

# Lei Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Causal relationship between gut microbiota and serum vitamin D: evidence from genetic correlation and Mendelian randomization study. <i>European Journal of Clinical Nutrition</i> , 2022, 76, 1017-1023.	2.9	11
2	Mendelian Randomization Analysis Reveals Causal Effects of Plasma Proteome on Body Composition Traits. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, e2133-e2140.	3.6	5
3	Pleiotropic genomic variants at 17q21.31 associated with bone mineral density and body fat mass: a bivariate genome-wide association analysis. <i>European Journal of Human Genetics</i> , 2021, 29, 553-563.	2.8	3
4	Three pleiotropic loci associated with bone mineral density and lean body mass. <i>Molecular Genetics and Genomics</i> , 2021, 296, 55-65.	2.1	4
5	Identification of pleiotropic loci underlying hip bone mineral density and trunk lean mass. <i>Journal of Human Genetics</i> , 2021, 66, 251-260.	2.3	3
6	Is the Townsend Deprivation Index a Reliable Predictor of Psychiatric Disorders?. <i>Biological Psychiatry</i> , 2021, 89, 839-841.	1.3	9
7	Bivariate genome-wide association analysis identified three pleiotropic loci underlying osteoporosis and obesity. <i>Clinical Genetics</i> , 2020, 97, 785-786.	2.0	1
8	A road map for understanding molecular and genetic determinants of osteoporosis. <i>Nature Reviews Endocrinology</i> , 2020, 16, 91-103.	9.6	200
9	Four pleiotropic loci associated with fat mass and lean mass. <i>International Journal of Obesity</i> , 2020, 44, 2113-2123.	3.4	2
10	The genetic architecture of appendicular lean mass characterized by association analysis in the UK Biobank study. <i>Communications Biology</i> , 2020, 3, 608.	4.4	83
11	Gene Expression and RNA Splicing Imputation Identifies Novel Candidate Genes Associated with Osteoporosis. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, e4742-e4757.	3.6	12
12	Whole-exome sequencing and genome-wide association studies identify novel sarcopenia risk genes in Han Chinese. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2020, 8, e1267.	1.2	6
13	Association of 3p27.1 Variants with Whole Body Lean Mass Identified by a Genome-wide Association Study. <i>Scientific Reports</i> , 2020, 10, 4293.	3.3	2
14	Replication of FTO Gene associated with lean mass in a Meta-Analysis of Genome-Wide Association Studies. <i>Scientific Reports</i> , 2020, 10, 5057.	3.3	12
15	Two novel pleiotropic loci associated with osteoporosis and abdominal obesity. <i>Human Genetics</i> , 2020, 139, 1023-1035.	3.8	8
16	Twelve New Genomic Loci Associated With Bone Mineral Density. <i>Frontiers in Endocrinology</i> , 2020, 11, 243.	3.5	10
17	Joint Association Analysis Identified 18 New Loci for Bone Mineral Density. <i>Journal of Bone and Mineral Research</i> , 2019, 34, 1086-1094.	2.8	27
18	Genetic risk factors identified in populations of European descent do not improve the prediction of osteoporotic fracture and bone mineral density in Chinese populations. <i>Scientific Reports</i> , 2019, 9, 6086.	3.3	6

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19	Identification of a 1p21 independent functional variant for abdominal obesity. <i>International Journal of Obesity</i> , 2019, 43, 2480-2490.	3.4	5
20	Two functional variants at 6p21.1 were associated with lean mass. <i>Skeletal Muscle</i> , 2019, 9, 28.	4.2	7
21	Joint study of two genome-wide association meta-analyses identified 20p12.1 and 20q13.33 for bone mineral density. <i>Bone</i> , 2018, 110, 378-385.	2.9	22
22	Genome-wide association study of lncRNA polymorphisms with bone mineral density. <i>Annals of Human Genetics</i> , 2018, 82, 244-253.	0.8	10
23	V-ATPases and osteoclasts: ambiguous future of V-ATPases inhibitors in osteoporosis. <i>Theranostics</i> , 2018, 8, 5379-5399.	10.0	47
24	Genomic variants at 20p11 associated with body fat mass in the European population. <i>Obesity</i> , 2017, 25, 757-764.	3.0	10
25	Gene-based genome-wide association study identified 19p13.3 for lean body mass. <i>Scientific Reports</i> , 2017, 7, 45025.	3.3	8
26	Bivariate genome-wide association analyses identified genetic pleiotropic effects for bone mineral density and alcohol drinking in Caucasians. <i>Journal of Bone and Mineral Metabolism</i> , 2017, 35, 649-658.	2.7	19
27	Identification of <i>IDUA</i> and <i>WNT16</i> Phosphorylation-Related Non-Synonymous Polymorphisms for Bone Mineral Density in Meta-Analyses of Genome-Wide Association Studies. <i>Journal of Bone and Mineral Research</i> , 2016, 31, 358-368.	2.8	24
28	Genome-wide association study in East Asians suggests UHMK1 as a novel bone mineral density susceptibility gene. <i>Bone</i> , 2016, 91, 113-121.	2.9	14
29	Genome-wide association meta-analyses identified 1q43 and 2q32.2 for hip Ward's triangle areal bone mineral density. <i>Bone</i> , 2016, 91, 1-10.	2.9	14
30	Exploring the Major Sources and Extent of Heterogeneity in a Genome-Wide Association Meta-Analysis. <i>Annals of Human Genetics</i> , 2016, 80, 113-122.	0.8	9
31	A new method for estimating effect size distribution and heritability from genome-wide association summary results. <i>Human Genetics</i> , 2016, 135, 171-184.	3.8	5
32	Attenuated Monocyte Apoptosis, a New Mechanism for Osteoporosis Suggested by a Transcriptome-Wide Expression Study of Monocytes. <i>PLoS ONE</i> , 2015, 10, e0116792.	2.5	26
33	Identification of a novel <i>FGFRL1</i> MicroRNA target site polymorphism for bone mineral density in meta-analyses of genome-wide association studies. <i>Human Molecular Genetics</i> , 2015, 24, 4710-4727.	2.9	22
34	Genome-Wide Association Study Identified Copy Number Variants Important for Appendicular Lean Mass. <i>PLoS ONE</i> , 2014, 9, e89776.	2.5	12
35	Genome-wide Association Studies for Osteoporosis: A 2013 Update. <i>Journal of Bone Metabolism</i> , 2014, 21, 99.	1.3	57
36	Integrative Analysis of GWASs, Human Protein Interaction, and Gene Expression Identified Gene Modules Associated With BMDs. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2014, 99, E2392-E2399.	3.6	10

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37	FISH: fast and accurate diploid genotype imputation via segmental hidden Markov model. <i>Bioinformatics</i> , 2014, 30, 1876-1883.	4.1	27
38	Meta-analysis of genome-wide association data identifies novel susceptibility loci for obesity. <i>Human Molecular Genetics</i> , 2014, 23, 820-830.	2.9	73
39	On individual genome-wide association studies and their meta-analysis. <i>Human Genetics</i> , 2014, 133, 265-279.	3.8	30
40	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. <i>Human Molecular Genetics</i> , 2014, 23, 1923-1933.	2.9	130
41	Trps1 Differentially Modulates the Bone Mineral Density between Male and Female Mice and Its Polymorphism Associates with BMD Differently between Women and Men. <i>PLoS ONE</i> , 2014, 9, e84485.	2.5	16
42	Gene-gene interaction between <i>RBMS3</i> and <i>ZNF516</i> influences bone mineral density. <i>Journal of Bone and Mineral Research</i> , 2013, 28, 828-837.	2.8	21
43	Genome-wide approaches for identifying genetic risk factors for osteoporosis. <i>Genome Medicine</i> , 2013, 5, 44.	8.2	23
44	On Genome-Wide Association Studies and Their Meta-Analyses: Lessons Learned From Osteoporosis Studies. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013, 98, E1278-E1282.	3.6	18
45	Bivariate Genome-Wide Association Analyses Identified Genes with Pleiotropic Effects for Femoral Neck Bone Geometry and Age at Menarche. <i>PLoS ONE</i> , 2013, 8, e60362.	2.5	18
46	Genome-wide association study of copy number variation identified gremlin1 as a candidate gene for lean body mass. <i>Journal of Human Genetics</i> , 2012, 57, 33-37.	2.3	30
47	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. <i>Bone</i> , 2012, 51, 1000-1007.	2.9	11
48	Bivariate genome-wide association study suggests that the DARC gene influences lean body mass and age at menarche. <i>Science China Life Sciences</i> , 2012, 55, 516-520.	4.9	10
49	Testing Rare Variants for Association with Diseases: A Bayesian Marker Selection Approach. <i>Annals of Human Genetics</i> , 2012, 76, 74-85.	0.8	6
50	Genome-Wide Association Study of Copy Number Variants Suggests LTBP1 and FGD4 Are Important for Alcohol Drinking. <i>PLoS ONE</i> , 2012, 7, e30860.	2.5	23
51	Comparative studies of <i>de novo</i> assembly tools for next-generation sequencing technologies. <i>Bioinformatics</i> , 2011, 27, 2031-2037.	4.1	109
52	<i>IL21R</i> and <i>PTH</i> may underlie variation of femoral neck bone mineral density as revealed by a genome-wide association study. <i>Journal of Bone and Mineral Research</i> , 2010, 25, 1042-1048.	2.8	36
53	Evaluation of Compressive Strength Index of the Femoral Neck in Caucasians and Chinese. <i>Calcified Tissue International</i> , 2010, 87, 324-332.	3.1	44
54	Pathway-based genome-wide association analysis identified the importance of regulation-of-autophagy pathway for ultradistal radius BMD. <i>Journal of Bone and Mineral Research</i> , 2010, 25, 1572-1580.	2.8	103

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55	Analyses and Comparison of Imputation-Based Association Methods. PLoS ONE, 2010, 5, e10827.	2.5	34
56	Improved Detection of Rare Genetic Variants for Diseases. PLoS ONE, 2010, 5, e13857.	2.5	5
57	Efficient Utilization of Rare Variants for Detection of Disease-Related Genomic Regions. PLoS ONE, 2010, 5, e14288.	2.5	20
58	Univariate/Multivariate Genome-Wide Association Scans Using Data from Families and Unrelated Samples. PLoS ONE, 2009, 4, e6502.	2.5	29
59	Genome-Wide Association Analyses Identify SPOCK as a Key Novel Gene Underlying Age at Menarche. PLoS Genetics, 2009, 5, e1000420.	3.5	59
60	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
61	A multilocus linkage disequilibrium measure based on mutual information theory and its applications. Genetica, 2009, 137, 355-364.	1.1	18
62	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
63	Multivariate Association Test Using Haplotype Trend Regression. Annals of Human Genetics, 2009, 73, 456-464.	0.8	14
64	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
65	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
66	Family-Based Bivariate Association Tests for Quantitative Traits. PLoS ONE, 2009, 4, e8133.	2.5	7
67	Genome-wide association scans identified CTNBL1 as a novel gene for obesity. Human Molecular Genetics, 2008, 17, 1803-1813.	2.9	168
68	Analyses and Comparison of Accuracy of Different Genotype Imputation Methods. PLoS ONE, 2008, 3, e3551.	2.5	117