Hou-Feng Zheng

List of Publications by Year
in descending order

65	8,530	159585 30	106344 65
papers	citations	h-index	g-index

74	74	74	15250
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Response to: â€˜Correspondence on â€˜Systemic evaluation of the relationship between psoriasis, psoriatic arthritis and osteoporosis: observational and Mendelian randomisation studyâ€™ by Lee. Annals of the Rheumatic Diseases, 2022, 81, e229-e229.	0.9	1
2	Genetically Determined Circulating Levels of Cytokines and the Risk of Rheumatoid Arthritis. Frontiers in Genetics, 2022, 13, 802464.	2.3	5
3	PAGEANT: personal access to genome and analysis of natural traits. Nucleic Acids Research, 2022, 50, e39-e39.	14.5	1
4	Identification of clinically actionable secondary genetic variants from wholeâ€genome sequencing in a largeâ€scale Chinese population. Clinical and Translational Medicine, 2022, 12, e866.	4.0	4
5	General and abdominal obesity operate differently as influencing factors of fracture risk in old adults. IScience, 2022, 25, 104466.	4.1	6
6	Genomic analyses of 10,376 individuals in the Westlake BioBank for Chinese (WBBC) pilot project. Nature Communications, 2022, 13, .	12.8	41
7	Oncogenic TRIB2 interacts with and regulates PKM2 to promote aerobic glycolysis and lung cancer cell procession. Cell Death Discovery, 2022, 8, .	4.7	7
8	Factors influencing peak bone mass gain. Frontiers of Medicine, 2021, 15, 53-69.	3.4	70
9	Twelve years of GWAS discoveries for osteoporosis and related traits: advances, challenges and applications. Bone Research, 2021, 9, 23.	11.4	85
10	Cohort profile: the Westlake BioBank for Chinese (WBBC) pilot project. BMJ Open, 2021, 11, e045564.	1.9	12
11	Integrative analysis of genomic and epigenomic data reveal underlying superenhancer-mediated microRNA regulatory network for human bone mineral density. Human Molecular Genetics, 2021, 30, 2177-2189.	2.9	4
12	Observational and genetic evidence highlight the association of human sleep behaviors with the incidence of fracture. Communications Biology, 2021, 4, 1339.	4.4	15
13	Genotype imputation and reference panel: a systematic evaluation on haplotype size and diversity. Briefings in Bioinformatics, 2020, 21, 1806-1817.	6.5	27
14	Response to: â€˜Correspondence on â€˜Systemic evaluation of the relationship between psoriasis, psoriatic arthritis and osteoporosis: observational and Mendelian randomisation studyâ€™â€™ by Cui et al. Annals of the Rheumatic Diseases, 2020, , annrheumdis-2020-219183.	0.9	0
15	Systemic evaluation of the relationship between psoriasis, psoriatic arthritis and osteoporosis: observational and Mendelian randomisation study. Annals of the Rheumatic Diseases, 2020, 79, 1460-1467.	0.9	41
16	Identification of PIEZO1 polymorphisms for human bone mineral density. Bone, 2020, 133, 115247.	2.9	30
17	Relationship between alcohol use, blood pressure and hypertension: an association study and a Mendelian randomisation study. Journal of Epidemiology and Community Health, 2019, 73, 796-801.	3.7	25
18	Effect of CD14 polymorphisms on the risk of cardiovascular disease: evidence from a meta-analysis. Lipids in Health and Disease, 2019, 18, 74.	3.0	9

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19	Exome-wide rare variant analyses of two bone mineral density phenotypes: the challenges of analyzing rare genetic variation. Scientific Reports, 2018, 8, 220.	3.3	2
20	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. American Journal of Human Genetics, 2018, 102, 88-102.	6.2	252
21	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	12.8	181
22	Comprehensive assessment of the association between genes on JAK-STAT pathway (IFIH1, TYK2, IL-10) and systemic lupus erythematosus: a meta-analysis. Archives of Dermatological Research, 2018, 310, 711-728.	1.9	15
23	Assessment of the genetic and clinical determinants of fracture risk: genome wide association and mendelian randomisation study. BMJ: British Medical Journal, 2018, 362, k3225.	2.3	190
24	A regulatory mutant on <scp>TRIM</scp>26 conferring the risk of nasopharyngeal carcinoma by inducing low immune response. Cancer Medicine, 2018, 7, 3848-3861.	2.8	14
25	Reproduction and In-Depth Evaluation of Genome-Wide Association Studies and Genome-Wide Meta-analyses Using Summary Statistics. G3: Genes, Genomes, Genetics, 2017, 7, 943-952.	1.8	3
26	Genome-wide association study meta-analysis for quantitative ultrasound parameters of bone identifies five novel loci for broadband ultrasound attenuation. Human Molecular Genetics, 2017, 26, 2791-2802.	2.9	32
27	Associations between PTPN22 and TLR9 polymorphisms and systemic lupus erythematosus: a comprehensive meta-analysis. Archives of Dermatological Research, 2017, 309, 461-477.	1.9	11
28	A combined reference panel from the 1000â€‰Genomes and UK10K projects improved rare variant imputation in European and Chinese samples. Scientific Reports, 2016, 6, 39313.	3.3	32
29	Comprehensive Assessment of the Association between FCGRs polymorphisms and the risk of systemic lupus erythematosus: Evidence from a Meta-Analysis. Scientific Reports, 2016, 6, 31617.	3.3	30
30	A method for analyzing multiple continuous phenotypes in rare variant association studies allowing for flexible correlations in variant effects. European Journal of Human Genetics, 2016, 24, 1344-1351.	2.8	21
31	Genome-wide association study using family-based cohorts identifies the WLS and CCDC170/ESR1 loci as associated with bone mineral density. BMC Genomics, 2016, 17, 136.	2.8	44
32	Probiotic and anti-inflammatory attributes of an isolate Lactobacillus helveticus NS8 from Mongolian fermented koumiss. BMC Microbiology, 2015, 15, 196.	3.3	78
33	Performance of Genotype Imputation for Low Frequency and Rare Variants from the 1000 Genomes. PLoS ONE, 2015, 10, e0116487.	2.5	62
34	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	12.8	75
35	Ethnicity-stratified analysis of the association between IL-18 polymorphisms and systemic lupus erythematosus in a European population: a meta-analysis. Archives of Dermatological Research, 2015, 307, 747-755.	1.9	3
36	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	27.8	483

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37	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
38	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. Nature Communications, 2015, 6, 8111.	12.8	300
39	Gene-gene and gene-environment interactions detected by transcriptome sequence analysis in twins. Nature Genetics, 2015, 47, 88-91.	21.4	215
40	Genetic determinants of heel bone properties: genome-wide association meta-analysis and replication in the GEFOS/GENOMOS consortium. Human Molecular Genetics, 2014, 23, 3054-3068.	2.9	90
41	Expression of Phosphofructokinase in Skeletal Muscle Is Influenced by Genetic Variation and Associated With Insulin Sensitivity. Diabetes, 2014, 63, 1154-1165.	0.6	41
42	Genetic interactions affecting human gene expression identified by variance association mapping. ELife, 2014, 3, e01381.	6.0	137
43	Association between CYP1A1 polymorphisms and esophageal cancer: a meta-analysis. Molecular Biology Reports, 2013, 40, 6035-6042.	2.3	13
44	Meta-analysis of genome-wide studies identifies WNT16 and ESR1 SNPs associated with bone mineral density in premenopausal women. Journal of Bone and Mineral Research, 2013, 28, 547-558.	2.8	87
45	Empirical power of very rare variants for common traits and disease: results from sanger sequencing 1998 individuals. European Journal of Human Genetics, 2013, 21, 1027-1030.	2.8	11
46	An example design of large-scale next-generation sequencing study for bone mineral density. IBMS BoneKEy, 2013, 10, .	0.0	2
47	Meta-analysis of genome-wide studies identifiesMEF2CSNPs associated with bone mineral density at forearm. Journal of Medical Genetics, 2013, 50, 473-478.	3.2	22
48	Imputation of Variants from the 1000 Genomes Project Modestly Improves Known Associations and Can Identify Low-frequency Variant - Phenotype Associations Undetected by HapMap Based Imputation. PLoS ONE, 2013, 8, e64343.	2.5	61
49	Association between C-reactive protein gene +1059 G/C polymorphism and the risk of coronary heart disease: a meta-analysis. Chinese Medical Journal, 2013, 126, 4780-5.	2.3	4
50	Meta-Analysis of Genome-Wide Scans for Total Body BMD in Children and Adults Reveals Allelic Heterogeneity and Age-Specific Effects at the WNT16 Locus. PLoS Genetics, 2012, 8, e1002718.	3.5	142
51	WNT16 Influences Bone Mineral Density, Cortical Bone Thickness, Bone Strength, and Osteoporotic Fracture Risk. PLoS Genetics, 2012, 8, e1002745.	3.5	240
52	Effect of Genome-Wide Genotyping and Reference Panels on Rare Variants Imputation. Journal of Genetics and Genomics, 2012, 39, 545-550.	3.9	40
53	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. Nature Genetics, 2012, 44, 491-501.	21.4	1,100
54	Assessment of gene-by-sex interaction effect on bone mineral density. Journal of Bone and Mineral Research, 2012, 27, 2051-2064.	2.8	47

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55	Genetics of osteoporosis from genome-wide association studies: advances and challenges. Nature Reviews Genetics, 2012, 13, 576-588.	16.3	269
56	Variants in MHC, LCE and IL12B have epistatic effects on psoriasis risk in Chinese population. Journal of Dermatological Science, 2011, 61, 124-128.	1.9	33
57	Association of HLA haplotype with keloids in Chinese Hans. Burns, 2011, 37, 794-799.	1.9	4
58	Insights into the genetics of osteoporosis from recent genome-wide association studies. Expert Reviews in Molecular Medicine, 2011, 13, e28.	3.9	30
59	The association of the BLK gene with SLE was replicated in Chinese Han. Archives of Dermatological Research, 2010, 302, 619-624.	1.9	27
60	Genome-wide association study of esophageal squamous cell carcinoma in Chinese subjects identifies a susceptibility locus at PLCE1. Nature Genetics, 2010, 42, 759-763.	21.4	383
61	A single nucleotide polymorphism of MHC region is associated with subphenotypes of Psoriasis in Chinese population. Journal of Dermatological Science, 2010, 59, 50-52.	1.9	6
62	Psoriasis genome-wide association study identifies susceptibility variants within LCE gene cluster at 1q21. Nature Genetics, 2009, 41, 205-210.	21.4	410
63	Genome-wide association study in a Chinese Han population identifies nine new susceptibility loci for systemic lupus erythematosus. Nature Genetics, 2009, 41, 1234-1237.	21.4	868
64	Genetic Structure of the Han Chinese Population Revealed by Genome-wide SNP Variation. American Journal of Human Genetics, 2009, 85, 775-785.	6.2	316
65	Genomewide Association Study of Leprosy. New England Journal of Medicine, 2009, 361, 2609-2618.	27.0	682