

Tie-Lin Yang

List of Publications by Year in descending order

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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	PopLDdecay: a fast and effective tool for linkage disequilibrium decay analysis based on variant call format files. <i>Bioinformatics</i> , 2019, 35, 1786-1788.	1.8	818
2	Genomic insights into the formation of human populations in East Asia. <i>Nature</i> , 2021, 591, 413-419.	13.7	216
3	Genome-wide Copy-Number-Variation Study Identified a Susceptibility Gene, UGT2B17, for Osteoporosis. <i>American Journal of Human Genetics</i> , 2008, 83, 663-674.	2.6	209
4	A road map for understanding molecular and genetic determinants of osteoporosis. <i>Nature Reviews Endocrinology</i> , 2020, 16, 91-103.	4.3	200
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, 388-398.	2.6	187
6	LDBlockShow: a fast and convenient tool for visualizing linkage disequilibrium and haplotype blocks based on variant call format files. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	177
7	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. <i>Human Molecular Genetics</i> , 2014, 23, 1923-1933.	1.4	130
8	A programmable polymer library that enables the construction of stimuli-responsive nanocarriers containing logic gates. <i>Nature Chemistry</i> , 2020, 12, 381-390.	6.6	122
9	Polymorphisms of the low-density lipoprotein receptor-related protein 5 (LRP5) gene are associated with obesity phenotypes in a large family-based association study. <i>Journal of Medical Genetics</i> , 2006, 43, 798-803.	1.5	106
10	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, 418-423.	2.6	103
11	Pathway-based genome-wide association analysis identified the importance of regulation-of-autophagy pathway for ultradistal radius BMD. <i>Journal of Bone and Mineral Research</i> , 2010, 25, 1572-1580.	3.1	103
12	Genome-Wide Association Study Identifies ALDH7A1 as a Novel Susceptibility Gene for Osteoporosis. <i>PLoS Genetics</i> , 2010, 6, e1000806.	1.5	101
13	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. <i>Journal of Bone and Mineral Research</i> , 2006, 21, 1678-1695.	3.1	85
14	Genome-wide association study suggested copy number variation may be associated with body mass index in the Chinese population. <i>Journal of Human Genetics</i> , 2009, 54, 199-202.	1.1	78
15	An Osteoporosis Risk SNP at 1p36.12 Acts as an Allele-Specific Enhancer to Modulate LINC00339 Expression via Long-Range Loop Formation. <i>American Journal of Human Genetics</i> , 2018, 102, 776-793.	2.6	78
16	Molecular Genetic Studies of Gene Identification for Osteoporosis: The 2009 Update. <i>Endocrine Reviews</i> , 2010, 31, 447-505.	8.9	76
17	In Vivo Genome-Wide Expression Study on Human Circulating B Cells Suggests a Novel <i>ESR1</i> and <i>MAPK3</i> Network for Postmenopausal Osteoporosis. <i>Journal of Bone and Mineral Research</i> , 2008, 23, 644-654.	3.1	70
18	ERK-mediated phosphorylation regulates SOX10 sumoylation and targets expression in mutant BRAF melanoma. <i>Nature Communications</i> , 2018, 9, 28.	5.8	60

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19	Whole Genome Distribution and Ethnic Differentiation of Copy Number Variation in Caucasian and Asian Populations. <i>PLoS ONE</i> , 2009, 4, e7958.	1.1	51
20	Suggestion of GLYAT gene underlying variation of bone size and body lean mass as revealed by a bivariate genome-wide association study. <i>Human Genetics</i> , 2013, 132, 189-199.	1.8	50
21	Genomewide Linkage Scan for Quantitative Trait Loci Underlying Variation in Age at Menarche. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2006, 91, 1009-1014.	1.8	49
22	Polymorphisms of estrogen-biosynthesis genes CYP17 and CYP19 may influence age at menarche: a genetic association study in Caucasian females. <i>Human Molecular Genetics</i> , 2006, 15, 2401-2408.	1.4	47
23	V-ATPases and osteoclasts: ambiguous future of V-ATPases inhibitors in osteoporosis. <i>Theranostics</i> , 2018, 8, 5379-5399.	4.6	47
24	Polymorphism in the insulin-like growth factor 1 gene is associated with age at menarche in caucasian females. <i>Human Reproduction</i> , 2007, 22, 1789-1794.	0.4	43
25	Genome-wide association study for femoral neck bone geometry. <i>Journal of Bone and Mineral Research</i> , 2010, 25, 320-329.	3.1	43
26	Deficiency of <i>ATP6V1H</i> Causes Bone Loss by Inhibiting Bone Resorption and Bone Formation through the TGF- β 1 Pathway. <i>Theranostics</i> , 2016, 6, 2183-2195.	4.6	43
27	Genome-wide copy number variation study and gene expression analysis identify ABI3BP as a susceptibility gene for Kashin-Beck disease. <i>Human Genetics</i> , 2014, 133, 793-799.	1.8	42
28	Matrine suppresses cardiac fibrosis by inhibiting the TGF- β 2/Smad pathway in experimental diabetic cardiomyopathy. <i>Molecular Medicine Reports</i> , 2018, 17, 1775-1781.	1.1	41
29	Genetic and Environmental Correlations of Bone Mineral Density at Different Skeletal Sites in Females and Males. <i>Calcified Tissue International</i> , 2006, 78, 212-217.	1.5	39
30	Genome-wide association scan for stature in Chinese: evidence for ethnic specific loci. <i>Human Genetics</i> , 2009, 125, 1-9.	1.8	39
31	The Fat Mass and Obesity Associated Gene, FTO, Is Also Associated with Osteoporosis Phenotypes. <i>PLoS ONE</i> , 2011, 6, e27312.	1.1	38
32	Multiple Functional Variants at 13q14 Risk Locus for Osteoporosis Regulate <i>RANKL</i> Expression Through Long-Range Super-Enhancer. <i>Journal of Bone and Mineral Research</i> , 2018, 33, 1335-1346.	3.1	38
33	Genetic variants in the SOX6 gene are associated with bone mineral density in both Caucasian and Chinese populations. <i>Osteoporosis International</i> , 2012, 23, 781-787.	1.3	37
34	<i>IL21R</i> and <i>PTH</i> 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, 1042-1048.	3.1	36
35	RTN4-mediated suppression of Sirtuin 2 activity ameliorates β -amyloid pathology and cognitive impairment in Alzheimer's disease mouse model. <i>Aging Cell</i> , 2020, 19, e13194.	3.0	36
36	Runs of Homozygosity Identify a Recessive Locus 12q21.31 for Human Adult Height. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2010, 95, 3777-3782.	1.8	33

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37	Mitochondria-Wide Association Study of Common Variants in Osteoporosis. <i>Annals of Human Genetics</i> , 2011, 75, 569-574.	0.3	33
38	Genome-wide copy number variation association study suggested VPS13B gene for osteoporosis in Caucasians. <i>Osteoporosis International</i> , 2010, 21, 579-587.	1.3	32
39	<i>HMGA2</i> Is Confirmed To Be Associated with Human Adult Height. <i>Annals of Human Genetics</i> , 2010, 74, 11-16.	0.3	32
40	Comprehensive review and annotation of susceptibility SNPs associated with obesity-related traits. <i>Obesity Reviews</i> , 2018, 19, 917-930.	3.1	31
41	Genomewide Linkage Scan for Combined Obesity Phenotypes using Principal Component Analysis. <i>Annals of Human Genetics</i> , 2008, 72, 319-326.	0.3	30
42	Genetic Association Study of Common Mitochondrial Variants on Body Fat Mass. <i>PLoS ONE</i> , 2011, 6, e21595.	1.1	30
43	Genome-wide association study of copy number variation identified <i>gremlin1</i> as a candidate gene for lean body mass. <i>Journal of Human Genetics</i> , 2012, 57, 33-37.	1.1	30
44	Bidirectional two-sample Mendelian randomization analysis identifies causal associations between relative carbohydrate intake and depression. <i>Nature Human Behaviour</i> , 2022, 6, 1569-1576.	6.2	30
45	Brief Report: Genome-Wide Association Study Identifies <i>ITPR2</i> as a Susceptibility Gene for Kashin-Beck Disease in Han Chinese. <i>Arthritis and Rheumatology</i> , 2015, 67, 176-181.	2.9	29
46	Integrating Epigenomic Elements and GWASs Identifies BDNF Gene Affecting Bone Mineral Density and Osteoporotic Fracture Risk. <i>Scientific Reports</i> , 2016, 6, 30558.	1.6	29
47	Genome-wide association study identifies two novel loci containing <i>FLNB</i> and <i>SBF2</i> genes underlying stature variation. <i>Human Molecular Genetics</i> , 2009, 18, 1661-1669.	1.4	27
48	Matrine-Type Alkaloids Inhibit Advanced Glycation End Products Induced Reactive Oxygen Species-Mediated Apoptosis of Aortic Endothelial Cells In Vivo and In Vitro by Targeting MKK3 and p38MAPK Signaling. <i>Journal of the American Heart Association</i> , 2017, 6, .	1.6	26
49	An Allele-Specific Functional SNP Associated with Two Systemic Autoimmune Diseases Modulates IRF5 Expression by Long-Range Chromatin Loop Formation. <i>Journal of Investigative Dermatology</i> , 2020, 140, 348-360.e11.	0.3	25
50	Identification of <i>IDUA</i> and <i>WNT16</i> 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, 358-368.	3.1	24
51	Polymorphisms in the estrogen receptor genes are associated with hip fractures in Chinese. <i>Bone</i> , 2008, 43, 910-914.	1.4	23
52	Phenome-wide investigation of the causal associations between childhood BMI and adult trait outcomes: a two-sample Mendelian randomization study. <i>Genome Medicine</i> , 2021, 13, 48.	3.6	23
53	Genome-Wide Association Study of Copy Number Variants Suggests <i>LTBP1</i> and <i>FGD4</i> Are Important for Alcohol Drinking. <i>PLoS ONE</i> , 2012, 7, e30860.	1.1	23
54	Copy Number Variations at the Prader-Willi Syndrome Region on Chromosome 15 and associations with Obesity in Whites. <i>Obesity</i> , 2011, 19, 1229-1234.	1.5	22

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55	Identification of a novel <i>FGFR1</i> MicroRNA target site polymorphism for bone mineral density in meta-analyses of genome-wide association studies. <i>Human Molecular Genetics</i> , 2015, 24, 4710-4727.	1.4	22
56	Gene-gene interaction between <i>RBMS3</i> and <i>ZNF516</i> influences bone mineral density. <i>Journal of Bone and Mineral Research</i> , 2013, 28, 828-837.	3.1	21
57	Epigenomic elements analyses for promoters identify <i>ESRRG</i> as a new susceptibility gene for obesity-related traits. <i>International Journal of Obesity</i> , 2016, 40, 1170-1176.	1.6	21
58	Tissue-specific pathway association analysis using genome-wide association study summaries. <i>Bioinformatics</i> , 2017, 33, 243-247.	1.8	21
59	Impact of female cigarette smoking on circulating B cells in vivo: the suppressed <i>ICOSLG</i> , <i>TCF3</i> , and <i>VCAM1</i> gene functional network may inhibit normal cell function. <i>Immunogenetics</i> , 2010, 62, 237-251.	1.2	20
60	The regulation-of-autophagy pathway may influence Chinese stature variation: evidence from elder adults. <i>Journal of Human Genetics</i> , 2010, 55, 441-447.	1.1	20
61	Are bone mineral density loci associated with hip osteoporotic fractures? A validation study on previously reported genome-wide association loci in a Chinese population. <i>Genetics and Molecular Research</i> , 2012, 11, 202-210.	0.3	20
62	Comprehensive functional annotation of susceptibility SNPs prioritized 10 genes for schizophrenia. <i>Translational Psychiatry</i> , 2019, 9, 56.	2.4	20
63	Copy Number Variation on Chromosome 10q26.3 for Obesity Identified by a Genome-Wide Study. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013, 98, E191-E195.	1.8	19
64	Ethnic differentiation of copy number variation on chromosome 16p12.3 for association with obesity phenotypes in European and Chinese populations. <i>International Journal of Obesity</i> , 2013, 37, 188-190.	1.6	19
65	Associations of Plasma <i>FGF2</i> Levels and Polymorphisms in the <i>FGF2</i> Gene with Obesity Phenotypes in Han Chinese Population. <i>Scientific Reports</i> , 2016, 6, 19868.	1.6	19
66	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.	1.1	18
67	A follow-up association study of two genetic variants for bone mineral density variation in Caucasians. <i>Osteoporosis International</i> , 2012, 23, 1867-1875.	1.3	17
68	Functional analyses reveal the essential role of <i>SOX6</i> and <i>RUNX2</i> in the communication of chondrocyte and osteoblast. <i>Osteoporosis International</i> , 2015, 26, 553-561.	1.3	17
69	Causal Associations Between Blood Lipids and COVID-19 Risk: A Two-Sample Mendelian Randomization Study. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 2802-2810.	1.1	15
70	SNP-SNP interactions between <i>WNT4</i> and <i>WNT5A</i> were associated with obesity related traits in Han Chinese Population. <i>Scientific Reports</i> , 2017, 7, 43939.	1.6	14
71	Genetic substructure and admixture of Mongolians and Kazakhs inferred from genome-wide array genotyping. <i>Annals of Human Biology</i> , 2020, 47, 620-628.	0.4	14
72	Associations of plasma uromodulin and genetic variants with blood pressure responses to dietary salt interventions. <i>Journal of Clinical Hypertension</i> , 2021, 23, 1897-1906.	1.0	14

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73	Comprehensive association analyses of IGF1, ESR2, and CYP17 genes with adult height in Caucasians. <i>European Journal of Human Genetics</i> , 2008, 16, 1380-1387.	1.4	13
74	A genome-wide association analysis implicates SOX6 as a candidate gene for wrist bone mass. <i>Science China Life Sciences</i> , 2010, 53, 1065-1072.	2.3	13
75	Genome-Wide Survey of Runs of Homozygosity Identifies Recessive Loci for Bone Mineral Density in Caucasian and Chinese Populations. <i>Journal of Bone and Mineral Research</i> , 2015, 30, 2119-2126.	3.1	13
76	A functional SNP regulated by miR-196a-3p in the 3'UTR of <i>FGF2</i> is associated with bone mineral density in the Chinese population. <i>Human Mutation</i> , 2017, 38, 725-735.	1.1	13
77	Multimiomics dissection of molecular regulatory mechanisms underlying autoimmune-associated noncoding SNPs. <i>JCI Insight</i> , 2020, 5, .	2.3	13
78	MetaDecoder: a novel method for clustering metagenomic contigs. <i>Microbiome</i> , 2022, 10, 46.	4.9	13
79	A genome wide association study between copy number variation (CNV) and human height in Chinese population. <i>Journal of Genetics and Genomics</i> , 2010, 37, 779-785.	1.7	12
80	Genome-Wide Association Study Identified Copy Number Variants Important for Appendicular Lean Mass. <i>PLoS ONE</i> , 2014, 9, e89776.	1.1	12
81	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.	1.4	12
82	Gene expression profiles indicate tissue-specific obesity regulation changes and strong obesity relevant tissues. <i>International Journal of Obesity</i> , 2018, 42, 363-369.	1.6	12
83	An integrative multi-omics network-based approach identifies key regulators for breast cancer. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2826-2835.	1.9	12
84	Associations of plasma PAPP-A2 and genetic variations with salt sensitivity, blood pressure changes and hypertension incidence in Chinese adults. <i>Journal of Hypertension</i> , 2021, 39, 1817-1825.	0.3	12
85	Associations of corin genetic polymorphisms with salt sensitivity, blood pressure changes, and hypertension incidence in Chinese adults. <i>Journal of Clinical Hypertension</i> , 2021, 23, 2115-2123.	1.0	12
86	Regulatory element-based prediction identifies new susceptibility regulatory variants for osteoporosis. <i>Human Genetics</i> , 2017, 136, 963-974.	1.8	11
87	Integrating regulatory features data for prediction of functional disease-associated SNPs. <i>Briefings in Bioinformatics</i> , 2019, 20, 26-32.	3.2	11
88	ANKRD7 and CYTL1 are novel risk genes for alcohol drinking behavior. <i>Chinese Medical Journal</i> , 2012, 125, 1127-34.	0.9	11
89	Exome sequencing identified FGF12 as a novel candidate gene for Kashin-Beck disease. <i>Functional and Integrative Genomics</i> , 2016, 16, 13-17.	1.4	10
90	An Intronic Risk SNP rs12454712 for Central Obesity Acts As an Allele-Specific Enhancer To Regulate <i>BCL2</i> Expression. <i>Diabetes</i> , 2021, 70, 1679-1688.	0.3	10

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91	Association analyses of CYP19 gene polymorphisms with height variation in a large sample of Caucasian nuclear families. <i>Human Genetics</i> , 2006, 120, 119-125.	1.8	9
92	Replication of Caucasian Loci Associated with Osteoporosis-related Traits in East Asians. <i>Journal of Bone Metabolism</i> , 2016, 23, 233.	0.5	9
93	A bivariate genome-wide association study identifies ADAM12 as a novel susceptibility gene for Kashin-Beck disease. <i>Scientific Reports</i> , 2016, 6, 31792.	1.6	9
94	A family-based association study identified CYP17 as a candidate gene for obesity susceptibility in Caucasians. <i>Genetics and Molecular Research</i> , 2012, 11, 1967-1974.	0.3	8
95	Epigenetic Element-Based Transcriptome-Wide Association Study Identifies Novel Genes for Bipolar Disorder. <i>Schizophrenia Bulletin</i> , 2021, 47, 1642-1652.	2.3	8
96	DDRS: Detection of drug response SNPs specifically in patients receiving drug treatment. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3650-3657.	1.9	7
97	Associations of Serum Uromodulin and Its Genetic Variants With Blood Pressure and Hypertension in Chinese Adults. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 710023.	1.1	7
98	Individualized pathway activity algorithm identifies oncogenic pathways in pan-cancer analysis. <i>EBioMedicine</i> , 2022, 79, 104014.	2.7	7
99	Variations in RANK gene are associated with adult height in Caucasians. <i>American Journal of Human Biology</i> , 2007, 19, 559-565.	0.8	6
100	Bivariate genome linkage analysis suggests pleiotropic effects on chromosomes 20p and 3p for body fat mass and lean mass. <i>Genetical Research</i> , 2008, 90, 259-268.	0.3	6
101	Genome-wide association study identifies HMG3 locus for spine bone size variation in Chinese. <i>Human Genetics</i> , 2012, 131, 463-469.	1.8	6
102	Copy Number Variation. , 2013, , 123-132.		6
103	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, 166-169.	1.0	6
104	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.	1.1	6
105	A transcriptome-wide association study identifies novel susceptibility genes for psoriasis. <i>Human Molecular Genetics</i> , 2021, 31, 300-308.	1.4	6
106	Molecular genetic studies of gene identification for osteoporosis. <i>Expert Review of Endocrinology and Metabolism</i> , 2008, 3, 223-267.	1.2	5
107	Copy Number Variation in CNP267 Region May Be Associated with Hip Bone Size. <i>PLoS ONE</i> , 2011, 6, e22035.	1.1	5
108	Nuclear receptor NR5A2 and bone: gene expression and association with bone mineral density. <i>European Journal of Endocrinology</i> , 2012, 166, 69-75.	1.9	5

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109	Association analyses of FGFR2 gene polymorphisms with femoral neck bone mineral density in Chinese Han population. <i>Molecular Genetics and Genomics</i> , 2015, 290, 485-491.	1.0	5
110	Epistatic Interactions between Genomic Regions Containing the COL1A1 Gene and Genes Regulating Osteoclast Differentiation may Influence Femoral Neck Bone Mineral Density. <i>Annals of Human Genetics</i> , 2007, 71, 152-159.	0.3	4
111	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.	1.6	4
112	A Chinese case of Nakajo's Nishimura syndrome with novel compound heterozygous mutations of the PSMB8 gene. <i>BMC Medical Genetics</i> , 2020, 21, 126.	2.1	4
113	An Osteoporosis Susceptibility Allele at 11p15 Regulates SOX6 Expression by Modulating TCF4 Chromatin Binding. <i>Journal of Bone and Mineral Research</i> , 2020, 37, 1147-1155.	3.1	4
114	Transcription Factor Enrichment Analysis in Enhancers Identifies EZH2 as a Susceptibility Gene for Osteoporosis. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, e1152-e1161.	1.8	3
115	Modeling circRNA expression pattern with integrated sequence and epigenetic features demonstrates the potential involvement of H3K79me2 in circRNA expression. <i>Bioinformatics</i> , 2020, 36, 4739-4748.	1.8	3
116	A trans-ethnic two-stage polygenic scoring analysis detects genetic correlation between osteoporosis and schizophrenia. <i>Clinical and Translational Medicine</i> , 2020, 9, 21.	1.7	2
117	Genome-Wide Association Study Identified CNP12587 Region Underlying Height Variation in Chinese Females. <i>PLoS ONE</i> , 2012, 7, e44292.	1.1	2
118	Large Multicohort Study Reveals a Prostate Cancer Susceptibility Allele at 5p15 Regulating TERT via Androgen Signaling-Orchestrated Chromatin Binding of E2F1 and MYC. <i>Frontiers in Oncology</i> , 2021, 11, 754206.	1.3	2
119	Transcriptome-wide association study identifies multiple genes and pathways associated with thyroid function. <i>Human Molecular Genetics</i> , 2021, , .	1.4	2
120	ExsgRNA: reduce off-target efficiency by on-target mismatched sgRNA. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	2
121	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.	2.5	1
122	PPARGC1B gene is associated with Kashin-Beck disease in Han Chinese. <i>Functional and Integrative Genomics</i> , 2016, 16, 459-463.	1.4	1
123	Runs of homozygosity associate with decreased risks of lung cancer in never-smoking East Asian females. <i>Journal of Cancer</i> , 2018, 9, 3858-3866.	1.2	1
124	Copy Number Variation. , 2018, , 43-54.		1
125	Addressing the Missing Heritability Problem With the Help of Regulatory Features. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431986086.	0.6	0
126	Epigenomic data facilitate genetic studies for osteoporosis in post-GWAS era. <i>Annals of Translational Medicine</i> , 2017, 5, 93-93.	0.7	0