

# Wanjun Gu

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

56

papers

5,231

citations

27

h-index

61

g-index

61

ext. papers

6,095

ext. citations

8.4

avg, IF

5.01

L-index

#	Paper	IF	Citations
56	The Evolution of G-quadruplex Structure in mRNA Untranslated Region. <i>Evolutionary Bioinformatics</i> , <b>2021</b> , 17, 11769343211035140	1.9	1
55	Identifying disease-associated signaling pathways through a novel effector gene analysis. <i>PeerJ</i> , <b>2020</b> , 8, e9695	3.1	1
54	Technical progress in circulating tumor DNA analysis using next generation sequencing. <i>Molecular and Cellular Probes</i> , <b>2020</b> , 49, 101480	3.3	10
53	Peripheral blood non-canonical small non-coding RNAs as novel biomarkers in lung cancer. <i>Molecular Cancer</i> , <b>2020</b> , 19, 159	42.1	13
52	The potential of using blood circular RNA as liquid biopsy biomarker for human diseases. <i>Protein and Cell</i> , <b>2020</b> , 1	7.2	44
51	Signaling Pathway Analysis Combined With the Strength Variations of Interactions Between Genes Under Different Conditions. <i>IEEE Access</i> , <b>2020</b> , 8, 138036-138045	3.5	1
50	Denosing Autoencoder, A Deep Learning Algorithm, Aids the Identification of A Novel Molecular Signature of Lung Adenocarcinoma. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2020</b> , 18, 468-480	6.5	4
49	. <i>IEEE Access</i> , <b>2019</b> , 7, 69172-69183	3.5	3
48	A Pathway-Based Strategy to Identify Biomarkers for Lung Cancer Diagnosis and Prognosis. <i>Evolutionary Bioinformatics</i> , <b>2019</b> , 15, 1176934319838494	1.9	5
47	Two Distinct Subtypes Revealed in Blood Transcriptome of Breast Cancer Patients With an Unsupervised Analysis. <i>Frontiers in Oncology</i> , <b>2019</b> , 9, 985	5.3	7
46	Potential Diagnostic Power of Blood Circular RNA Expression in Active Pulmonary Tuberculosis. <i>EBioMedicine</i> , <b>2018</b> , 27, 18-26	8.8	43
45	Identification of circular RNAs in human aortic valves. <i>Gene</i> , <b>2018</b> , 642, 135-144	3.8	12
44	Rat BodyMap transcriptomes reveal unique circular RNA features across tissue types and developmental stages. <i>Rna</i> , <b>2018</b> , 24, 1443-1456	5.8	35
43	Quantifying circular RNA expression from RNA-seq data using model-based framework. <i>Bioinformatics</i> , <b>2017</b> , 33, 2131-2139	7.2	39
42	Genome Sequence and Analysis of Peptoclostridium difficile Strain ZJCDC-S82. <i>Evolutionary Bioinformatics</i> , <b>2016</b> , 12, 41-9	1.9	7
41	Comparative Transcriptome Analysis Reveals Substantial Tissue Specificity in Human Aortic Valve. <i>Evolutionary Bioinformatics</i> , <b>2016</b> , 12, 175-84	1.9	5
40	Expression of nuclear factor, erythroid 2-like 2-mediated genes differentiates tuberculosis. <i>Tuberculosis</i> , <b>2016</b> , 99, 56-62	2.6	17

39	Ion channel gene expression predicts survival in glioma patients. <i>Scientific Reports</i> , <b>2015</b> , 5, 11593	4.9	27
38	Functional and Structural Consequence of Rare Exonic Single Nucleotide Polymorphisms: One Story, Two Tales. <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 2929-40	3.9	9
37	The role of RNA structure at 5' untranslated region in microRNA-mediated gene regulation. <i>Rna</i> , <b>2014</b> , 20, 1369-75	5.8	59
36	The impact of RNA structure on coding sequence evolution in both bacteria and eukaryotes. <i>BMC Evolutionary Biology</i> , <b>2014</b> , 14, 87	3	6
35	Ion channel gene expression in lung adenocarcinoma: potential role in prognosis and diagnosis. <i>PLoS ONE</i> , <b>2014</b> , 9, e86569	3.7	27
34	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , <b>2014</b> , 3, 27	7.6	50
33	Expression profiling of mitochondrial voltage-dependent anion channel-1 associated genes predicts recurrence-free survival in human carcinomas. <i>PLoS ONE</i> , <b>2014</b> , 9, e110094	3.7	22
32	The Burmese python genome reveals the molecular basis for extreme adaptation in snakes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 20645-50	11.5	203
31	Expression profiling of ion channel genes predicts clinical outcome in breast cancer. <i>Molecular Cancer</i> , <b>2013</b> , 12, 106	42.1	69
30	Biological basis of miRNA action when their targets are located in human protein coding region. <i>PLoS ONE</i> , <b>2013</b> , 8, e63403	3.7	19
29	Tracking miRNA precursor metabolic products and processing sites through completely analyzing high-throughput sequencing data. <i>Molecular Biology Reports</i> , <b>2012</b> , 39, 2031-8	2.8	14
28	Phylogenetics, likelihood, evolution and complexity. <i>Bioinformatics</i> , <b>2012</b> , 28, 2989-90	7.2	7
27	Non-silent story on synonymous sites in voltage-gated ion channel genes. <i>PLoS ONE</i> , <b>2012</b> , 7, e48541	3.7	9
26	Selection on synonymous sites for increased accessibility around miRNA binding sites in plants. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 3037-44	8.3	42
25	Translation Efficiency in Upstream Region of microRNA Targets in <i>Arabidopsis thaliana</i> . <i>Evolutionary Bioinformatics</i> , <b>2012</b> , 8, 565-74	1.9	4
24	Sequencing the genome of the Burmese python ( <i>Python molurus bivittatus</i> ) as a model for studying extreme adaptations in snakes. <i>Genome Biology</i> , <b>2011</b> , 12, 406	18.3	50
23	A comprehensive survey of miRNA repertoire and 3' addition events in the placentas of patients with pre-eclampsia from high-throughput sequencing. <i>PLoS ONE</i> , <b>2011</b> , 6, e21072	3.7	79
22	Discovery of highly divergent repeat landscapes in snake genomes using high-throughput sequencing. <i>Genome Biology and Evolution</i> , <b>2011</b> , 3, 641-53	3.9	74

21	Repetitive elements may comprise over two-thirds of the human genome. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002384	384	689
20	Cross-mapping events in miRNAs reveal potential miRNA-mimics and evolutionary implications. <i>PLoS ONE</i> , <b>2011</b> , 6, e20517	3.7	24
19	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , <b>2010</b> , 463, 311-7	50.4	864
18	The genome of a songbird. <i>Nature</i> , <b>2010</b> , 464, 757-62	50.4	655
17	Detecting positive and purifying selection at synonymous sites in yeast and worm. <i>Molecular Biology and Evolution</i> , <b>2010</b> , 27, 1912-22	8.3	50
16	Rapid likelihood analysis on large phylogenies using partial sampling of substitution histories. <i>Molecular Biology and Evolution</i> , <b>2010</b> , 27, 249-65	8.3	21
15	A universal trend of reduced mRNA stability near the translation-initiation site in prokaryotes and eukaryotes. <i>PLoS Computational Biology</i> , <b>2010</b> , 6, e1000664	5	208
14	Rapid identification of thousands of copperhead snake ( <i>Agkistrodon contortrix</i> ) microsatellite loci from modest amounts of 454 shotgun genome sequence. <i>Molecular Ecology Resources</i> , <b>2010</b> , 10, 341-7	8.4	167
13	Dynamic nucleotide mutation gradients and control region usage in squamate reptile mitochondrial genomes. <i>Cytogenetic and Genome Research</i> , <b>2009</b> , 127, 112-27	1.9	20
12	Evidence for an ancient adaptive episode of convergent molecular evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 8986-91	11.5	233
11	Structural, biochemical, and in vivo characterization of the first virally encoded cyclophilin from the Mimivirus. <i>Journal of Molecular Biology</i> , <b>2008</b> , 378, 71-86	6.5	24
10	Adaptive evolution and functional redesign of core metabolic proteins in snakes. <i>PLoS ONE</i> , <b>2008</b> , 3, e2201	3.7	91
9	Identification of repeat structure in large genomes using repeat probability clouds. <i>Analytical Biochemistry</i> , <b>2008</b> , 380, 77-83	3.1	37
8	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , <b>2007</b> , 447, 167-77	50.4	577
7	Evolutionary dynamics of transposable elements in the short-tailed opossum <i>Monodelphis domestica</i> . <i>Genome Research</i> , <b>2007</b> , 17, 992-1004	9.7	109
6	SINEs, evolution and genome structure in the opossum. <i>Gene</i> , <b>2007</b> , 396, 46-58	3.8	17
5	Analysis of synonymous codon usage in H5N1 virus and other influenza A viruses. <i>BioSystems</i> , <b>2005</b> , 81, 77-86	1.9	118
4	The relationship between synonymous codon usage and protein structure in <i>Escherichia coli</i> and <i>Homo sapiens</i> . <i>BioSystems</i> , <b>2004</b> , 73, 89-97	1.9	83

3	Analysis of synonymous codon usage in SARS Coronavirus and other viruses in the Nidovirales. <i>Virus Research</i> , <b>2004</b> , 101, 155-61	6.4	151
2	Folding type specific secondary structure propensities of synonymous codons. <i>IEEE Transactions on Nanobioscience</i> , <b>2003</b> , 2, 150-7	3.4	21
1	Cluster analysis of the codon use frequency of MHC genes from different species. <i>BioSystems</i> , <b>2002</b> , 65, 199-207	1.9	45