

Wanjun Gu

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

6,562
citations

182225

30
h-index

150775

59
g-index

61
all docs

61
docs citations

61
times ranked

12475
citing authors

#	ARTICLE	IF	CITATIONS
1	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	13.7	1,058
2	Repetitive Elements May Comprise Over Two-Thirds of the Human Genome. <i>PLoS Genetics</i> , 2011, 7, e1002384.	1.5	907
3	The genome of a songbird. <i>Nature</i> , 2010, 464, 757-762.	13.7	770
4	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	13.7	661
5	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, 8986-8991.	3.3	284
6	A Universal Trend of Reduced mRNA Stability near the Translation-Initiation Site in Prokaryotes and Eukaryotes. <i>PLoS Computational Biology</i> , 2010, 6, e1000664.	1.5	266
7	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, 20645-20650.	3.3	260
8	Analysis of synonymous codon usage in SARS Coronavirus and other viruses in the Nidovirales. <i>Virus Research</i> , 2004, 101, 155-161.	1.1	186
9	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, 341-347.	2.2	179
10	Analysis of synonymous codon usage in H5N1 virus and other influenza A viruses. <i>BioSystems</i> , 2005, 81, 77-86.	0.9	140
11	Evolutionary dynamics of transposable elements in the short-tailed opossum <i>Monodelphis domestica</i> . <i>Genome Research</i> , 2007, 17, 992-1004.	2.4	137
12	Adaptive Evolution and Functional Redesign of Core Metabolic Proteins in Snakes. <i>PLoS ONE</i> , 2008, 3, e2201.	1.1	113
13	The potential of using blood circular RNA as liquid biopsy biomarker for human diseases. <i>Protein and Cell</i> , 2021, 12, 911-946.	4.8	101
14	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.	0.9	99
15	The role of RNA structure at 5' untranslated region in microRNA-mediated gene regulation. <i>Rna</i> , 2014, 20, 1369-1375.	1.6	89
16	A Comprehensive Survey of miRNA Repertoire and Addition Events in the Placentas of Patients with Pre-Eclampsia from High-Throughput Sequencing. <i>PLoS ONE</i> , 2011, 6, e21072.	1.1	88
17	Discovery of Highly Divergent Repeat Landscapes in Snake Genomes Using High-Throughput Sequencing. <i>Genome Biology and Evolution</i> , 2011, 3, 641-653.	1.1	87
18	Expression profiling of ion channel genes predicts clinical outcome in breast cancer. <i>Molecular Cancer</i> , 2013, 12, 106.	7.9	85

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19	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , 2014, 3, 27.	3.3	72
20	Detecting Positive and Purifying Selection at Synonymous Sites in Yeast and Worm. <i>Molecular Biology and Evolution</i> , 2010, 27, 1912-1922.	3.5	62
21	Potential Diagnostic Power of Blood Circular RNA Expression in Active Pulmonary Tuberculosis. <i>EBioMedicine</i> , 2018, 27, 18-26.	2.7	61
22	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.	13.9	58
23	Selection on Synonymous Sites for Increased Accessibility around miRNA Binding Sites in Plants. <i>Molecular Biology and Evolution</i> , 2012, 29, 3037-3044.	3.5	57
24	Quantifying circular RNA expression from RNA-seq data using model-based framework. <i>Bioinformatics</i> , 2017, 33, 2131-2139.	1.8	57
25	Cluster analysis of the codon use frequency of MHC genes from different species. <i>BioSystems</i> , 2002, 65, 199-207.	0.9	52
26	Identification of repeat structure in large genomes using repeat probability clouds. <i>Analytical Biochemistry</i> , 2008, 380, 77-83.	1.1	51
27	Rat BodyMap transcriptomes reveal unique circular RNA features across tissue types and developmental stages. <i>Rna</i> , 2018, 24, 1443-1456.	1.6	50
28	Ion channel gene expression predicts survival in glioma patients. <i>Scientific Reports</i> , 2015, 5, 11593.	1.6	41
29	Peripheral blood non-canonical small non-coding RNAs as novel biomarkers in lung cancer. <i>Molecular Cancer</i> , 2020, 19, 159.	7.9	36
30	Ion Channel Gene Expression in Lung Adenocarcinoma: Potential Role in Prognosis and Diagnosis. <i>PLoS ONE</i> , 2014, 9, e86569.	1.1	33
31	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.	2.0	30
32	Expression of nuclear factor, erythroid 2-like 2-mediated genes differentiates tuberculosis. <i>Tuberculosis</i> , 2016, 99, 56-62.	0.8	30
33	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.	1.1	28
34	Cross-Mapping Events in miRNAs Reveal Potential miRNA-Mimics and Evolutionary Implications. <i>PLoS ONE</i> , 2011, 6, e20517.	1.1	25
35	Folding type specific secondary structure propensities of synonymous codons. <i>IEEE Transactions on Nanobioscience</i> , 2003, 2, 150-157.	2.2	23
36	Rapid Likelihood Analysis on Large Phylogenies Using Partial Sampling of Substitution Histories. <i>Molecular Biology and Evolution</i> , 2010, 27, 249-265.	3.5	23

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37	Biological Basis of miRNA Action when Their Targets Are Located in Human Protein Coding Region. PLoS ONE, 2013, 8, e63403.	1.1	23
38	Dynamic Nucleotide Mutation Gradients and Control Region Usage in Squamate Reptile Mitochondrial Genomes. Cytogenetic and Genome Research, 2009, 127, 112-127.	0.6	22
39	SINEs, evolution and genome structure in the opossum. Gene, 2007, 396, 46-58.	1.0	20
40	Technical progress in circulating tumor DNA analysis using next generation sequencing. Molecular and Cellular Probes, 2020, 49, 101480.	0.9	19
41	Denosing Autoencoder, A Deep Learning Algorithm, Aids the Identification of A Novel Molecular Signature of Lung Adenocarcinoma. Genomics, Proteomics and Bioinformatics, 2020, 18, 468-480.	3.0	18
42	Two Distinct Subtypes Revealed in Blood Transcriptome of Breast Cancer Patients With an Unsupervised Analysis. Frontiers in Oncology, 2019, 9, 985.	1.3	16
43	Tracking miRNA precursor metabolic products and processing sites through completely analyzing high-throughput sequencing data. Molecular Biology Reports, 2012, 39, 2031-2038.	1.0	14
44	Identification of circular RNAs in human aortic valves. Gene, 2018, 642, 135-144.	1.0	13
45	Non-Silent Story on Synonymous Sites in Voltage-Gated Ion Channel Genes. PLoS ONE, 2012, 7, e48541.	1.1	12
46	Functional and Structural Consequence of Rare Exonic Single Nucleotide Polymorphisms: One Story, Two Tales. Genome Biology and Evolution, 2015, 7, 2929-2940.	1.1	12
47	Phylogenetics, likelihood, evolution and complexity. Bioinformatics, 2012, 28, 2989-2990.	1.8	10
48	Genome Sequence and Analysis of <i>Peptoclostridium difficile</i> Strain ZJCDC-S82. Evolutionary Bioinformatics, 2016, 12, EBO.S32476.	0.6	9
49	The impact of RNA structure on coding sequence evolution in both bacteria and eukaryotes. BMC Evolutionary Biology, 2014, 14, 87.	3.2	8
50	Translation Efficiency in Upstream Region of microRNA Targets in <i>Arabidopsis thaliana</i> . Evolutionary Bioinformatics, 2012, 8, EBO.S10362.	0.6	6
51	Comparative Transcriptome Analysis Reveals Substantial Tissue Specificity in Human Aortic Valve. Evolutionary Bioinformatics, 2016, 12, EBO.S37594.	0.6	6
52	gwSPIA: Improved Signaling Pathway Impact Analysis With Gene Weights. IEEE Access, 2019, 7, 69172-69183.	2.6	6
53	A Pathway-Based Strategy to Identify Biomarkers for Lung Cancer Diagnosis and Prognosis. Evolutionary Bioinformatics, 2019, 15, 117693431983849.	0.6	6
54	The Evolution of G-quadruplex Structure in mRNA Untranslated Region. Evolutionary Bioinformatics, 2021, 17, 117693432110351.	0.6	6

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55	Signaling Pathway Analysis Combined With the Strength Variations of Interactions Between Genes Under Different Conditions. IEEE Access, 2020, 8, 138036-138045.	2.6	4
56	AQUARIUM: accurate quantification of circular isoforms using model-based strategy. Bioinformatics, 2021, 37, 4879-4881.	1.8	2
57	Identifying disease-associated signaling pathways through a novel effector gene analysis. PeerJ, 2020, 8, e9695.	0.9	1
58	Extended XOR Algorithm with Biotechnology Constraints for Data Security in DNA Storage. Current Bioinformatics, 2022, 17, 401-410.	0.7	1