

Hui Shen

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.

93 papers	1,685 citations	20 h-index	39 g-index
101 ext. papers	2,241 ext. citations	6.1 avg, IF	4.49 L-index

#	Paper	IF	Citations
93	Multi-omics research in sarcopenia: Current progress and future prospects.. <i>Ageing Research Reviews</i> , 2022 , 76, 101576	12	4
92	Network-Based Approach to Repurpose Approved Drugs for COVID-19 by Integrating GWAS and Text Mining Data. <i>Processes</i> , 2022 , 10, 326	2.9	0
91	Integration of the Human Gut Microbiome and Serum Metabolome Reveals Novel Biological Factors Involved in the Regulation of Bone Mineral Density.. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022 , 12, 853499	5.9	0
90	Associations of physical activity with sarcopenia and sarcopenic obesity in middle-aged and older adults: the Louisiana osteoporosis study.. <i>BMC Public Health</i> , 2022 , 22, 896	4.1	0
89	Integrative analysis of multi-omics data to detect the underlying molecular mechanisms for obesity in vivo in humans.. <i>Human Genomics</i> , 2022 , 16, 15	6.8	0
88	Evaluation of the Activity and Efficacy of Anidulafungin-Loaded Human Serum Albumin Nanoparticles Against .. <i>Frontiers in Microbiology</i> , 2021 , 12, 788442	5.7	1
87	Single-cell RNA sequencing deconvolutes the heterogeneity of human bone marrow-derived mesenchymal stem cells. <i>International Journal of Biological Sciences</i> , 2021 , 17, 4192-4206	11.2	4
86	Prioritization of Osteoporosis-Associated Genome-wide Association Study (GWAS) Single-Nucleotide Polymorphisms (SNPs) Using Epigenomics and Transcriptomics. <i>JBMR Plus</i> , 2021 , 5, e10481	3.9	2
85	Identification and Functional Characterization of Metabolites for Bone Mass in Peri- and Postmenopausal Chinese Women. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 , 106, e3159-e3177	5.6	3
84	Single-cell RNA sequencing of human femoral head. <i>Aging</i> , 2021 , 13, 15595-15619	5.6	1
83	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
82	GWA-based pleiotropic analysis identified potential SNPs and genes related to type 2 diabetes and obesity. <i>Journal of Human Genetics</i> , 2021 , 66, 297-306	4.3	5
81	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
80	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
79	The RNA methyltransferase NSUN6 suppresses pancreatic cancer development by regulating cell proliferation. <i>EBioMedicine</i> , 2021 , 63, 103195	8.8	19
78	A systematic dissection of human primary osteoblasts at single-cell resolution. <i>Aging</i> , 2021 , 13, 20629-20650	5.6	2
77	A generalized kernel machine approach to identify higher-order composite effects in multi-view datasets, with application to adolescent brain development and osteoporosis. <i>Journal of Biomedical Informatics</i> , 2021 , 120, 103854	10.2	0

76	Human gut microbiome impacts skeletal muscle mass via gut microbial synthesis of the short-chain fatty acid butyrate among healthy menopausal women. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2021 ,	10.3	5
75	A transcriptome-wide association study to detect novel genes for volumetric bone mineral density. <i>Bone</i> , 2021 , 153, 116106	4.7	1
74	A Review of Integrative Imputation for Multi-Omics Datasets. <i>Frontiers in Genetics</i> , 2020 , 11, 570255	4.5	20
73	Medium-coverage DNA sequencing in the design of the genetic association study. <i>European Journal of Human Genetics</i> , 2020 , 28, 1459-1466	5.3	0
72	Deoxycholic acid modulates the progression of gallbladder cancer through N-methyladenosine-dependent microRNA maturation. <i>Oncogene</i> , 2020 , 39, 4983-5000	9.2	17
71	Mendelian Randomization Identifies CpG Methylation Sites With Mediation Effects for Genetic Influences on BMD in Peripheral Blood Monocytes. <i>Frontiers in Genetics</i> , 2020 , 11, 60	4.5	4
70	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
69	Identification of novel functional CpG-SNPs associated with type 2 diabetes and coronary artery disease. <i>Molecular Genetics and Genomics</i> , 2020 , 295, 607-619	3.1	4
68	A trans-ethnic two-stage polygenetic scoring analysis detects genetic correlation between osteoporosis and schizophrenia. <i>Clinical and Translational Medicine</i> , 2020 , 9, 21	5.7	2
67	Osteoporosis- and obesity-risk interrelationships: an epigenetic analysis of GWAS-derived SNPs at the developmental gene. <i>Epigenetics</i> , 2020 , 15, 728-749	5.7	4
66	Quantification of aminobutyric acids and their clinical applications as biomarkers for osteoporosis. <i>Communications Biology</i> , 2020 , 3, 39	6.7	17
65	Two novel pleiotropic loci associated with osteoporosis and abdominal obesity. <i>Human Genetics</i> , 2020 , 139, 1023-1035	6.3	3
64	A road map for understanding molecular and genetic determinants of osteoporosis. <i>Nature Reviews Endocrinology</i> , 2020 , 16, 91-103	15.2	85
63	Tamoxifen inhibits cell proliferation by impaired glucose metabolism in gallbladder cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2020 , 24, 1599-1613	5.6	6
62	Multi-omics Data Integration for Identifying Osteoporosis Biomarkers and Their Biological Interaction and Causal Mechanisms. <i>IScience</i> , 2020 , 23, 100847	6.1	12
61	A novel computational strategy for DNA methylation imputation using mixture regression model (MRM). <i>BMC Bioinformatics</i> , 2020 , 21, 552	3.6	1
60	Four pleiotropic loci associated with fat mass and lean mass. <i>International Journal of Obesity</i> , 2020 , 44, 2113-2123	5.5	1
59	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

58	Geographical differences in osteoporosis, obesity, and sarcopenia related traits in white American cohorts. <i>Scientific Reports</i> , 2019 , 9, 12311	4.9	2
57	Integrative genomic analysis predicts novel functional enhancer-SNPs for bone mineral density. <i>Human Genetics</i> , 2019 , 138, 167-185	6.3	3
56	mA Regulates Neurogenesis and Neuronal Development by Modulating Histone Methyltransferase Ezh2. <i>Genomics, Proteomics and Bioinformatics</i> , 2019 , 17, 154-168	6.5	73
55	PLEK2 promotes gallbladder cancer invasion and metastasis through EGFR/CCL2 pathway. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019 , 38, 247	12.8	30
54	Identification of a 1p21 independent functional variant for abdominal obesity. <i>International Journal of Obesity</i> , 2019 , 43, 2480-2490	5.5	3
53	A Statistical Test for Differential Network Analysis Based on Inference of Gaussian Graphical Model. <i>Scientific Reports</i> , 2019 , 9, 10863	4.9	5
52	Variants in oxidative stress-related genes affect the chemosensitivity through Nrf2-mediated signaling pathway in biliary tract cancer. <i>EBioMedicine</i> , 2019 , 48, 143-160	8.8	9
51	Two functional variants at 6p21.1 were associated with lean mass. <i>Skeletal Muscle</i> , 2019 , 9, 28	5.1	6
50	Genome-wide CRISPR screen identifies ELP5 as a determinant of gemcitabine sensitivity in gallbladder cancer. <i>Nature Communications</i> , 2019 , 10, 5492	17.4	33
49	Circular RNA circERBB2 promotes gallbladder cancer progression by regulating PA2G4-dependent rDNA transcription. <i>Molecular Cancer</i> , 2019 , 18, 166	42.1	51
48	PCA-based GRS analysis enhances the effectiveness for genetic correlation detection. <i>Briefings in Bioinformatics</i> , 2019 , 20, 2291-2298	13.4	5
47	Assessing the Genetic Correlations Between Blood Plasma Proteins and Osteoporosis: A Polygenic Risk Score Analysis. <i>Calcified Tissue International</i> , 2019 , 104, 171-181	3.9	3
46	Detecting epistasis within chromatin regulatory circuitry reveals CAND2 as a novel susceptibility gene for obesity. <i>International Journal of Obesity</i> , 2019 , 43, 450-456	5.5	3
45	Inferring causal relationships between phenotypes using summary statistics from genome-wide association studies. <i>Human Genetics</i> , 2018 , 137, 247-255	6.3	1
44	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
43	Genome-wide association study of lncRNA polymorphisms with bone mineral density. <i>Annals of Human Genetics</i> , 2018 , 82, 244-253	2.2	9
42	Identification of Novel Potentially Pleiotropic Variants Associated With Osteoporosis and Obesity Using the cFDR Method. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018 , 103, 125-138	5.6	27
41	PLZF inhibits proliferation and metastasis of gallbladder cancer by regulating IFIT2. <i>Cell Death and Disease</i> , 2018 , 9, 71	9.8	17

40	Assessing the Associations of Blood Metabolites With Osteoporosis: A Mendelian Randomization Study. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018 , 103, 1850-1855	5.6	11
39	Metabolomic profiles associated with bone mineral density in US Caucasian women. <i>Nutrition and Metabolism</i> , 2018 , 15, 57	4.6	30
38	A joint analysis of metabolomic profiles associated with muscle mass and strength in Caucasian women. <i>Aging</i> , 2018 , 10, 2624-2635	5.6	11
37	Assessing the genetic correlations between early growth parameters and bone mineral density: A polygenic risk score analysis. <i>Bone</i> , 2018 , 116, 301-306	4.7	5
36	Meta-Analysis of Genome-Wide Association Studies Identifies Novel Functional CpG-SNPs Associated with Bone Mineral Density at Lumbar Spine. <i>International Journal of Genomics</i> , 2018 , 2018, 6407257	2.5	6
35	Genomic variants at 20p11 associated with body fat mass in the European population. <i>Obesity</i> , 2017 , 25, 757-764	8	9
34	Fat mass and obesity-associated (FTO) protein regulates adult neurogenesis. <i>Human Molecular Genetics</i> , 2017 , 26, 2398-2411	5.6	134
33	Systemic analysis of osteoblast-specific DNA methylation marks reveals novel epigenetic basis of osteoblast differentiation. <i>Bone Reports</i> , 2017 , 6, 109-119	2.6	12
32	A Systems Genetics Approach Identified GPD1L and its Molecular Mechanism for Obesity in Human Adipose Tissue. <i>Scientific Reports</i> , 2017 , 7, 1799	4.9	10
31	Increased detection of genetic loci associated with risk predictors of osteoporotic fracture using a pleiotropic cFDR method. <i>Bone</i> , 2017 , 99, 62-68	4.7	19
30	Multiple analyses indicate the specific association of NR1I3, C6 and TNN with low hip BMD risk. <i>Journal of Genetics and Genomics</i> , 2017 , 44, 327-330	4	2
29	Low-, high-coverage, and two-stage DNA sequencing in the design of the genetic association study. <i>Genetic Epidemiology</i> , 2017 , 41, 187-197	2.6	15
28	Tissue-specific pathway association analysis using genome-wide association study summaries. <i>Bioinformatics</i> , 2017 , 33, 243-247	7.2	18
27	Exome sequencing identified FGF12 as a novel candidate gene for Kashin-Beck disease. <i>Functional and Integrative Genomics</i> , 2016 , 16, 13-7	3.8	7
26	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
25	Integrating Epigenomic Elements and GWASs Identifies BDNF Gene Affecting Bone Mineral Density and Osteoporotic Fracture Risk. <i>Scientific Reports</i> , 2016 , 6, 30558	4.9	23
24	Genome-wide alteration of 5-hydroxymethylcytosine in a mouse model of Alzheimer's disease. <i>BMC Genomics</i> , 2016 , 17, 381	4.5	40
23	Network-based proteomic analysis for postmenopausal osteoporosis in Caucasian females. <i>Proteomics</i> , 2016 , 16, 12-28	4.8	28

22	PPARGC1B gene is associated with Kashin-Beck disease in Han Chinese. <i>Functional and Integrative Genomics</i> , 2016 , 16, 459-63	3.8	
21	miR-145 sensitizes gallbladder cancer to cisplatin by regulating multidrug resistance associated protein 1. <i>Tumor Biology</i> , 2016 , 37, 10553-62	2.9	42
20	Impact of diabetes mellitus on the survival of pancreatic cancer: a meta-analysis. <i>OncoTargets and Therapy</i> , 2016 , 9, 1679-88	4.4	9
19	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
18	A bivariate genome-wide association study identifies ADAM12 as a novel susceptibility gene for Kashin-Beck disease. <i>Scientific Reports</i> , 2016 , 6, 31792	4.9	6
17	SWGDT: A sliding window-based genotype dependence testing tool for genome-wide susceptibility gene scan. <i>Journal of Biomedical Informatics</i> , 2015 , 57, 38-41	10.2	1
16	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
15	Genome-wide pathway-based association study implicates complement system in the development of Kashin-Beck disease in Han Chinese. <i>Bone</i> , 2015 , 71, 36-41	4.7	9
14	Genetic analysis identifies DDR2 as a novel gene affecting bone mineral density and osteoporotic fractures in Chinese population. <i>PLoS ONE</i> , 2015 , 10, e0117102	3.7	5
13	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
12	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
11	Trans-omics pathway analysis suggests that eQTLs contribute to chondrocyte apoptosis of Kashin-Beck disease through regulating apoptosis pathway expression. <i>Gene</i> , 2014 , 553, 166-9	3.8	6
10	Replication of 6 obesity genes in a meta-analysis of genome-wide association studies from diverse ancestries. <i>PLoS ONE</i> , 2014 , 9, e96149	3.7	45
9	Characterization of the DNA methylome and its interindividual variation in human peripheral blood monocytes. <i>Epigenomics</i> , 2013 , 5, 255-69	4.4	18
8	Comprehensive characterization of human genome variation by high coverage whole-genome sequencing of forty four Caucasians. <i>PLoS ONE</i> , 2013 , 8, e59494	3.7	47
7	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
6	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
5	Genome-wide association and replication studies identified TRHR as an important gene for lean body mass. <i>American Journal of Human Genetics</i> , 2009 , 84, 418-23	11	89

4	Tests of linkage and/or association of genes for vitamin D receptor, osteocalcin, and parathyroid hormone with bone mineral density. <i>Journal of Bone and Mineral Research</i> , 2002 , 17, 678-86	6.3	91
3	A genomewide linkage scan for quantitative-trait loci for obesity phenotypes. <i>American Journal of Human Genetics</i> , 2002 , 70, 1138-51	11	144
2	Thermotolerance induced by heat shock in <i>Chlorella</i> . <i>Journal of Applied Phycology</i> , 1997 , 9, 471-475	3.2	5
1	ST-V-Net: incorporating shape prior into convolutional neural networks for proximal femur segmentation. <i>Complex & Intelligent Systems</i> , 1	7.1	1