Lei Zhang

List of Publications by Year
in descending order

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68 papers	2,239 citations	279798 23 h-index	243625 44 g-index
70 all docs	70 docs citations	70 times ranked	4132 citing authors

#	Article	IF	Citations
1	A road map for understanding molecular and genetic determinants of osteoporosis. Nature Reviews Endocrinology, 2020, 16, 91-103.	9.6	200
2	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
3	Genome-wide association scans identified CTNNBL1 as a novel gene for obesity. Human Molecular Genetics, 2008, 17, 1803-1813.	2.9	168
4	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. Human Molecular Genetics, 2014, 23, 1923-1933.	2.9	130
5	Analyses and Comparison of Accuracy of Different Genotype Imputation Methods. PLoS ONE, 2008, 3, e3551.	2.5	117
6	Comparative studies of de novo assembly tools for next-generation sequencing technologies. Bioinformatics, 2011, 27, 2031-2037.	4.1	109
7	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
8	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
9	The genetic architecture of appendicular lean mass characterized by association analysis in the UK Biobank study. Communications Biology, 2020, 3, 608.	4.4	83
10	Meta-analysis of genome-wide association data identifies novel susceptibility loci for obesity. Human Molecular Genetics, 2014, 23, 820-830.	2.9	73
11	Genome-Wide Association Analyses Identify SPOCK as a Key Novel Gene Underlying Age at Menarche. PLoS Genetics, 2009, 5, e1000420.	3.5	59
12	Genome-wide Association Studies for Osteoporosis: A 2013 Update. Journal of Bone Metabolism, 2014, 21, 99.	1.3	57
13	V-ATPases and osteoclasts: ambiguous future of V-ATPases inhibitors in osteoporosis. Theranostics, 2018, 8, 5379-5399.	10.0	47
14	Evaluation of Compressive Strength Index of the Femoral Neck in Caucasians and Chinese. Calcified Tissue International, 2010, 87, 324-332.	3.1	44
15	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
16	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
17	Analyses and Comparison of Imputation-Based Association Methods. PLoS ONE, 2010, 5, e10827.	2.5	34
18	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

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19	On individual genome-wide association studies and their meta-analysis. Human Genetics, 2014, 133, 265-279.	3.8	30
20	Univariate/Multivariate Genome-Wide Association Scans Using Data from Families and Unrelated Samples. PLoS ONE, 2009, 4, e6502.	2.5	29
21	FISH: fast and accurate diploid genotype imputation via segmental hidden Markov model. Bioinformatics, 2014, 30, 1876-1883.	4.1	27
22	Joint Association Analysis Identified 18 New Loci for Bone Mineral Density. Journal of Bone and Mineral Research, 2019, 34, 1086-1094.	2.8	27
23	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
24	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
25	Genome-wide approaches for identifying genetic risk factors for osteoporosis. Genome Medicine, 2013, 5, 44.	8.2	23
26	Genome-Wide Association Study of Copy Number Variants Suggests LTBP1 and FGD4 Are Important for Alcohol Drinking. PLoS ONE, 2012, 7, e30860.	2.5	23
27	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
28	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
29	Gene-gene interaction between RBMS3 and ZNF516 influences bone mineral density. Journal of Bone and Mineral Research, 2013, 28, 828-837.	2.8	21
30	Efficient Utilization of Rare Variants for Detection of Disease-Related Genomic Regions. PLoS ONE, 2010, 5, e14288.	2.5	20
31	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
32	A multilocus linkage disequilibrium measure based on mutual information theory and its applications. Genetica, 2009, 137, 355-364.	1.1	18
33	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
34	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
35	Trps1 Differentially Modulates the Bone Mineral Density between Male and Female Mice and Its Polymorphism Associates with BMD Differently between Women and Men. PLoS ONE, 2014, 9, e84485.	2.5	16
36	Multivariate Association Test Using Haplotype Trend Regression. Annals of Human Genetics, 2009, 73, 456-464.	0.8	14

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37	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
38	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
39	Genome-Wide Association Study Identified Copy Number Variants Important for Appendicular Lean Mass. PLoS ONE, 2014, 9, e89776.	2.5	12
40	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
41	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
42	Bivariate genome-wide association study suggests fatty acid desaturase genes and cadherin DCHS2 for variation of both compressive strength index and appendicular lean mass in males. Bone, 2012, 51, 1000-1007.	2.9	11
43	Causal relationship between gut microbiota and serum vitamin D: evidence from genetic correlation and Mendelian randomization study. European Journal of Clinical Nutrition, 2022, 76, 1017-1023.	2.9	11
44	Bivariate genome-wide association study suggests that the DARC gene influences lean body mass and age at menarche. Science China Life Sciences, 2012, 55, 516-520.	4.9	10
45	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
46	Genomic variants at 20p11 associated with body fat mass in the European population. Obesity, 2017, 25, 757-764.	3.0	10
47	Genomeâ€wide association study of lncRNA polymorphisms with bone mineral density. Annals of Human Genetics, 2018, 82, 244-253.	0.8	10
48	Twelve New Genomic Loci Associated With Bone Mineral Density. Frontiers in Endocrinology, 2020, 11, 243.	3.5	10
49	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
50	Is the Townsend Deprivation Index a Reliable Predictor of Psychiatric Disorders?. Biological Psychiatry, 2021, 89, 839-841.	1.3	9
51	Gene-based genome-wide association study identified 19p13.3 for lean body mass. Scientific Reports, 2017, 7, 45025.	3.3	8
52	Two novel pleiotropic loci associated with osteoporosis and abdominal obesity. Human Genetics, 2020, 139, 1023-1035.	3.8	8
53	Two functional variants at 6p21.1 were associated with lean mass. Skeletal Muscle, 2019, 9, 28.	4.2	7
54	Family-Based Bivariate Association Tests for Quantitative Traits. PLoS ONE, 2009, 4, e8133.	2.5	7

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55	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
56	Testing Rare Variants for Association with Diseases: A Bayesian Marker Selection Approach. Annals of Human Genetics, 2012, 76, 74-85.	0.8	6
57	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
58	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
59	A new method for estimating effect size distribution and heritability from genome-wide association summary results. Human Genetics, 2016, 135, 171-184.	3.8	5
60	Identification of a 1p21 independent functional variant for abdominal obesity. International Journal of Obesity, 2019, 43, 2480-2490.	3.4	5
61	Improved Detection of Rare Genetic Variants for Diseases. PLoS ONE, 2010, 5, e13857.	2.5	5
62	Mendelian Randomization Analysis Reveals Causal Effects of Plasma Proteome on Body Composition Traits. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e2133-e2140.	3.6	5
63	Three pleiotropic loci associated with bone mineral density and lean body mass. Molecular Genetics and Genomics, 2021, 296, 55-65.	2.1	4
64	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
65	Identification of pleiotropic loci underlying hip bone mineral density and trunk lean mass. Journal of Human Genetics, 2021, 66, 251-260.	2.3	3
66	Four pleiotropic loci associated with fat mass and lean mass. International Journal of Obesity, 2020, 44, 2113-2123.	3.4	2
67	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
68	Bivariate genomeâ€wide association analysis identified three pleiotropic loci underlying osteoporosis and obesity. Clinical Genetics, 2020, 97, 785-786.	2.0	1