

Wanjun Gu

List of Publications by Citations

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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 sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010 , 463, 311-7	50.4	864
55	Repetitive elements may comprise over two-thirds of the human genome. <i>PLoS Genetics</i> , 2011 , 7, e1002384	38.4	689
54	The genome of a songbird. <i>Nature</i> , 2010 , 464, 757-62	50.4	655
53	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007 , 447, 167-77	50.4	577
52	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> , 2009 , 106, 8986-91	11.5	233
51	A universal trend of reduced mRNA stability near the translation-initiation site in prokaryotes and eukaryotes. <i>PLoS Computational Biology</i> , 2010 , 6, e1000664	5	208
50	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> , 2013 , 110, 20645-50	11.5	203
49	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> , 2010 , 10, 341-7	8.4	167
48	Analysis of synonymous codon usage in SARS Coronavirus and other viruses in the Nidovirales. <i>Virus Research</i> , 2004 , 101, 155-61	6.4	151
47	Analysis of synonymous codon usage in H5N1 virus and other influenza A viruses. <i>BioSystems</i> , 2005 , 81, 77-86	1.9	118
46	Evolutionary dynamics of transposable elements in the short-tailed opossum <i>Monodelphis domestica</i> . <i>Genome Research</i> , 2007 , 17, 992-1004	9.7	109
45	Adaptive evolution and functional redesign of core metabolic proteins in snakes. <i>PLoS ONE</i> , 2008 , 3, e2201	3.7	91
44	The relationship between synonymous codon usage and protein structure in <i>Escherichia coli</i> and <i>Homo sapiens</i> . <i>BioSystems</i> , 2004 , 73, 89-97	1.9	83
43	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> , 2011 , 6, e21072	3.7	79
42	Discovery of highly divergent repeat landscapes in snake genomes using high-throughput sequencing. <i>Genome Biology and Evolution</i> , 2011 , 3, 641-53	3.9	74
41	Expression profiling of ion channel genes predicts clinical outcome in breast cancer. <i>Molecular Cancer</i> , 2013 , 12, 106	42.1	69
40	The role of RNA structure at 5' untranslated region in microRNA-mediated gene regulation. <i>Rna</i> , 2014 , 20, 1369-75	5.8	59

39	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , 2014 , 3, 27	7.6	50
38	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> , 2011 , 12, 406	18.3	50
37	Detecting positive and purifying selection at synonymous sites in yeast and worm. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1912-22	8.3	50
36	Cluster analysis of the codon use frequency of MHC genes from different species. <i>BioSystems</i> , 2002 , 65, 199-207	1.9	45
35	The potential of using blood circular RNA as liquid biopsy biomarker for human diseases. <i>Protein and Cell</i> , 2020 , 1	7.2	44
34	Potential Diagnostic Power of Blood Circular RNA Expression in Active Pulmonary Tuberculosis. <i>EBioMedicine</i> , 2018 , 27, 18-26	8.8	43
33	Selection on synonymous sites for increased accessibility around miRNA binding sites in plants. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3037-44	8.3	42
32	Quantifying circular RNA expression from RNA-seq data using model-based framework. <i>Bioinformatics</i> , 2017 , 33, 2131-2139	7.2	39
31	Identification of repeat structure in large genomes using repeat probability clouds. <i>Analytical Biochemistry</i> , 2008 , 380, 77-83	3.1	37
30	Rat BodyMap transcriptomes reveal unique circular RNA features across tissue types and developmental stages. <i>Rna</i> , 2018 , 24, 1443-1456	5.8	35
29	Ion channel gene expression predicts survival in glioma patients. <i>Scientific Reports</i> , 2015 , 5, 11593	4.9	27
28	Ion channel gene expression in lung adenocarcinoma: potential role in prognosis and diagnosis. <i>PLoS ONE</i> , 2014 , 9, e86569	3.7	27
27	Structural, biochemical, and in vivo characterization of the first virally encoded cyclophilin from the Mimivirus. <i>Journal of Molecular Biology</i> , 2008 , 378, 71-86	6.5	24
26	Cross-mapping events in miRNAs reveal potential miRNA-mimics and evolutionary implications. <i>PLoS ONE</i> , 2011 , 6, e20517	3.7	24
25	Expression profiling of mitochondrial voltage-dependent anion channel-1 associated genes predicts recurrence-free survival in human carcinomas. <i>PLoS ONE</i> , 2014 , 9, e110094	3.7	22
24	Rapid likelihood analysis on large phylogenies using partial sampling of substitution histories. <i>Molecular Biology and Evolution</i> , 2010 , 27, 249-65	8.3	21
23	Folding type specific secondary structure propensities of synonymous codons. <i>IEEE Transactions on Nanobioscience</i> , 2003 , 2, 150-7	3.4	21
22	Dynamic nucleotide mutation gradients and control region usage in squamate reptile mitochondrial genomes. <i>Cytogenetic and Genome Research</i> , 2009 , 127, 112-27	1.9	20

21	Biological basis of miRNA action when their targets are located in human protein coding region. <i>PLoS ONE</i> , 2013 , 8, e63403	3.7	19
20	SINEs, evolution and genome structure in the opossum. <i>Gene</i> , 2007 , 396, 46-58	3.8	17
19	Expression of nuclear factor, erythroid 2-like 2-mediated genes differentiates tuberculosis. <i>Tuberculosis</i> , 2016 , 99, 56-62	2.6	17
18	Tracking miRNA precursor metabolic products and processing sites through completely analyzing high-throughput sequencing data. <i>Molecular Biology Reports</i> , 2012 , 39, 2031-8	2.8	14
17	Peripheral blood non-canonical small non-coding RNAs as novel biomarkers in lung cancer. <i>Molecular Cancer</i> , 2020 , 19, 159	42.1	13
16	Identification of circular RNAs in human aortic valves. <i>Gene</i> , 2018 , 642, 135-144	3.8	12
15	Technical progress in circulating tumor DNA analysis using next generation sequencing. <i>Molecular and Cellular Probes</i> , 2020 , 49, 101480	3.3	10
14	Functional and Structural Consequence of Rare Exonic Single Nucleotide Polymorphisms: One Story, Two Tales. <i>Genome Biology and Evolution</i> , 2015 , 7, 2929-40	3.9	9
13	Non-silent story on synonymous sites in voltage-gated ion channel genes. <i>PLoS ONE</i> , 2012 , 7, e48541	3.7	9
12	Two Distinct Subtypes Revealed in Blood Transcriptome of Breast Cancer Patients With an Unsupervised Analysis. <i>Frontiers in Oncology</i> , 2019 , 9, 985	5.3	7
11	Phylogenetics, likelihood, evolution and complexity. <i>Bioinformatics</i> , 2012 , 28, 2989-90	7.2	7
10	Genome Sequence and Analysis of <i>Peptoclostridium difficile</i> Strain ZJCDC-S82. <i>Evolutionary Bioinformatics</i> , 2016 , 12, 41-9	1.9	7
9	The impact of RNA structure on coding sequence evolution in both bacteria and eukaryotes. <i>BMC Evolutionary Biology</i> , 2014 , 14, 87	3	6
8	A Pathway-Based Strategy to Identify Biomarkers for Lung Cancer Diagnosis and Prognosis. <i>Evolutionary Bioinformatics</i> , 2019 , 15, 1176934319838494	1.9	5
7	Comparative Transcriptome Analysis Reveals Substantial Tissue Specificity in Human Aortic Valve. <i>Evolutionary Bioinformatics</i> , 2016 , 12, 175-84	1.9	5
6	Translation Efficiency in Upstream Region of microRNA Targets in <i>Arabidopsis thaliana</i> . <i>Evolutionary Bioinformatics</i> , 2012 , 8, 565-74	1.9	4
5	Denosing Autoencoder, A Deep Learning Algorithm, Aids the Identification of A Novel Molecular Signature of Lung Adenocarcinoma. <i>Genomics, Proteomics and Bioinformatics</i> , 2020 , 18, 468-480	6.5	4
4	. <i>IEEE Access</i> , 2019 , 7, 69172-69183	3.5	3

3	Identifying disease-associated signaling pathways through a novel effector gene analysis. <i>PeerJ</i> , 2020 , 8, e9695	3.1	1
2	Signaling Pathway Analysis Combined With the Strength Variations of Interactions Between Genes Under Different Conditions. <i>IEEE Access</i> , 2020 , 8, 138036-138045	3.5	1
1	The Evolution of G-quadruplex Structure in mRNA Untranslated Region. <i>Evolutionary Bioinformatics</i> , 2021 , 17, 11769343211035140	1.9	1