

Yu-Fang Pei

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.

62

papers

1,376

citations

19

h-index

35

g-index

67

ext. papers

1,680

ext. citations

4.9

avg, IF

3.96

L-index

#	Paper	IF	Citations
62	Causal Relationship Between Gut Microbiota and Autoimmune Diseases: A Two-Sample Mendelian Randomization Study.. <i>Frontiers in Immunology</i> , 2021 , 12, 746998	8.4	4
61	Gut Microbiota and Psychiatric Disorders: A Two-Sample Mendelian Randomization Study.. <i>Frontiers in Microbiology</i> , 2021 , 12, 737197	5.7	2
60	Mendelian Randomization Analysis Reveals Causal Effects of the Human Gut Microbiota on Abdominal Obesity. <i>Journal of Nutrition</i> , 2021 , 151, 1401-1406	4.1	1
59	Is the Townsend Deprivation Index a Reliable Predictor of Psychiatric Disorders?. <i>Biological Psychiatry</i> , 2021 , 89, 839-841	7.9	0
58	Joint Genome-Wide Association Analyses Identified 49 Novel Loci For Age at Natural Menopause. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 , 106, 2574-2591	5.6	3
57	Assessing causal relationship from gut microbiota to heel bone mineral density. <i>Bone</i> , 2021 , 143, 115652-7	4.7	10
56	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
55	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
54	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
53	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
52	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
51	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
50	Effects of probiotics on type II diabetes mellitus: a meta-analysis. <i>Journal of Translational Medicine</i> , 2020 , 18, 30	8.5	36
49	Two novel pleiotropic loci associated with osteoporosis and abdominal obesity. <i>Human Genetics</i> , 2020 , 139, 1023-1035	6.3	3
48	Twelve New Genomic Loci Associated With Bone Mineral Density. <i>Frontiers in Endocrinology</i> , 2020 , 11, 243	5.7	7
47	Bivariate genome-wide association analysis identified three pleiotropic loci underlying osteoporosis and obesity. <i>Clinical Genetics</i> , 2020 , 97, 785-786	4	1
46	Four pleiotropic loci associated with fat mass and lean mass. <i>International Journal of Obesity</i> , 2020 , 44, 2113-2123	5.5	1

45	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
44	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
43	Identification of a 1p21 independent functional variant for abdominal obesity. <i>International Journal of Obesity</i> , 2019 , 43, 2480-2490	5.5	3
42	Two functional variants at 6p21.1 were associated with lean mass. <i>Skeletal Muscle</i> , 2019 , 9, 28	5.1	6
41	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
40	Gut microbiota profiling in Han Chinese with type 1 diabetes. <i>Diabetes Research and Clinical Practice</i> , 2018 , 141, 256-263	7.4	42
39	Negative Binomial Mixed Models for Analyzing Longitudinal Microbiome Data. <i>Frontiers in Microbiology</i> , 2018 , 9, 1683	5.7	26
38	Genomic variants at 20p11 associated with body fat mass in the European population. <i>Obesity</i> , 2017 , 25, 757-764	8	9
37	Gene-based genome-wide association study identified 19p13.3 for lean body mass. <i>Scientific Reports</i> , 2017 , 7, 45025	4.9	6
36	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
35	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
34	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
33	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
32	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
31	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
30	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
29	On individual genome-wide association studies and their meta-analysis. <i>Human Genetics</i> , 2014 , 133, 265-79	7.9	19
28	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

27	FISH: fast and accurate diploid genotype imputation via segmental hidden Markov model. <i>Bioinformatics</i> , 2014 , 30, 1876-83	7.2	18
26	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
25	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
24	On combining reference data to improve imputation accuracy. <i>PLoS ONE</i> , 2013 , 8, e55600	3.7	8
23	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
22	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
21	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
20	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
19	ANKRD7 and CYTL1 are novel risk genes for alcohol drinking behavior. <i>Chinese Medical Journal</i> , 2012 , 125, 1127-34	2.9	10
18	Copy number variations at the Prader-Willi syndrome region on chromosome 15 and associations with obesity in whites. <i>Obesity</i> , 2011 , 19, 1229-34	8	20
17	Biological pathway-based genome-wide association analysis identified the vasoactive intestinal peptide (VIP) pathway important for obesity. <i>Obesity</i> , 2010 , 18, 2339-46	8	48
16	Analyses and comparison of imputation-based association methods. <i>PLoS ONE</i> , 2010 , 5, e10827	3.7	26
15	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
14	Impact of female cigarette smoking on circulating B cells in vivo: the suppressed ICOSLG, TCF3, and VCAM1 gene functional network may inhibit normal cell function. <i>Immunogenetics</i> , 2010 , 62, 237-51	3.2	14
13	Design and Interpretation of Linkage and Association Studies on Osteoporosis. <i>Clinical Reviews in Bone and Mineral Metabolism</i> , 2010 , 8, 60-67	2.5	
12	Improved detection of rare genetic variants for diseases. <i>PLoS ONE</i> , 2010 , 5, e13857	3.7	4
11	Efficient utilization of rare variants for detection of disease-related genomic regions. <i>PLoS ONE</i> , 2010 , 5, e14288	3.7	17
10	Univariate/multivariate genome-wide association scans using data from families and unrelated samples. <i>PLoS ONE</i> , 2009 , 4, e6502	3.7	22

9	Genome-wide association analyses identify SPOCK as a key novel gene underlying age at menarche. <i>PLoS Genetics</i> , 2009 , 5, e1000420	6	55
8	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
7	Multivariate association test using haplotype trend regression. <i>Annals of Human Genetics</i> , 2009 , 73, 456-64	6.4	12
6	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
5	Genome-wide association and follow-up replication studies identified ADAMTS18 and TGFBR3 as bone mass candidate genes in different ethnic groups. <i>American Journal of Human Genetics</i> , 2009 , 84, 388-98	11	165
4	Family-based bivariate association tests for quantitative traits. <i>PLoS ONE</i> , 2009 , 4, e8133	3.7	7
3	Genome-wide association scans identified CTNBL1 as a novel gene for obesity. <i>Human Molecular Genetics</i> , 2008 , 17, 1803-13	5.6	152
2	Analyses and comparison of accuracy of different genotype imputation methods. <i>PLoS ONE</i> , 2008 , 3, e3551	3.7	100
1	CYP17 MspA1 polymorphism and age at menarche: a meta-analysis. <i>Disease Markers</i> , 2008 , 25, 87-95	3.2	4