

Lei Zhang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

67
papers

1,655
citations

19
h-index

39
g-index

70
ext. papers

1,988
ext. citations

5
avg, IF

4.16
L-index

#	Paper	IF	Citations
67	Is the Townsend Deprivation Index a Reliable Predictor of Psychiatric Disorders?. <i>Biological Psychiatry</i> , 2021 , 89, 839-841	7.9	0
66	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	5.3	1
65	Three pleiotropic loci associated with bone mineral density and lean body mass. <i>Molecular Genetics and Genomics</i> , 2021 , 296, 55-65	3.1	2
64	Identification of pleiotropic loci underlying hip bone mineral density and trunk lean mass. <i>Journal of Human Genetics</i> , 2021 , 66, 251-260	4.3	0
63	Mendelian randomization analysis reveals causal effects of plasma proteome on body composition traits.. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 ,	5.6	1
62	Whole-exome sequencing and genome-wide association studies identify novel sarcopenia risk genes in Han Chinese. <i>Molecular Genetics & Genomic Medicine</i> , 2020 , 8, e1267	2.3	3
61	Association of 3p27.1 Variants with Whole Body Lean Mass Identified by a Genome-wide Association Study. <i>Scientific Reports</i> , 2020 , 10, 4293	4.9	2
60	Replication of FTO Gene associated with lean mass in a Meta-Analysis of Genome-Wide Association Studies. <i>Scientific Reports</i> , 2020 , 10, 5057	4.9	5
59	Two novel pleiotropic loci associated with osteoporosis and abdominal obesity. <i>Human Genetics</i> , 2020 , 139, 1023-1035	6.3	3
58	Twelve New Genomic Loci Associated With Bone Mineral Density. <i>Frontiers in Endocrinology</i> , 2020 , 11, 243	5.7	7
57	Bivariate genome-wide association analysis identified three pleiotropic loci underlying osteoporosis and obesity. <i>Clinical Genetics</i> , 2020 , 97, 785-786	4	1
56	A road map for understanding molecular and genetic determinants of osteoporosis. <i>Nature Reviews Endocrinology</i> , 2020 , 16, 91-103	15.2	85
55	Four pleiotropic loci associated with fat mass and lean mass. <i>International Journal of Obesity</i> , 2020 , 44, 2113-2123	5.5	1
54	The genetic architecture of appendicular lean mass characterized by association analysis in the UK Biobank study. <i>Communications Biology</i> , 2020 , 3, 608	6.7	7
53	Gene Expression and RNA Splicing Imputation Identifies Novel Candidate Genes Associated with Osteoporosis. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020 , 105,	5.6	5
52	Joint Association Analysis Identified 18 New Loci for Bone Mineral Density. <i>Journal of Bone and Mineral Research</i> , 2019 , 34, 1086-1094	6.3	15
51	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	4.9	4

50	Identification of a 1p21 independent functional variant for abdominal obesity. <i>International Journal of Obesity</i> , 2019 , 43, 2480-2490	5.5	3
49	Two functional variants at 6p21.1 were associated with lean mass. <i>Skeletal Muscle</i> , 2019 , 9, 28	5.1	6
48	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	4.7	14
47	Genome-wide association study of lncRNA polymorphisms with bone mineral density. <i>Annals of Human Genetics</i> , 2018 , 82, 244-253	2.2	9
46	V-ATPases and osteoclasts: ambiguous future of V-ATPases inhibitors in osteoporosis. <i>Theranostics</i> , 2018 , 8, 5379-5399	12.1	26
45	Genomic variants at 20p11 associated with body fat mass in the European population. <i>Obesity</i> , 2017 , 25, 757-764	8	9
44	Gene-based genome-wide association study identified 19p13.3 for lean body mass. <i>Scientific Reports</i> , 2017 , 7, 45025	4.9	6
43	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	2.9	9
42	Genome-wide association study in East Asians suggests UHMK1 as a novel bone mineral density susceptibility gene. <i>Bone</i> , 2016 , 91, 113-21	4.7	9
41	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	4.7	9
40	Exploring the Major Sources and Extent of Heterogeneity in a Genome-Wide Association Meta-Analysis. <i>Annals of Human Genetics</i> , 2016 , 80, 113-22	2.2	7
39	A new method for estimating effect size distribution and heritability from genome-wide association summary results. <i>Human Genetics</i> , 2016 , 135, 171-84	6.3	5
38	Identification of IDUA and WNT16 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, 358-68	6.3	20
37	Identification of a novel FGFR1 MicroRNA target site polymorphism for bone mineral density in meta-analyses of genome-wide association studies. <i>Human Molecular Genetics</i> , 2015 , 24, 4710-27	5.6	19
36	Attenuated monocyte apoptosis, a new mechanism for osteoporosis suggested by a transcriptome-wide expression study of monocytes. <i>PLoS ONE</i> , 2015 , 10, e0116792	3.7	19
35	Meta-analysis of genome-wide association data identifies novel susceptibility loci for obesity. <i>Human Molecular Genetics</i> , 2014 , 23, 820-30	5.6	62
34	On individual genome-wide association studies and their meta-analysis. <i>Human Genetics</i> , 2014 , 133, 265-73	7.9	19
33	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. <i>Human Molecular Genetics</i> , 2014 , 23, 1923-33	5.6	113

32	Genome-wide association study identified copy number variants important for appendicular lean mass. <i>PLoS ONE</i> , 2014 , 9, e89776	3.7	9
31	Genome-wide Association Studies for Osteoporosis: A 2013 Update. <i>Journal of Bone Metabolism</i> , 2014 , 21, 99-116	2.7	48
30	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, E2392-9	5.6	7
29	FISH: fast and accurate diploid genotype imputation via segmental hidden Markov model. <i>Bioinformatics</i> , 2014 , 30, 1876-83	7.2	18
28	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	3.7	12
27	Gene-gene interaction between RBMS3 and ZNF516 influences bone mineral density. <i>Journal of Bone and Mineral Research</i> , 2013 , 28, 828-37	6.3	14
26	Genome-wide approaches for identifying genetic risk factors for osteoporosis. <i>Genome Medicine</i> , 2013 , 5, 44	14.4	17
25	On genome-wide association studies and their meta-analyses: lessons learned from osteoporosis studies. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013 , 98, E1278-82	5.6	16
24	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	3.7	12
23	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, 1000-7	4.7	10
22	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, 516-20	8.5	7
21	Testing rare variants for association with diseases: a Bayesian marker selection approach. <i>Annals of Human Genetics</i> , 2012 , 76, 74-85	2.2	6
20	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, 33-7	4.3	28
19	Genome-wide association study of copy number variants suggests LTBP1 and FGD4 are important for alcohol drinking. <i>PLoS ONE</i> , 2012 , 7, e30860	3.7	12
18	Comparative studies of de novo assembly tools for next-generation sequencing technologies. <i>Bioinformatics</i> , 2011 , 27, 2031-7	7.2	103
17	Analyses and comparison of imputation-based association methods. <i>PLoS ONE</i> , 2010 , 5, e10827	3.7	26
16	IL21R and PTH 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, 1042-8	6.3	30
15	Evaluation of compressive strength index of the femoral neck in Caucasians and chinese. <i>Calcified Tissue International</i> , 2010 , 87, 324-32	3.9	37

14	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, 1572-80	6.3	82
13	Improved detection of rare genetic variants for diseases. <i>PLoS ONE</i> , 2010 , 5, e13857	3.7	4
12	Efficient utilization of rare variants for detection of disease-related genomic regions. <i>PLoS ONE</i> , 2010 , 5, e14288	3.7	17
11	Univariate/multivariate genome-wide association scans using data from families and unrelated samples. <i>PLoS ONE</i> , 2009 , 4, e6502	3.7	22
10	Genome-wide association analyses identify SPOCK as a key novel gene underlying age at menarche. <i>PLoS Genetics</i> , 2009 , 5, e1000420	6	55
9	Powerful bivariate genome-wide association analyses suggest the SOX6 gene influencing both obesity and osteoporosis phenotypes in males. <i>PLoS ONE</i> , 2009 , 4, e6827	3.7	78
8	A multilocus linkage disequilibrium measure based on mutual information theory and its applications. <i>Genetica</i> , 2009 , 137, 355-64	1.5	14
7	A PCA-based method for ancestral informative markers selection in structured populations. <i>Science in China Series C: Life Sciences</i> , 2009 , 52, 972-6		2
6	Multivariate association test using haplotype trend regression. <i>Annals of Human Genetics</i> , 2009 , 73, 456-64		12
5	Tests of association for quantitative traits in nuclear families using principal components to correct for population stratification. <i>Annals of Human Genetics</i> , 2009 , 73, 601-13	2.2	27
4	Genome-wide association and follow-up replication studies identified ADAMTS18 and TGFB3 as bone mass candidate genes in different ethnic groups. <i>American Journal of Human Genetics</i> , 2009 , 84, 388-98	11	165
3	Family-based bivariate association tests for quantitative traits. <i>PLoS ONE</i> , 2009 , 4, e8133	3.7	7
2	Genome-wide association scans identified CTNBL1 as a novel gene for obesity. <i>Human Molecular Genetics</i> , 2008 , 17, 1803-13	5.6	152
1	Analyses and comparison of accuracy of different genotype imputation methods. <i>PLoS ONE</i> , 2008 , 3, e3551	3.7	100