Hui Shen

List of Publications by Year
in descending order

98 papers	2,766 citations	218677 26 h-index	214800 47 g-index
101 all docs	101 docs citations	101 times ranked	4292 citing authors

#	Article	IF	Citations
1	Fat mass and obesity-associated (FTO) protein regulates adult neurogenesis. Human Molecular Genetics, 2017, 26, 2398-2411.	2.9	221
2	A road map for understanding molecular and genetic determinants of osteoporosis. Nature Reviews Endocrinology, 2020, 16, 91-103.	9.6	200
3	A Genomewide Linkage Scan for Quantitative-Trait Loci for Obesity Phenotypes. American Journal of Human Genetics, 2002, 70, 1138-1151.	6.2	151
4	m6A Regulates Neurogenesis and Neuronal Development by Modulating Histone Methyltransferase Ezh2. Genomics, Proteomics and Bioinformatics, 2019, 17, 154-168.	6.9	135
5	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. Human Molecular Genetics, 2014, 23, 1923-1933.	2.9	130
6	Tests of Linkage and/or Association of Genes for Vitamin D Receptor, Osteocalcin, and Parathyroid Hormone With Bone Mineral Density. Journal of Bone and Mineral Research, 2002, 17, 678-686.	2.8	109
7	Genome-wide Association and Replication Studies Identified TRHR as an Important Gene for Lean Body Mass. American Journal of Human Genetics, 2009, 84, 418-423.	6.2	103
8	Meta-analysis of genome-wide association data identifies novel susceptibility loci for obesity. Human Molecular Genetics, 2014, 23, 820-830.	2.9	73
9	Circular RNA circERBB2 promotes gallbladder cancer progression by regulating PA2G4-dependent rDNA transcription. Molecular Cancer, 2019, 18, 166.	19.2	71
10	Comprehensive Characterization of Human Genome Variation by High Coverage Whole-Genome Sequencing of Forty Four Caucasians. PLoS ONE, 2013, 8, e59494.	2.5	62
11	A Review of Integrative Imputation for Multi-Omics Datasets. Frontiers in Genetics, 2020, 11, 570255.	2.3	57
12	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
13	PLEK2 promotes gallbladder cancer invasion and metastasis through EGFR/CCL2 pathway. Journal of Experimental and Clinical Cancer Research, 2019, 38, 247.	8.6	56
14	Genome-wide CRISPR screen identifies ELP5 as a determinant of gemcitabine sensitivity in gallbladder cancer. Nature Communications, 2019, 10, 5492.	12.8	54
15	Metabolomic profiles associated with bone mineral density in US Caucasian women. Nutrition and Metabolism, 2018, 15, 57.	3.0	51
16	miR-145 sensitizes gallbladder cancer to cisplatin by regulating multidrug resistance associated protein 1. Tumor Biology, 2016, 37, 10553-10562.	1.8	50
17	Genome-wide alteration of 5-hydroxymenthylcytosine in a mouse model of Alzheimer's disease. BMC Genomics, 2016, 17, 381.	2.8	48
18	Multi-omics Data Integration for Identifying Osteoporosis Biomarkers and Their Biological Interaction and Causal Mechanisms. IScience, 2020, 23, 100847.	4.1	48

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19	Deoxycholic acid modulates the progression of gallbladder cancer through N6-methyladenosine-dependent microRNA maturation. Oncogene, 2020, 39, 4983-5000.	5.9	48
20	Human gut microbiome impacts skeletal muscle mass via gut microbial synthesis of the short€chain fatty acid butyrate among healthy menopausal women. Journal of Cachexia, Sarcopenia and Muscle, 2021, 12, 1860-1870.	7.3	48
21	The RNA methyltransferase NSUN6 suppresses pancreatic cancer development by regulating cell proliferation. EBioMedicine, 2021, 63, 103195.	6.1	45
22	Network€based proteomic analysis for postmenopausal osteoporosis in Caucasian females. Proteomics, 2016, 16, 12-28.	2.2	40
23	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
24	Quantification of aminobutyric acids and their clinical applications as biomarkers for osteoporosis. Communications Biology, 2020, 3, 39.	4.4	39
25	Single-cell RNA sequencing deconvolutes the *in vivo* heterogeneity of human bone marrow-derived mesenchymal stem cells. International Journal of Biological Sciences, 2021, 17, 4192-4206.	6.4	39
26	PLZF inhibits proliferation and metastasis of gallbladder cancer by regulating IFIT2. Cell Death and Disease, 2018, 9, 71.	6.3	36
27	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
28	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
29	Integrating Epigenomic Elements and GWASs Identifies BDNF Gene Affecting Bone Mineral Density and Osteoporotic Fracture Risk. Scientific Reports, 2016, 6, 30558.	3.3	29
30	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
31	Multi-omics research in sarcopenia: Current progress and future prospects. Ageing Research Reviews, 2022, 76, 101576.	10.9	24
32	Identification of a novel *FGFRL1* MicroRNA 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
33	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
34	Tissue-specific pathway association analysis using genome-wide association study summaries. Bioinformatics, 2017, 33, 243-247.	4.1	21
35	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
36	Variants in oxidative stress-related genes affect the chemosensitivity through Nrf2-mediated signaling pathway in biliary tract cancer. EBioMedicine, 2019, 48, 143-160.	6.1	20

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37	Characterization of the DNA methylome and its interindividual variation in human peripheral blood monocytes. Epigenomics, 2013, 5, 255-269.	2.1	19
38	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
39	A systematic dissection of human primary osteoblasts in vivo at single-cell resolution. Aging, 2021, 13, 20629-20650.	3.1	19
40	A joint analysis of metabolomic profiles associated with muscle mass and strength in Caucasian women. Aging, 2018, 10, 2624-2635.	3.1	18
41	O-GlcNAc transferase Ogt regulates embryonic neuronal development through modulating Wnt/Î²-catenin signaling. Human Molecular Genetics, 2021, 31, 57-68.	2.9	17
42	Systemic analysis of osteoblast-specific DNA methylation marks reveals novel epigenetic basis of osteoblast differentiation. Bone Reports, 2017, 6, 109-119.	0.4	15
43	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
44	A Systems Genetics Approach Identified GPD1L and its Molecular Mechanism for Obesity in Human Adipose Tissue. Scientific Reports, 2017, 7, 1799.	3.3	14
45	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
46	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
47	Single-cell RNA sequencing of human femoral head in vivo. Aging, 2021, 13, 15595-15619.	3.1	13
48	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
49	Impact of diabetes mellitus on the survival of pancreatic cancer: a meta-analysis. OncoTargets and Therapy, 2016, 9, 1679.	2.0	12
50	A Statistical Test for Differential Network Analysis Based on Inference of Gaussian Graphical Model. Scientific Reports, 2019, 9, 10863.	3.3	12
51	A novel computational strategy for DNA methylation imputation using mixture regression model (MRM). BMC Bioinformatics, 2020, 21, 552.	2.6	12
52	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
53	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
54	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

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55	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
56	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
57	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
58	Exome sequencing identified FGF12 as a novel candidate gene for Kashin-Beck disease. Functional and Integrative Genomics, 2016, 16, 13-17.	3.5	10
59	Genomic variants at 20p11 associated with body fat mass in the European population. Obesity, 2017, 25, 757-764.	3.0	10
60	Genome‐wide association study of lncRNA polymorphisms with bone mineral density. Annals of Human Genetics, 2018, 82, 244-253.	0.8	10
61	Tamoxifen inhibits cell proliferation by impaired glucose metabolism in gallbladder cancer. Journal of Cellular and Molecular Medicine, 2020, 24, 1599-1613.	3.6	10
62	Associations of physical activity with sarcopenia and sarcopenic obesity in middle-aged and older adults: the Louisiana osteoporosis study. BMC Public Health, 2022, 22, 896.	2.9	10
63	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
64	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
65	Meta-Analysis of Genome-Wide Association Studies Identifies Novel Functional CpG-SNPs Associated with Bone Mineral Density at Lumbar Spine. International Journal of Genomics, 2018, 2018, 1-11.	1.6	9
66	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
67	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
68	Inferring causal relationships between phenotypes using summary statistics from genome-wide association studies. Human Genetics, 2018, 137, 247-255.	3.8	8
69	Two novel pleiotropic loci associated with osteoporosis and abdominal obesity. Human Genetics, 2020, 139, 1023-1035.	3.8	8
70	ST-V-Net: incorporating shape prior into convolutional neural networks for proximal femur segmentation. Complex & Intelligent Systems, 2023, 9, 2747-2758.	6.5	8
71	A multiethnic whole genome sequencing study to identify novel loci for bone mineral density. Human Molecular Genetics, 2022, 31, 1067-1081.	2.9	8
72	Two functional variants at 6p21.1 were associated with lean mass. Skeletal Muscle, 2019, 9, 28.	4.2	7

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73	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
74	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
75	Geographical differences in osteoporosis, obesity, and sarcopenia related traits in white American cohorts. Scientific Reports, 2019, 9, 12311.	3.3	6
76	PCA-based GRS analysis enhances the effectiveness for genetic correlation detection. Briefings in Bioinformatics, 2019, 20, 2291-2298.	6.5	6
77	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
78	Thermotolerance induced by heat shock in Chlorella. Journal of Applied Phycology, 1997, 9, 471-475.	2.8	5
79	Identification of a 1p21 independent functional variant for abdominal obesity. International Journal of Obesity, 2019, 43, 2480-2490.	3.4	5
80	Epigenomic and Transcriptomic Prioritization of Candidate Obesity-Risk Regulatory GWAS SNPs. International Journal of Molecular Sciences, 2022, 23, 1271.	4.1	5
81	Pathway-based metabolomics study of sarcopenia-related traits in two US cohorts. Aging, 2022, 14, 2101-2112.	3.1	5
82	Integrative genomic analysis predicts novel functional enhancer-SNPs for bone mineral density. Human Genetics, 2019, 138, 167-185.	3.8	4
83	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
84	Three pleiotropic loci associated with bone mineral density and lean body mass. Molecular Genetics and Genomics, 2021, 296, 55-65.	2.1	4
85	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
86	Identification of pleiotropic loci underlying hip bone mineral density and trunk lean mass. Journal of Human Genetics, 2021, 66, 251-260.	2.3	3
87	A transcriptome-wide association study to detect novel genes for volumetric bone mineral density. Bone, 2021, 153, 116106.	2.9	3
88	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
89	Four pleiotropic loci associated with fat mass and lean mass. International Journal of Obesity, 2020, 44, 2113-2123.	3.4	2
90	Medium-coverage DNA sequencing in the design of the genetic association study. European Journal of Human Genetics, 2020, 28, 1459-1466.	2.8	2

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91	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
92	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
93	A generalized kernel machine approach to identify higher-order composite effects in multi-view datasets, with application to adolescent brain development and osteoporosis. Journal of Biomedical Informatics, 2021, 120, 103854.	4.3	2
94	Identification and Functional Characterization of Metabolites for Skeletal Muscle Mass in Early Postmenopausal Chinese Women. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2022, 77, 2346-2355.	3.6	2
95	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
96	PPARGC1B gene is associated with Kashin-Beck disease in Han Chinese. Functional and Integrative Genomics, 2016, 16, 459-463.	3.5	1
97	Evaluation of the in vitro Activity and in vivo Efficacy of Anidulafungin-Loaded Human Serum Albumin Nanoparticles Against Candida albicans. Frontiers in Microbiology, 2021, 12, 788442.	3.5	1
98	Network-Based Approach to Repurpose Approved Drugs for COVID-19 by Integrating GWAS and Text Mining Data. Processes, 2022, 10, 326.	2.8	1