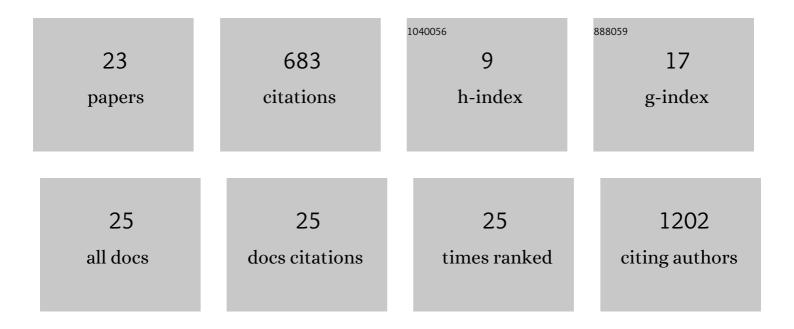
## Wenyu Zhang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3596177/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Tracing the Origin and Evolutionary Fate of Recent Gene Retrocopies in Natural Populations of the House Mouse. Molecular Biology and Evolution, 2022, 39, .	8.9	6
2	The mutational load in natural populations is significantly affected by high primary rates of retroposition. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	8
3	Testing Implications of the Omnigenic Model for the Genetic Analysis of Loci Identified through Genome-wide Association. Current Biology, 2021, 31, 1092-1098.e6.	3.9	15
4	ldentification of a genetic network for an ecologically relevant behavioural phenotype in Drosophila melanogaster. Molecular Ecology, 2020, 29, 502-518.	3.9	3
5	Dedicated transcriptomics combined with power analysis lead to functional understanding of genes with weak phenotypic changes in knockout lines. PLoS Computational Biology, 2020, 16, e1008354.	3.2	6
6	Title is missing!. , 2020, 16, e1008354.		0
7	Title is missing!. , 2020, 16, e1008354.		0
8	Title is missing!. , 2020, 16, e1008354.		0
9	Title is missing!. , 2020, 16, e1008354.		0
10	Title is missing!. , 2020, 16, e1008354.		0
11	Title is missing!. , 2020, 16, e1008354.		0
12	Origination and evolution of orphan genes and de novo genes in the genome of Caenorhabditis elegans. Science China Life Sciences, 2019, 62, 579-593.	4.9	21
13	Topological evolution of coexpression networks by new gene integration maintains the hierarchical and modular structures in human ancestors. Science China Life Sciences, 2019, 62, 594-608.	4.9	8
14	MicroRNA biomarker identification for pediatric acute myeloid leukemia based on a novel bioinformatics model. Oncotarget, 2015, 6, 26424-26436.	1.8	45
15	New genes drive the evolution of gene interaction networks in the human and mouse genomes. Genome Biology, 2015, 16, 202.	8.8	88
16	Screening key microRNAs for castration-resistant prostate cancer based on miRNA/mRNA functional synergistic network. Oncotarget, 2015, 6, 43819-43830.	1.8	65
17	Evaluation and Comparison of Multiple Aligners for Next-Generation Sequencing Data Analysis. BioMed Research International, 2014, 2014, 1-16.	1.9	52
18	Amino acid contact energy networks impact protein structure and evolution. Journal of Theoretical Biology, 2014, 355, 95-104.	1.7	18

WENYU ZHANG

#	Article	IF	CITATIONS
19	Identification of candidate miRNA biomarkers from miRNA regulatory network with application to prostate cancer. Journal of Translational Medicine, 2014, 12, 66.	4.4	94
20	Clear cell renal cell carcinoma associated microRNA expression signatures identified by an integrated bioinformatics analysis. Journal of Translational Medicine, 2013, 11, 169.	4.4	52
21	Identification of Cancer MicroRNA Biomarkers Based on miRNA–mRNA Network. Translational Bioinformatics, 2013, , 153-167.	0.0	1
22	A Practical Comparison of De Novo Genome Assembly Software Tools for Next-Generation Sequencing Technologies. PLoS ONE, 2011, 6, e17915.	2.5	194
23	Construction and Application of an Electronic Spatiotemporal Expression Profile and Gene Ontology Analysis Platform Based on the EST Database of the Silkworm,Bombyx mori. Journal of Insect Science, 2010, 10, 1-14.	1.5	5