Medical Imaging, 2018, 37, 860-870.	8.9	17
71	Assessing the Associations of Blood Metabolites With Osteoporosis: A Mendelian Randomization Study. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 1850-1855.	3.6	19
72	Improved detection of genetic loci in estimated glomerular filtration rate and type 2 diabetes using a pleiotropic cFDR method. Molecular Genetics and Genomics, 2018, 293, 225-235.	2.1	14

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73	Age at menarche and osteoporosis: A Mendelian randomization study. Bone, 2018, 117, 91-97.	2.9	39
74	Identification of potential functional genes in papillary thyroid cancer by coâ€'expression network analysis. Oncology Letters, 2018, 16, 4871-4878.	1.8	13
75	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.	2.3	5
76	Identification of novel variants associated with osteoporosis, type 2 diabetes and potentially pleiotropic loci using pleiotropic cFDR method. Bone, 2018, 117, 6-14.	2.9	19
77	Assessing the genetic correlations between early growth parameters and bone mineral density: A polygenic risk score analysis. Bone, 2018, 116, 301-306.	2.9	9
78	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
79	Copy Number Variation. , 2018, , 43-54.		1
80	Transcriptomic Data Identified Key Transcription Factors for Osteoporosis in Caucasian Women. Calcified Tissue International, 2018, 103, 581-588.	3.1	14
81	Metabolomic profiles associated with bone mineral density in US Caucasian women. Nutrition and Metabolism, 2018, 15, 57.	3.0	51
82	Genetically driven adiposity traits increase the risk of coronary artery disease independent of blood pressure, dyslipidaemia, glycaemic traits. European Journal of Human Genetics, 2018, 26, 1547-1553.	2.8	8
83	A joint analysis of metabolomic profiles associated with muscle mass and strength in Caucasian women. Aging, 2018, 10, 2624-2635.	3.1	18
84	Genomic variants at 20p11 associated with body fat mass in the European population. Obesity, 2017, 25, 757-764.	3.0	10
85	SNP-SNP interactions between WNT4 and WNT5A were associated with obesity related traits in Han Chinese Population. Scientific Reports, 2017, 7, 43939.	3.3	14
86	Comparison of statistical methods for subnetwork detection in the integration of gene expression and protein interaction network. BMC Bioinformatics, 2017, 18, 149.	2.6	29
87	A Statistical Approach to Fine Mapping for the Identification of Potential Causal Variants Related to Bone Mineral Density. Journal of Bone and Mineral Research, 2017, 32, 1651-1658.	2.8	12
88	A Systemic Analysis of Transcriptomic and Epigenomic Data To Reveal Regulation Patterns for Complex Disease. G3: Genes, Genomes, Genetics, 2017, 7, 2271-2279.	1.8	7
89	Increased identification of novel variants in type 2 diabetes, birth weight and their pleiotropic loci. Journal of Diabetes, 2017, 9, 898-907.	1.8	21
90	Mass spectrometry based proteomics profiling of human monocytes. Protein and Cell, 2017, 8, 123-133.	11.0	6

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91	Regulatory element-based prediction identifies new susceptibility regulatory variants for osteoporosis. Human Genetics, 2017, 136, 963-974.	3.8	11
92	A Systems Genetics Approach Identified GPD1L and its Molecular Mechanism for Obesity in Human Adipose Tissue. Scientific Reports, 2017, 7, 1799.	3.3	14
93	Increased detection of genetic loci associated with risk predictors of osteoporotic fracture using a pleiotropic cFDR method. Bone, 2017, 99, 62-68.	2.9	30
94	Gene-based genome-wide association study identified 19p13.3 for lean body mass. Scientific Reports, 2017, 7, 45025.	3.3	8
95	SNP rs11185644 of RXRA gene is identified for dose-response variability to vitamin D3 supplementation: a randomized clinical trial. Scientific Reports, 2017, 7, 40593.	3.3	25
96	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.	2.7	19
97	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
98	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
99	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.	3.9	2
100	Association Between Gut Microbiota and Bone Health: Potential Mechanisms and Prospective. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 3635-3646.	3.6	103
101	Connections between the human gut microbiome and gestational diabetes mellitus. GigaScience, 2017, 6, 1-12.	6.4	204
102	Novel Common Variants Associated with Obesity and Type 2 Diabetes Detected Using a cFDR Method. Scientific Reports, 2017, 7, 16397.	3.3	11
103	Genetic sharing with coronary artery disease identifies potential novel loci for bone mineral density. Bone, 2017, 103, 70-77.	2.9	19
104	Low-, high-coverage, and two-stage DNA sequencing in the design of the genetic association study. Genetic Epidemiology, 2017, 41, 187-197.	1.3	20
105	Tissue-specific pathway association analysis using genome-wide association study summaries. Bioinformatics, 2017, 33, 243-247.	4.1	21
106	Functional relevance for associations between osteoporosis and genetic variants. PLoS ONE, 2017, 12, e0174808.	2.5	13
107	Identification of novel genetic loci for osteoporosis and/or rheumatoid arthritis using cFDR approach. PLoS ONE, 2017, 12, e0183842.	2.5	12
108	Replication of Caucasian Loci Associated with Osteoporosis-related Traits in East Asians. Journal of Bone Metabolism, 2016, 23, 233.	1.3	9

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109	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
110	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
111	Effect of short-term room temperature storage on the microbial community in infant fecal samples. Scientific Reports, 2016, 6, 26648.	3.3	39
112	A bivariate genome-wide association study identifies ADAM12 as a novel susceptibility gene for Kashin-Beck disease. Scientific Reports, 2016, 6, 31792.	3.3	9
113	The Next Generation Sequencing and Applications in Clinical Research. Translational Bioinformatics, 2016, , 83-113.	0.0	0
114	Biostatistics, Data Mining and Computational Modeling. Translational Bioinformatics, 2016, , 23-57.	0.0	2
115	Quantitative proteomics and integrative network analysis identified novel genes and pathways related to osteoporosis. Journal of Proteomics, 2016, 142, 45-52.	2.4	21
116	Genome-wide association study in East Asians suggests UHMK1 as a novel bone mineral density susceptibility gene. Bone, 2016, 91, 113-121.	2.9	14
117	Genome-wide association meta-analyses identified 1q43 and 2q32.2 for hip Ward's triangle areal bone mineral density. Bone, 2016, 91, 1-10.	2.9	14
118	Integrating Epigenomic Elements and GWASs Identifies BDNF Gene Affecting Bone Mineral Density and Osteoporotic Fracture Risk. Scientific Reports, 2016, 6, 30558.	3.3	29
119	An integrative imputation method based on multi-omics datasets. BMC Bioinformatics, 2016, 17, 247.	2.6	29
120	Networkâ€based proteomic analysis for postmenopausal osteoporosis in Caucasian females. Proteomics, 2016, 16, 12-28.	2.2	40
121	PPARGC1B gene is associated with Kashin-Beck disease in Han Chinese. Functional and Integrative Genomics, 2016, 16, 459-463.	3.5	1
122	Exploring the Major Sources and Extent of Heterogeneity in a Genomeâ€Wide Association Metaâ€Analysis. Annals of Human Genetics, 2016, 80, 113-122.	0.8	9
123	Unified tests for fine-scale mapping and identifying sparse high-dimensional sequence associations. Bioinformatics, 2016, 32, 330-337.	4.1	5
124	RNA-sequencing study of peripheral blood monocytes in chronic periodontitis. Gene, 2016, 581, 152-160.	2.2	21
125	Exome sequencing identified FGF12 as a novel candidate gene for Kashin-Beck disease. Functional and Integrative Genomics, 2016, 16, 13-17.	3.5	10
126	A Sparse Model Based Detection of Copy Number Variations From Exome Sequencing Data. IEEE Transactions on Biomedical Engineering, 2016, 63, 496-505.	4.2	5

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127	Network-Based Meta-Analyses of Associations of Multiple Gene Expression Profiles with Bone Mineral Density Variations in Women. PLoS ONE, 2016, 11, e0147475.	2.5	12
128	Unified tests for fine scale mapping and identifying sparse high-dimensional sequence associations. , 2015, , .		0
129	Genome-Wide Survey of Runs of Homozygosity Identifies Recessive Loci for Bone Mineral Density in Caucasian and Chinese Populations. Journal of Bone and Mineral Research, 2015, 30, 2119-2126.	2.8	13
130	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
131	Genetic Analysis Identifies DDR2 as a Novel Gene Affecting Bone Mineral Density and Osteoporotic Fractures in Chinese Population. PLoS ONE, 2015, 10, e0117102.	2.5	6
132	SWGDT: A sliding window-based genotype dependence testing tool for genome-wide susceptibility gene scan. Journal of Biomedical Informatics, 2015, 57, 38-41.	4.3	1
133	Identification of a novelFGFRL1MicroRNA target site polymorphism for bone mineral density in meta-analyses of genome-wide association studies. Human Molecular Genetics, 2015, 24, 4710-4727.	2.9	22
134	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
135	MicroRNAâ€“mRNA interaction analysis to detect potential dysregulation in complex diseases. Network Modeling Analysis in Health Informatics and Bioinformatics, 2015, 4, 1.	2.1	10
136	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
137	Genome-wide pathway-based association study implicates complement system in the development of Kashin-Beck disease in Han Chinese. Bone, 2015, 71, 36-41.	2.9	12
138	Integrative Analysis of Transcriptomic and Epigenomic Data to Reveal Regulation Patterns for BMD Variation. PLoS ONE, 2015, 10, e0138524.	2.5	25
139	Genome-Wide Association Study Identified Copy Number Variants Important for Appendicular Lean Mass. PLoS ONE, 2014, 9, e89776.	2.5	12
140	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
141	Integrative analysis of multiple diverse omics datasets by sparse group multitask regression. Frontiers in Cell and Developmental Biology, 2014, 2, 62.	3.7	23
142	Genome-wide Association Studies for Osteoporosis: A 2013 Update. Journal of Bone Metabolism, 2014, 21, 99.	1.3	57
143	Mutant ZP1 in Familial Infertility. New England Journal of Medicine, 2014, 370, 1220-1226.	27.0	114
144	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.	1.7	3

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145	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.	3.6	10
146	FISH: fast and accurate diploid genotype imputation via segmental hidden Markov model. Bioinformatics, 2014, 30, 1876-1883.	4.1	27
147	Population clustering based on copy number variations detected from next generation sequencing data. Journal of Bioinformatics and Computational Biology, 2014, 12, 1450021.	0.8	0
148	Is GSN significant for hip BMD in female Caucasians?. Bone, 2014, 63, 69-75.	2.9	21
149	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
150	Meta-analysis of genome-wide association data identifies novel susceptibility loci for obesity. Human Molecular Genetics, 2014, 23, 820-830.	2.9	73
151	On individual genome-wide association studies and their meta-analysis. Human Genetics, 2014, 133, 265-279.	3.8	30
152	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. Human Molecular Genetics, 2014, 23, 1923-1933.	2.9	130
153	Common Copy Number Variation Detection From Multiple Sequenced Samples. IEEE Transactions on Biomedical Engineering, 2014, 61, 928-937.	4.2	22
154	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.	2.2	6
155	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
156	A Unified Sparse Representation for Sequence Variant Identification for Complex Traits. Genetic Epidemiology, 2014, 38, 671-679.	1.3	9
157	CNV-TV: A robust method to discover copy number variation from short sequencing reads. BMC Bioinformatics, 2013, 14, 150.	2.6	38
158	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
159	Characterization of the DNA methylome and its interindividual variation in human peripheral blood monocytes. Epigenomics, 2013, 5, 255-269.	2.1	19
160	Group sparse canonical correlation analysis for genomic data integration. BMC Bioinformatics, 2013, 14, 245.	2.6	91
161	Gene-gene interaction between RBMS3 and ZNF516 influences bone mineral density. Journal of Bone and Mineral Research, 2013, 28, 828-837.	2.8	21
162	Genome-wide approaches for identifying genetic risk factors for osteoporosis. Genome Medicine, 2013, 5, 44.	8.2	23

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163	Copy Number Variation on Chromosome 10q26.3 for Obesity Identified by a Genome-Wide Study. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E191-E195.	3.6	19
164	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
165	Genome-wide association study identified UQCC locus for spine bone size in humans. Bone, 2013, 53, 129-133.	2.9	16
166	On Genome-Wide Association Studies and Their Meta-Analyses: Lessons Learned From Osteoporosis Studies. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E1278-E1282.	3.6	18
167	Wnt/Î²-catenin signaling activates bone morphogenetic protein 2 expression in osteoblasts. Bone, 2013, 52, 145-156.	2.9	243
168	Rare ADH Variant Constellations are Specific for Alcohol Dependence. Alcohol and Alcoholism, 2013, 48, 9-14.	1.6	30
169	Meta-analysis identifies aMECOMgene as a novel predisposing factor of osteoporotic fracture. Journal of Medical Genetics, 2013, 50, 212-219.	3.2	30
170	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
171	Copy Number Variation. , 2013, , 123-132.		6
172	Modeling exome sequencing data with generalized Gaussian distribution with application to copy number variation detection. , 2013, , .		0
173	Association of rare PTP4A1-PHF3-EYS variants with alcohol dependence. Journal of Human Genetics, 2013, 58, 178-179.	2.3	10
174	Bivariate Genome-Wide Association Analyses Identified Genes with Pleiotropic Effects for Femoral Neck Bone Geometry and Age at Menarche. PLoS ONE, 2013, 8, e60362.	2.5	18
175	On Combining Reference Data to Improve Imputation Accuracy. PLoS ONE, 2013, 8, e55600.	2.5	8
176	Comparative Studies of Copy Number Variation Detection Methods for Next-Generation Sequencing Technologies. PLoS ONE, 2013, 8, e59128.	2.5	138
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