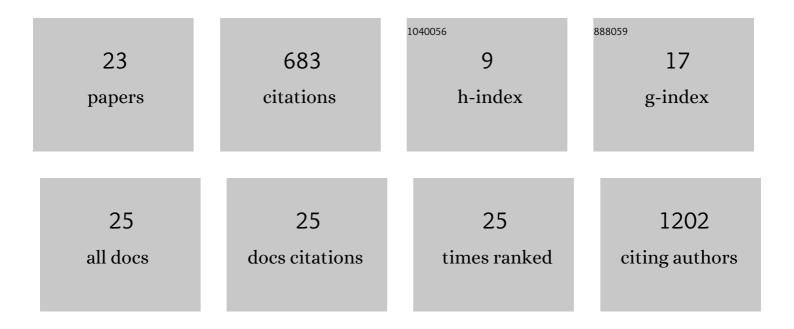
Wenyu Zhang

List of Publications by Year in descending order

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Μεννή Ζηλνίς

#	Article	IF	CITATIONS
1	A Practical Comparison of De Novo Genome Assembly Software Tools for Next-Generation Sequencing Technologies. PLoS ONE, 2011, 6, e17915.	2.5	194
2	Identification of candidate miRNA biomarkers from miRNA regulatory network with application to prostate cancer. Journal of Translational Medicine, 2014, 12, 66.	4.4	94
3	New genes drive the evolution of gene interaction networks in the human and mouse genomes. Genome Biology, 2015, 16, 202.	8.8	88
4	Screening key microRNAs for castration-resistant prostate cancer based on miRNA/mRNA functional synergistic network. Oncotarget, 2015, 6, 43819-43830.	1.8	65
5	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
6	Evaluation and Comparison of Multiple Aligners for Next-Generation Sequencing Data Analysis. BioMed Research International, 2014, 2014, 1-16.	1.9	52
7	MicroRNA biomarker identification for pediatric acute myeloid leukemia based on a novel bioinformatics model. Oncotarget, 2015, 6, 26424-26436.	1.8	45
8	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
9	Amino acid contact energy networks impact protein structure and evolution. Journal of Theoretical Biology, 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. Current Biology, 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. Science China Life Sciences, 2019, 62, 594-608.	4.9	8
12	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
13	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
14	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
15	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
16	Identification of a genetic network for an ecologically relevant behavioural phenotype in Drosophila melanogaster. Molecular Ecology, 2020, 29, 502-518.	3.9	3
17	Identification of Cancer MicroRNA Biomarkers Based on miRNA–mRNA Network. Translational Bioinformatics, 2013, , 153-167.	0.0	1

