

Zhong Wang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5414173/publications.pdf>

Version: 2024-02-01

50
papers

23,501
citations

201385

27
h-index

233125

45
g-index

59
all docs

59
docs citations

59
times ranked

34167
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA-Seq: a revolutionary tool for transcriptomics. <i>Nature Reviews Genetics</i> , 2009, 10, 57-63.	7.7	10,529
2	The Transcriptional Landscape of the Yeast Genome Defined by RNA Sequencing. <i>Science</i> , 2008, 320, 1344-1349.	6.0	2,180
3	MetaBAT 2: an adaptive binning algorithm for robust and efficient genome reconstruction from metagenome assemblies. <i>PeerJ</i> , 2019, 7, e7359.	0.9	1,704
4	MetaBAT, an efficient tool for accurately reconstructing single genomes from complex microbial communities. <i>PeerJ</i> , 2015, 3, e1165.	0.9	1,546
5	Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen. <i>Science</i> , 2011, 331, 463-467.	6.0	1,135
6	Next-generation transcriptome assembly. <i>Nature Reviews Genetics</i> , 2011, 12, 671-682.	7.7	1,073
7	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012, 30, 693-700.	9.4	946
8	A novel class of small RNAs in mouse spermatogenic cells. <i>Genes and Development</i> , 2006, 20, 1709-1714.	2.7	761
9	Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	9.0	635
10	Widespread Polycistronic Transcripts in Fungi Revealed by Single-Molecule mRNA Sequencing. <i>PLoS ONE</i> , 2015, 10, e0132628.	1.1	340
11	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. <i>Genome Research</i> , 2014, 24, 1517-1525.	2.4	332
12	Nanos Maintains Germline Stem Cell Self-Renewal by Preventing Differentiation. <i>Science</i> , 2004, 303, 2016-2019.	6.0	223
13	Rnnotator: an automated de novo transcriptome assembly pipeline from stranded RNA-Seq reads. <i>BMC Genomics</i> , 2010, 11, 663.	1.2	201
14	Comprehensive annotation of the transcriptome of the human fungal pathogen <i>Candida albicans</i> using RNA-seq. <i>Genome Research</i> , 2010, 20, 1451-1458.	2.4	191
15	Validation of two ribosomal RNA removal methods for microbial metatranscriptomics. <i>Nature Methods</i> , 2010, 7, 807-812.	9.0	184
16	Close association of RNA polymerase II and many transcription factors with Pol III genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3639-3644.	3.3	167
17	ALE: a generic assembly likelihood evaluation framework for assessing the accuracy of genome and metagenome assemblies. <i>Bioinformatics</i> , 2013, 29, 435-443.	1.8	155
18	Regulatory Relationship among piwi, pumilio, and bag-of-marbles in <i>Drosophila</i> Germline Stem Cell Self-Renewal and Differentiation. <i>Current Biology</i> , 2005, 15, 171-178.	1.8	139

#	ARTICLE	IF	CITATIONS
19	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	9.0	133
20	De novo transcriptome assembly of drought tolerant CAM plants, <i>Agave deserti</i> and <i>Agave tequilana</i> . <i>BMC Genomics</i> , 2013, 14, 563.	1.2	115
21	BioPig: a Hadoop-based analytic toolkit for large-scale sequence data. <i>Bioinformatics</i> , 2013, 29, 3014-3019.	1.8	101
22	Evidence of Influence of Genomic DNA Sequence on Human X Chromosome Inactivation. <i>PLoS Computational Biology</i> , 2006, 2, e113.	1.5	84
23	Evolution of extreme resistance to ionizing radiation via genetic adaptation of DNA repair. <i>ELife</i> , 2014, 3, e01322.	2.8	80
24	Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in <i>Agave</i> . <i>BMC Genomics</i> , 2018, 19, 588.	1.2	64
25	The Division of <i>Drosophila</i> Germline Stem Cells and Their Precursors Requires a Specific Cyclin. <i>Current Biology</i> , 2005, 15, 328-333.	1.8	61
26	The Prevalence and Regulation of Antisense Transcripts in <i>Schizosaccharomyces pombe</i> . <i>PLoS ONE</i> , 2010, 5, e15271.	1.1	50
27	Statistical methods for identifying differentially expressed genes in RNA-Seq experiments. <i>Cell and Bioscience</i> , 2012, 2, 26.	2.1	41
28	The arrest gene is required for germline cyst formation during <i>Drosophila</i> oogenesis. <i>Genesis</i> , 2001, 29, 196-209.	0.8	31
29	A near complete snapshot of the <i>Zea mays</i> seedling transcriptome revealed from ultra-deep sequencing. <i>Scientific Reports</i> , 2015, 4, 4519.	1.6	28
30	Identification of Genes Critical for Resistance to Infection by West Nile Virus Using RNA-Seq Analysis. <i>Viruses</i> , 2013, 5, 1664-1681.	1.5	25
31	Identification of somatic mutations in human prostate cancer by RNA-Seq. <i>Gene</i> , 2013, 519, 343-347.	1.0	24
32	Sex-lethal is a target of Bruno-mediated translational repression in promoting the differentiation of stem cell progeny during <i>Drosophila</i> oogenesis. <i>Developmental Biology</i> , 2007, 302, 160-168.	0.9	23
33	PIWI Proteins Are Dispensable for Mouse Somatic Development and Reprogramming of Fibroblasts into Pluripotent Stem Cells. <i>PLoS ONE</i> , 2014, 9, e97821.	1.1	23
34	Identification of novel biomass-degrading enzymes from genomic dark matter: Populating genomic sequence space with functional annotation. <i>Biotechnology and Bioengineering</i> , 2014, 111, 1550-1565.	1.7	22
35	SpaRC: scalable sequence clustering using Apache Spark. <i>Bioinformatics</i> , 2019, 35, 760-768.	1.8	15
36	A case study of tuning MapReduce for efficient Bioinformatics in the cloud. <i>Parallel Computing</i> , 2017, 61, 83-95.	1.3	14

#	ARTICLE	IF	CITATIONS
37	Evidence for sequence biases associated with patterns of histone methylation. BMC Genomics, 2012, 13, 367.	1.2	12
38	De novo Nanopore read quality improvement using deep learning. BMC Bioinformatics, 2019, 20, 552.	1.2	10
39	Computational Strategies for Scalable Genomics Analysis. Genes, 2019, 10, 1017.	1.0	9
40	Reconstructing single genomes from complex microbial communities. IT - Information Technology, 2016, 58, 133-139.	0.6	7
41	A quantitative model of transcriptional differentiation driving host-pathogen interactions. Briefings in Bioinformatics, 2013, 14, 713-723.	3.2	6
42	A bi-Poisson model for clustering gene expression profiles by RNA-seq. Briefings in Bioinformatics, 2014, 15, 534-541.	3.2	6
43	A multi-Poisson dynamic mixture model to cluster developmental patterns of gene expression by RNA-seq. Briefings in Bioinformatics, 2015, 16, 205-215.	3.2	6
44	Deconvolute individual genomes from metagenome sequences through short read clustering. PeerJ, 2020, 8, e8966.	0.9	5
45	Prediction of protein solubility in E. coli. , 2012, , .		4
46	Combining Hadoop with MPI to Solve Metagenomics Problems that are both Data- and Compute-intensive. International Journal of Parallel Programming, 2018, 46, 762-775.	1.1	3
47	Automatic Outlier Detection for Genome Assembly Quality Assessment. , 2013, , .		1
48	Performance evaluation and tuning of BioPig for genomic analysis. , 2015, , .		1
49	A Scalable Pipeline for Transcriptome Profiling Tasks with On-Demand Computing Clouds. , 2016, , .		0
50	Evidence of Influence of Genomic DNA Sequence on Human X Chromosome Inactivation. PLoS Computational Biology, 2005, preprint, e113.	1.5	0