

# Wenyu Zhang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3596177/publications.pdf>

Version: 2024-02-01

23  
papers

683  
citations

1040056

9  
h-index

888059

17  
g-index

25  
all docs

25  
docs citations

25  
times ranked

1202  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Practical Comparison of De Novo Genome Assembly Software Tools for Next-Generation Sequencing Technologies. <i>PLoS ONE</i> , 2011, 6, e17915.	2.5	194
2	Identification of candidate miRNA biomarkers from miRNA regulatory network with application to prostate cancer. <i>Journal of Translational Medicine</i> , 2014, 12, 66.	4.4	94
3	New genes drive the evolution of gene interaction networks in the human and mouse genomes. <i>Genome Biology</i> , 2015, 16, 202.	8.8	88
4	Screening key microRNAs for castration-resistant prostate cancer based on miRNA/mRNA functional synergistic network. <i>Oncotarget</i> , 2015, 6, 43819-43830.	1.8	65
5	Clear cell renal cell carcinoma associated microRNA expression signatures identified by an integrated bioinformatics analysis. <i>Journal of Translational Medicine</i> , 2013, 11, 169.	4.4	52
6	Evaluation and Comparison of Multiple Aligners for Next-Generation Sequencing Data Analysis. <i>BioMed Research International</i> , 2014, 2014, 1-16.	1.9	52
7	MicroRNA biomarker identification for pediatric acute myeloid leukemia based on a novel bioinformatics model. <i>Oncotarget</i> , 2015, 6, 26424-26436.	1.8	45
8	Origination and evolution of orphan genes and de novo genes in the genome of <i>Caenorhabditis elegans</i> . <i>Science China Life Sciences</i> , 2019, 62, 579-593.	4.9	21
9	Amino acid contact energy networks impact protein structure and evolution. <i>Journal of Theoretical Biology</i> , 2014, 355, 95-104.	1.7	18
10	Testing Implications of the Omnigenic Model for the Genetic Analysis of Loci Identified through Genome-wide Association. <i>Current Biology</i> , 2021, 31, 1092-1098.e6.	3.9	15
11	Topological evolution of coexpression networks by new gene integration maintains the hierarchical and modular structures in human ancestors. <i>Science China Life Sciences</i> , 2019, 62, 594-608.	4.9	8
12	The mutational load in natural populations is significantly affected by high primary rates of retroposition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	8
13	Dedicated transcriptomics combined with power analysis lead to functional understanding of genes with weak phenotypic changes in knockout lines. <i>PLoS Computational Biology</i> , 2020, 16, e1008354.	3.2	6
14	Tracing the Origin and Evolutionary Fate of Recent Gene Retrocopies in Natural Populations of the House Mouse. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	6
15	Construction and Application of an Electronic Spatiotemporal Expression Profile and Gene Ontology Analysis Platform Based on the EST Database of the Silkworm, <i>Bombyx mori</i> . <i>Journal of Insect Science</i> , 2010, 10, 1-14.	1.5	5
16	Identification of a genetic network for an ecologically relevant behavioural phenotype in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2020, 29, 502-518.	3.9	3
17	Identification of Cancer MicroRNA Biomarkers Based on miRNA-mRNA Network. <i>Translational Bioinformatics</i> , 2013, , 153-167.	0.0	1
18	Title is missing!. , 2020, 16, e1008354.		0

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 16, e1008354.		0
20	Title is missing!. , 2020, 16, e1008354.		0
21	Title is missing!. , 2020, 16, e1008354.		0
22	Title is missing!. , 2020, 16, e1008354.		0
23	Title is missing!. , 2020, 16, e1008354.		0