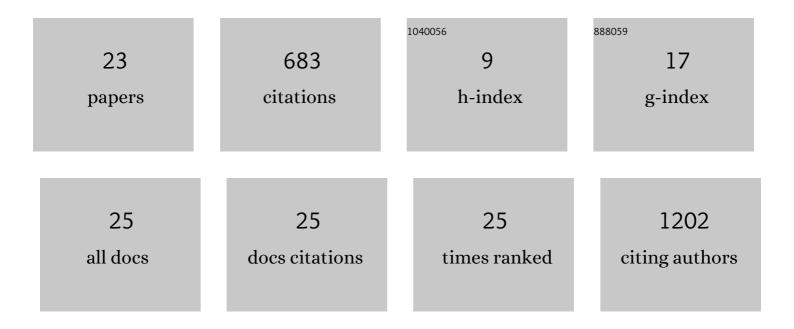
Wenyu Zhang

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 |
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