Tie-Lin Yang

List of Publications by Year
in descending order

126 papers	4,892 citations	126708 33 h-index	118652 62 g-index
134 all docs	134 docs citations	134 times ranked	7545 citing authors

#	Article	IF	Citations
1	MetaDecoder: a novel method for clustering metagenomic contigs. Microbiome, 2022, 10, 46.	4.9	13
2	ExsgRNA: reduce off-target efficiency by on-target mismatched sgRNA. Briefings in Bioinformatics, 2022, 23, .	3.2	2
3	Individualized pathway activity algorithm identifies oncogenic pathways in pan-cancer analysis. EBioMedicine, 2022, 79, 104014.	2.7	7
4	Bidirectional two-sample Mendelian randomization analysis identifies causal associations between relative carbohydrate intake and depression. Nature Human Behaviour, 2022, 6, 1569-1576.	6.2	30
5	LDBlockShow: a fast and convenient tool for visualizing linkage disequilibrium and haplotype blocks based on variant call format files. Briefings in Bioinformatics, 2021, 22, .	3.2	177
6	Genomic insights into the formation of human populations in East Asia. Nature, 2021, 591, 413-419.	13.7	216
7	Epigenetic Element-Based Transcriptome-Wide Association Study Identifies Novel Genes for Bipolar Disorder. Schizophrenia Bulletin, 2021, 47, 1642-1652.	2.3	8
8	Associations of plasma PAPP-A2 and genetic variations with salt sensitivity, blood pressure changes and hypertension incidence in Chinese adults. Journal of Hypertension, 2021, 39, 1817-1825.	0.3	12
9	Phenome-wide investigation of the causal associations between childhood BMI and adult trait outcomes: a two-sample Mendelian randomization study. Genome Medicine, 2021, 13, 48.	3.6	23
10	An Intronic Risk SNP rs12454712 for Central Obesity Acts As an Allele-Specific Enhancer To Regulate BCL2 Expression. Diabetes, 2021, 70, 1679-1688.	0.3	10
11	Associations of plasma uromodulin and genetic variants with blood pressure responses to dietary salt interventions. Journal of Clinical Hypertension, 2021, 23, 1897-1906.	1.0	14
12	A transcriptome-wide association study identifies novel susceptibility genes for psoriasis. Human Molecular Genetics, 2021, 31, 300-308.	1.4	6
13	Causal Associations Between Blood Lipids and COVID-19 Risk: A Two-Sample Mendelian Randomization Study. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 2802-2810.	1.1	15
14	DDRS: Detection of drug response SNPs specifically in patients receiving drug treatment. Computational and Structural Biotechnology Journal, 2021, 19, 3650-3657.	1.9	7
15	Large Multicohort Study Reveals a Prostate Cancer Susceptibility Allele at 5p15 Regulating TERT via Androgen Signaling-Orchestrated Chromatin Binding of E2F1 and MYC. Frontiers in Oncology, 2021, 11, 754206.	1.3	2
16	Associations of Serum Uromodulin and Its Genetic Variants With Blood Pressure and Hypertension in Chinese Adults. Frontiers in Cardiovascular Medicine, 2021, 8, 710023.	1.1	7
17	Associations of corin genetic polymorphisms with salt sensitivity, blood pressure changes, and hypertension incidence in Chinese adults. Journal of Clinical Hypertension, 2021, 23, 2115-2123.	1.0	12
18	Transcriptome-wide association study identifies multiple genes and pathways associated with thyroid function. Human Molecular Genetics, 2021, , .	1.4	2

#	Article	IF	Citations
19	An Allele-Specific Functional SNP Associated with Two Systemic Autoimmune Diseases Modulates IRF5 Expression by Long-Range Chromatin Loop Formation. Journal of Investigative Dermatology, 2020, 140, 348-360.e11.	0.3	25
20	Transcription Factor Enrichment Analysis in Enhancers Identifies EZH2 as a Susceptibility Gene for Osteoporosis. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e1152-e1161.	1.8	3
21	A road map for understanding molecular and genetic determinants of osteoporosis. Nature Reviews Endocrinology, 2020, 16, 91-103.	4.3	200
22	Genetic substructure and admixture of Mongolians and Kazakhs inferred from genome-wide array genotyping. Annals of Human Biology, 2020, 47, 620-628.	0.4	14
23	RTN4Bâ€mediated suppression of Sirtuin 2 activity ameliorates Î²â€amyloid pathology and cognitive impairment in Alzheimer's disease mouse model. Aging Cell, 2020, 19, e13194.	3.0	36
24	An integrative multi-omics network-based approach identifies key regulators for breast cancer. Computational and Structural Biotechnology Journal, 2020, 18, 2826-2835.	1.9	12
25	Modeling circRNA expression pattern with integrated sequence and epigenetic features demonstrates the potential involvement of H3K79me2 in circRNA expression. Bioinformatics, 2020, 36, 4739-4748.	1.8	3
26	A Chinese case of Nakajoâ€“Nishimura syndrome with novel compound heterozygous mutations of the PSMB8 gene. BMC Medical Genetics, 2020, 21, 126.	2.1	4
27	A programmable polymer library that enables the construction of stimuli-responsive nanocarriers containing logic gates. Nature Chemistry, 2020, 12, 381-390.	6.6	122
28	A transâ€ethnic twoâ€stage polygenetic scoring analysis detects genetic correlation between osteoporosis and schizophrenia. Clinical and Translational Medicine, 2020, 9, 21.	1.7	2
29	Multiomics dissection of molecular regulatory mechanisms underlying autoimmune-associated noncoding SNPs. JCI Insight, 2020, 5, .	2.3	13
30	An Osteoporosis Susceptibility Allele at 11p15 Regulates SOX6 Expression by Modulating TCF4 Chromatin Binding. Journal of Bone and Mineral Research, 2020, 37, 1147-1155.	3.1	4
31	Addressing the Missing Heritability Problem With the Help of Regulatory Features. Evolutionary Bioinformatics, 2019, 15, 117693431986086.	0.6	0
32	Comprehensive functional annotation of susceptibility SNPs prioritized 10 genes for schizophrenia. Translational Psychiatry, 2019, 9, 56.	2.4	20
33	PopLDdecay: a fast and effective tool for linkage disequilibrium decay analysis based on variant call format files. Bioinformatics, 2019, 35, 1786-1788.	1.8	818
34	Integrating regulatory features data for prediction of functional disease-associated SNPs. Briefings in Bioinformatics, 2019, 20, 26-32.	3.2	11
35	Detecting epistasis within chromatin regulatory circuitry reveals CAND2 as a novel susceptibility gene for obesity. International Journal of Obesity, 2019, 43, 450-456.	1.6	4
36	Matrine suppresses cardiac fibrosis by inhibiting the TGFâ€Î²/Smad pathway in experimental diabetic cardiomyopathy. Molecular Medicine Reports, 2018, 17, 1775-1781.	1.1	41

#	Article	IF	Citations
37	ERK-mediated phosphorylation regulates SOX10 sumoylation and targets expression in mutant BRAF melanoma. Nature Communications, 2018, 9, 28.	5.8	60
38	An Osteoporosis Risk SNP at 1p36.12 Acts as an Allele-Specific Enhancer to Modulate LINC00339 Expression via Long-Range Loop Formation. American Journal of Human Genetics, 2018, 102, 776-793.	2.6	78
39	Multiple Functional Variants at 13q14 Risk Locus for Osteoporosis Regulate RANKL Expression Through Long-Range Super-Enhancer. Journal of Bone and Mineral Research, 2018, 33, 1335-1346.	3.1	38
40	Comprehensive review and annotation of susceptibility SNPs associated with obesityâ€related traits. Obesity Reviews, 2018, 19, 917-930.	3.1	31
41	Gene expression profiles indicate tissue-specific obesity regulation changes and strong obesity relevant tissues. International Journal of Obesity, 2018, 42, 363-369.	1.6	12
42	V-ATPases and osteoclasts: ambiguous future of V-ATPases inhibitors in osteoporosis. Theranostics, 2018, 8, 5379-5399.	4.6	47
43	Runs of homozygosity associate with decreased risks of lung cancer in never-smoking East Asian females. Journal of Cancer, 2018, 9, 3858-3866.	1.2	1
44	Copy Number Variation. , 2018, , 43-54.		1
45	SNP-SNP interactions between WNT4 and WNT5A were associated with obesity related traits in Han Chinese Population. Scientific Reports, 2017, 7, 43939.	1.6	14
46	Regulatory element-based prediction identifies new susceptibility regulatory variants for osteoporosis. Human Genetics, 2017, 136, 963-974.	1.8	11
47	A functional SNP regulated by miR-196a-3p in the 3â€²UTR ofFGF2is associated with bone mineral density in the Chinese population. Human Mutation, 2017, 38, 725-735.	1.1	13
48	Matrineâ€Type Alkaloids Inhibit Advanced Glycation End Products Induced Reactive Oxygen Speciesâ€Mediated Apoptosis of Aortic Endothelial Cells In Vivo and In Vitro by Targeting MKK3 and p38MAPK Signaling. Journal of the American Heart Association, 2017, 6, .	1.6	26
49	Tissue-specific pathway association analysis using genome-wide association study summaries. Bioinformatics, 2017, 33, 243-247.	1.8	21
50	Epigenomic data facilitate genetic studies for osteoporosis in post-GWAS era. Annals of Translational Medicine, 2017, 5, 93-93.	0.7	0
51	Replication of Caucasian Loci Associated with Osteoporosis-related Traits in East Asians. Journal of Bone Metabolism, 2016, 23, 233.	0.5	9
52	Deficiency of ATP6V1H Causes Bone Loss by Inhibiting Bone Resorption and Bone Formation through the TGF-Î²1 Pathway. Theranostics, 2016, 6, 2183-2195.	4.6	43
53	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.	3.1	24
54	A bivariate genome-wide association study identifies ADAM12 as a novel susceptibility gene for Kashin-Beck disease. Scientific Reports, 2016, 6, 31792.	1.6	9

#	Article	IF	Citations
55	Epigenomic elements analyses for promoters identify ESRRG as a new susceptibility gene for obesity-related traits. International Journal of Obesity, 2016, 40, 1170-1176.	1.6	21
56	Associations of Plasma FGF2 Levels and Polymorphisms in the FGF2 Gene with Obesity Phenotypes in Han Chinese Population. Scientific Reports, 2016, 6, 19868.	1.6	19
57	Integrating Epigenomic Elements and GWASs Identifies BDNF Gene Affecting Bone Mineral Density and Osteoporotic Fracture Risk. Scientific Reports, 2016, 6, 30558.	1.6	29
58	PPARGC1B gene is associated with Kashin-Beck disease in Han Chinese. Functional and Integrative Genomics, 2016, 16, 459-463.	1.4	1
59	Exome sequencing identified FGF12 as a novel candidate gene for Kashin-Beck disease. Functional and Integrative Genomics, 2016, 16, 13-17.	1.4	10
60	Genome-Wide Survey of Runs of Homozygosity Identifies Recessive Loci for Bone Mineral Density in Caucasian and Chinese Populations. Journal of Bone and Mineral Research, 2015, 30, 2119-2126.	3.1	13
61	Genetic Analysis Identifies DDR2 as a Novel Gene Affecting Bone Mineral Density and Osteoporotic Fractures in Chinese Population. PLoS ONE, 2015, 10, e0117102.	1.1	6
62	Functional analyses reveal the essential role of SOX6 and RUNX2 in the communication of chondrocyte and osteoblast. Osteoporosis International, 2015, 26, 553-561.	1.3	17
63	SWGDT: A sliding window-based genotype dependence testing tool for genome-wide susceptibility gene scan. Journal of Biomedical Informatics, 2015, 57, 38-41.	2.5	1
64	Identification of a novelFGFRL1MicroRNA target site polymorphism for bone mineral density in meta-analyses of genome-wide association studies. Human Molecular Genetics, 2015, 24, 4710-4727.	1.4	22
65	Brief Report: Genomeâ€Wide Association Study Identifies ITPR2 as a Susceptibility Gene for Kashinâ€Beck Disease in Han Chinese. Arthritis and Rheumatology, 2015, 67, 176-181.	2.9	29
66	Association analyses of FGFR2 gene polymorphisms with femoral neck bone mineral density in Chinese Han population. Molecular Genetics and Genomics, 2015, 290, 485-491.	1.0	5
67	Genome-wide pathway-based association study implicates complement system in the development of Kashin-Beck disease in Han Chinese. Bone, 2015, 71, 36-41.	1.4	12
68	Genome-Wide Association Study Identified Copy Number Variants Important for Appendicular Lean Mass. PLoS ONE, 2014, 9, e89776.	1.1	12
69	Genome-wide copy number variation study and gene expression analysis identify ABI3BP as a susceptibility gene for Kashinâ€“Beck disease. Human Genetics, 2014, 133, 793-799.	1.8	42
70	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. Human Molecular Genetics, 2014, 23, 1923-1933.	1.4	130
71	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.	1.0	6
72	Gene-gene interaction between RBMS3 and ZNF516 influences bone mineral density. Journal of Bone and Mineral Research, 2013, 28, 828-837.	3.1	21

#	Article	IF	Citations
73	Copy Number Variation on Chromosome 10q26.3 for Obesity Identified by a Genome-Wide Study. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E191-E195.	1.8	19
74	Suggestion of GLYAT gene underlying variation of bone size and body lean mass as revealed by a bivariate genome-wide association study. Human Genetics, 2013, 132, 189-199.	1.8	50
75	Copy Number Variation. , 2013, , 123-132.		6
76	Ethnic differentiation of copy number variation on chromosome 16p12.3 for association with obesity phenotypes in European and Chinese populations. International Journal of Obesity, 2013, 37, 188-190.	1.6	19
77	Bivariate Genome-Wide Association Analyses Identified Genes with Pleiotropic Effects for Femoral Neck Bone Geometry and Age at Menarche. PLoS ONE, 2013, 8, e60362.	1.1	18
78	Nuclear receptor NR5A2 and bone: gene expression and association with bone mineral density. European Journal of Endocrinology, 2012, 166, 69-75.	1.9	5
79	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.	1.1	30
80	Are bone mineral density loci associated with hip osteoporotic fractures? A validation study on previously reported genome-wide association loci in a Chinese population. Genetics and Molecular Research, 2012, 11, 202-210.	0.3	20
81	A family-based association study identified CYP17 as a candidate gene for obesity susceptibility in Caucasians. Genetics and Molecular Research, 2012, 11, 1967-1974.	0.3	8
82	A follow-up association study of two genetic variants for bone mineral density variation in Caucasians. Osteoporosis International, 2012, 23, 1867-1875.	1.3	17
83	Genetic variants in the SOX6 gene are associated with bone mineral density in both Caucasian and Chinese populations. Osteoporosis International, 2012, 23, 781-787.	1.3	37
84	Genome-wide association study identifies HMGN3 locus for spine bone size variation in Chinese. Human Genetics, 2012, 131, 463-469.	1.8	6
85	Genome-Wide Association Study of Copy Number Variants Suggests LTBP1 and FGD4 Are Important for Alcohol Drinking. PLoS ONE, 2012, 7, e30860.	1.1	23
86	Genome-Wide Association Study Identified CNP12587 Region Underlying Height Variation in Chinese Females. PLoS ONE, 2012, 7, e44292.	1.1	2
87	ANKRD7 and CYTL1 are novel risk genes for alcohol drinking behavior. Chinese Medical Journal, 2012, 125, 1127-34.	0.9	11
88	Copy Number Variations at the Praderâ€“Willi Syndrome Region on Chromosome 15 and associations with Obesity in Whites. Obesity, 2011, 19, 1229-1234.	1.5	22
89	Genetic Association Study of Common Mitochondrial Variants on Body Fat Mass. PLoS ONE, 2011, 6, e21595.	1.1	30
90	Copy Number Variation in CNP267 Region May Be Associated with Hip Bone Size. PLoS ONE, 2011, 6, e22035.	1.1	5

#	Article	IF	Citations
91	The Fat Mass and Obesity Associated Gene, FTO, Is Also Associated with Osteoporosis Phenotypes. PLoS ONE, 2011, 6, e27312.	1.1	38
92	Mitochondria-Wide Association Study of Common Variants in Osteoporosis. Annals of Human Genetics, 2011, 75, 569-574.	0.3	33
93	IL21R and PTH may underlie variation of femoral neck bone mineral density as revealed by a genome-wide association study. Journal of Bone and Mineral Research, 2010, 25, 1042-1048.	3.1	36
94	Genome-wide association study for femoral neck bone geometry. Journal of Bone and Mineral Research, 2010, 25, 320-329.	3.1	43
95	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. Immunogenetics, 2010, 62, 237-251.	1.2	20
96	Genome-wide copy number variation association study suggested VPS13B gene for osteoporosis in Caucasians. Osteoporosis International, 2010, 21, 579-587.	1.3	32
97	A genome-wide association analysis implicates SOX6 as a candidate gene for wrist bone mass. Science China Life Sciences, 2010, 53, 1065-1072.	2.3	13
98	Pathway-based genome-wide association analysis identified the importance of regulation-of-autophagy pathway for ultradistal radius BMD. Journal of Bone and Mineral Research, 2010, 25, 1572-1580.	3.1	103
99	HMGA2 Is Confirmed To Be Associated with Human Adult Height. Annals of Human Genetics, 2010, 74, 11-16.	0.3	32
100	Molecular Genetic Studies of Gene Identification for Osteoporosis: The 2009 Update. Endocrine Reviews, 2010, 31, 447-505.	8.9	76
101	Genome-Wide Association Study Identifies ALDH7A1 as a Novel Susceptibility Gene for Osteoporosis. PLoS Genetics, 2010, 6, e1000806.	1.5	101
102	Runs of Homozygosity Identify a Recessive Locus 12q21.31 for Human Adult Height. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 3777-3782.	1.8	33
103	The regulation-of-autophagy pathway may influence Chinese stature variation: evidence from elder adults. Journal of Human Genetics, 2010, 55, 441-447.	1.1	20
104	A genome wide association study between copy number variation (CNV) and human height in Chinese population. Journal of Genetics and Genomics, 2010, 37, 779-785.	1.7	12
105	Genome-wide association study identifies two novel loci containing FLNB and SBF2 genes underlying stature variation. Human Molecular Genetics, 2009, 18, 1661-1669.	1.4	27
106	Genome-wide association study suggested copy number variation may be associated with body mass index in the Chinese population. Journal of Human Genetics, 2009, 54, 199-202.	1.1	78
107	Genome-wide association scan for stature in Chinese: evidence for ethnic specific loci. Human Genetics, 2009, 125, 1-9.	1.8	39
108	Genome-wide Association and Follow-Up Replication Studies Identified ADAMTS18 and TGFBR3 as Bone Mass Candidate Genes in Different Ethnic Groups. American Journal of Human Genetics, 2009, 84, 388-398.	2.6	187

#	Article	IF	Citations
109	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.	2.6	103
110	Whole Genome Distribution and Ethnic Differentiation of Copy Number Variation in Caucasian and Asian Populations. PLoS ONE, 2009, 4, e7958.	1.1	51
111	In Vivo Genome-Wide Expression Study on Human Circulating B Cells Suggests a Novel ESR1 and MAPK3 Network for Postmenopausal Osteoporosis. Journal of Bone and Mineral Research, 2008, 23, 644-654.	3.1	70
112	Genome-wide Copy-Number-Variation Study Identified a Susceptibility Gene, UGT2B17, for Osteoporosis. American Journal of Human Genetics, 2008, 83, 663-674.	2.6	209
113	Comprehensive association analyses of IGF1, ESR2, and CYP17 genes with adult height in Caucasians. European Journal of Human Genetics, 2008, 16, 1380-1387.	1.4	13
114	Genomewide Linkage Scan for Combined Obesity Phenotypes using Principal Component Analysis. Annals of Human Genetics, 2008, 72, 319-326.	0.3	30
115	Molecular genetic studies of gene identification for osteoporosis. Expert Review of Endocrinology and Metabolism, 2008, 3, 223-267.	1.2	5
116	Polymorphisms in the estrogen receptor genes are associated with hip fractures in Chinese. Bone, 2008, 43, 910-914.	1.4	23
117	Bivariate genome linkage analysis suggests pleiotropic effects on chromosomes 20p and 3p for body fat mass and lean mass. Genetical Research, 2008, 90, 259-268.	0.3	6
118	Polymorphism in the insulin-like growth factor 1 gene is associated with age at menarche in caucasian females. Human Reproduction, 2007, 22, 1789-1794.	0.4	43
119	Variations in RANK gene are associated with adult height in Caucasians. American Journal of Human Biology, 2007, 19, 559-565.	0.8	6
120	Epistatic Interactions between Genomic Regions Containing the COL1A1 Gene and Genes Regulating Osteoclast Differentiation may Influence Femoral Neck Bone Mineral Density. Annals of Human Genetics, 2007, 71, 152-159.	0.3	4
121	Robust and Comprehensive Analysis of 20 Osteoporosis Candidate Genes by Very High-Density Single-Nucleotide Polymorphism Screen Among 405 White Nuclear Families Identified Significant Association and Gene-Gene Interaction. Journal of Bone and Mineral Research, 2006, 21, 1678-1695.	3.1	85
122	Association analyses of CYP19 gene polymorphisms with height variation in a large sample of Caucasian nuclear families. Human Genetics, 2006, 120, 119-125.	1.8	9
123	Genetic and Environmental Correlations of Bone Mineral Density at Different Skeletal Sites in Females and Males. Calcified Tissue International, 2006, 78, 212-217.	1.5	39
124	Genomewide Linkage Scan for Quantitative Trait Loci Underlying Variation in Age at Menarche. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 1009-1014.	1.8	49
125	Polymorphisms of the low-density lipoprotein receptor-related protein 5 (LRP5) gene are associated with obesity phenotypes in a large family-based association study. Journal of Medical Genetics, 2006, 43, 798-803.	1.5	106
126	Polymorphisms of estrogen-biosynthesis genes CYP17 and CYP19 may influence age at menarche: a genetic association study in Caucasian females. Human Molecular Genetics, 2006, 15, 2401-2408.	1.4	47