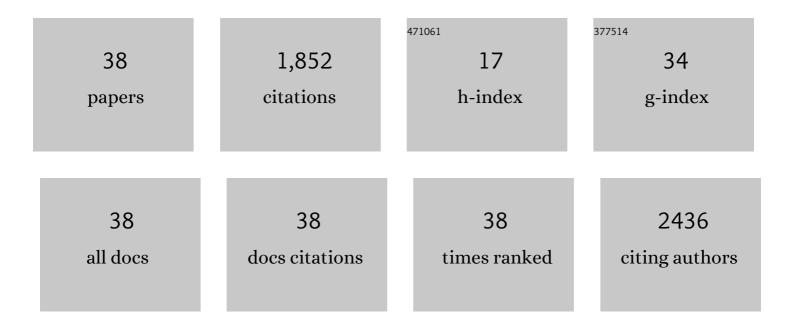
Tianhua Niu

List of Publications by Year in descending order

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Τιλνημιλ Νιιι

#	Article	IF	CITATIONS
1	Bayesian Haplotype Inference for Multiple Linked Single-Nucleotide Polymorphisms. American Journal of Human Genetics, 2002, 70, 157-169.	2.6	591
2	SeqVISTA: a graphical tool for sequence feature visualization and comparison. BMC Bioinformatics, 2003, 4, 1.	1.2	179
3	Algorithms for inferring haplotypes. Genetic Epidemiology, 2004, 27, 334-347.	0.6	157
4	The insulin-like growth factor-I gene and osteoporosis: A critical appraisal. Gene, 2005, 361, 38-56.	1.0	138
5	A genome-wide scan for loci linked to forearm bone mineral density. Human Genetics, 1999, 104, 226-233.	1.8	131
6	Angiotensin Converting Enzyme Gene Insertion/Deletion Polymorphism and Cardiovascular Disease. Drugs, 2002, 62, 977-993.	4.9	106
7	A 500-kb region on chromosome 16p13.1 contains the pseudoxanthoma elasticum locus: high-resolution mapping and genomic structure. Journal of Molecular Medicine, 2000, 78, 36-46.	1.7	63
8	Breast cancer survival predicted by TP53 mutation status differs markedly depending on treatment. Breast Cancer Research, 2018, 20, 115.	2.2	63
9	Association between polymorphism of the dopamine transporter gene and early smoking onset: an interaction risk on nicotine dependence. Journal of Human Genetics, 2004, 49, 35-39.	1.1	48
10	The Effects of a Low-Carbohydrate Diet vs. a Low-Fat Diet on Novel Cardiovascular Risk Factors: A Randomized Controlled Trial. Nutrients, 2015, 7, 7978-7994.	1.7	42
11	Machine Learning-Augmented Propensity Score-Adjusted Multilevel Mixed Effects Panel Analysis of Hands-On Cooking and Nutrition Education versus Traditional Curriculum for Medical Students as Preventive Cardiology: Multisite Cohort Study of 3,248 Trainees over 5 Years. BioMed Research International, 2018, 2018, 1-10.	0.9	34
12	A novel gene panel for prediction of lymph-node metastasis and recurrence in patients with thyroid cancer. Surgery, 2020, 167, 73-79.	1.0	31
13	Role of TNF in the Altered Interaction of Dormant Mycobacterium tuberculosis with Host Macrophages. PLoS ONE, 2014, 9, e95220.	1.1	30
14	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. Journal of Bone and Mineral Research, 2016, 31, 358-368.	3.1	24
15	Androgen receptor-deficient islet Î ² -cells exhibit alteration in genetic markers of insulin secretion and inflammation. A transcriptome analysis in the male mouse. Journal of Diabetes and Its Complications, 2017, 31, 787-795.	1.2	24
16	Identification of a novel <i>FGFRL1</i> MicroRNA 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
17	Critical assessment of coalescent simulators in modeling recombination hotspots in genomic sequences. BMC Bioinformatics, 2014, 15, 3.	1.2	21
18	KCNJ11, ABCC8 and TCF7L2 polymorphisms and the response to sulfonylurea treatment in patients with type 2 diabetes: a bioinformatics assessment. BMC Medical Genetics, 2017, 18, 64.	2.1	21

Τιανήμα Νιυ

#	Article	IF	CITATIONS
19	Mycobacterium tuberculosis sensor kinase DosS modulates the autophagosome in a DosR-independent manner. Communications Biology, 2019, 2, 349.	2.0	19
20	A meta-analysis of associations of LEPR Q223R and K109R polymorphisms with Type 2 diabetes risk. PLoS ONE, 2018, 13, e0189366.	1.1	16
21	Air Pollution and its Health Effects in Beijing. EcoHealth, 1998, 4, 199-209.	0.2	12
22	Network-Based Meta-Analyses of Associations of Multiple Gene Expression Profiles with Bone Mineral Density Variations in Women. PLoS ONE, 2016, 11, e0147475.	1.1	12
23	SNPicker: a graphical tool for primer picking in designing mutagenic endonuclease restriction assays. Bioinformatics, 2004, 20, 3263-3265.	1.8	11
24	Candidate Genes for Osteoporosis. Molecular Diagnosis and Therapy, 2001, 1, 11-19.	3.3	10
25	Sequencing-relative to hybridization-based transcriptomics approaches better define Mycobacterium tuberculosis stress-response regulons. Tuberculosis, 2016, 101, S9-S17.	0.8	10
26	D919G polymorphism of methionine synthase gene is associated with blood pressure response to benazepril in Chinese hypertensive patients. Journal of Human Genetics, 2004, 49, 296-301.	1.1	8
27	An Expectation-Maximization–Likelihood-Ratio Test for Handling Missing Data. Genetics, 2005, 169, 1021-1031.	1.2	7
28	A Novel Controlled PTEN-Knockout Mouse Model for Prostate Cancer Study. Frontiers in Molecular Biosciences, 2021, 8, 696537.	1.6	7
29	Meta-analysis and machine learning-augmented mixed effects cohort analysis of improved diets among 5847 medical trainees, providers and patients. Public Health Nutrition, 2021, , 1-9.	1.1	5
30	Peripheral Blood Markers Correlate with the Progression of Active Tuberculosis Relative to Latent Control of Mycobacterium tuberculosis Infection in Macaques. Pathogens, 2022, 11, 544.	1.2	3
31	A Statistical Procedure for Detecting Highly Correlated Genes with a Pre-Specified Candidate Gene in Microarray Analysis. Communications in Statistics - Theory and Methods, 2008, 37, 2991-3007.	0.6	2
32	SET levels contribute to cohesion fatigue. Molecular Biology of the Cell, 2021, 32, 1256-1266.	0.9	2
33	Observation of null alleles of microsatellite markers in a Chinese population. GeneScreen, 2000, 1, 41-45.	0.7	1
34	Dynamic visual data mining: biological sequence analysis and annotation using SeqVISTA. International Journal of Bioinformatics Research and Applications, 2005, 1, 18.	0.1	1
35	Genetic alterations of interleukin-17 and related genes in human prostate cancer. American Journal of Clinical and Experimental Urology, 2019, 7, 352-377.	0.4	1
36	Computational Advances in Cardiovascular Health. Computational and Mathematical Methods in Medicine, 2019, 2019, 1-2.	0.7	0

#	Article	IF	CITATIONS
37	IN SILICO BIOLOGY: HAPLOTYPE INFERENCE, LINKAGE DISEQUILIBRIUM ANALYSIS, AND MICROARRAY-BASED GENE SELECTION TECHNIQUES. , 2005, , .		Ο
38	Genome and transcriptome profiling of family in human prostate cancer. American Journal of Clinical and Experimental Urology, 2020, 8, 116-128.	0.4	0