

Wenyan Nong

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

1,060
citations

516710

16
h-index

454955

30
g-index

51
all docs

51
docs citations

51
times ranked

1835
citing authors

#	ARTICLE	IF	CITATIONS
1	Long-term effect of plastic feeding on growth and transcriptomic response of mealworms (<i>Tenebrio</i>) Tj ETQq1 1 0.784314 rgBT /Over	8.2	23
2	Differential microRNA expression, microRNA arm switching, and microRNA:long noncoding RNA interaction in response to salinity stress in soybean. <i>BMC Genomics</i> , 2022, 23, 65.	2.8	13
3	Population Genomics, Transcriptional Response to Heat Shock, and Gut Microbiota of the Hong Kong Oyster <i>Magallana hongkongensis</i> . <i>Journal of Marine Science and Engineering</i> , 2022, 10, 237.	2.6	1
4	Chromosomal level genome of <i>Ilex asprella</i> and insight into antiviral triterpenoid pathway. <i>Genomics</i> , 2022, 114, 110366.	2.9	9
5	Genome of the ramshorn snail <i>Biomphalaria straminea</i> -an obligate intermediate host of schistosomiasis.. <i>GigaScience</i> , 2022, 11, .	6.4	11
6	Comparative Genomics Reveals Insights into the Divergent Evolution of Astigmatic Mites and Household Pest Adaptations. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	13
7	Myriapod genomes reveal ancestral horizontal gene transfer and hormonal gene loss in millipedes. <i>Nature Communications</i> , 2022, 13, .	12.8	12
8	ProBioQuest: a database and semantic analysis engine for literature, clinical trials and patents related to probiotics. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	2
9	Horseshoe crab genomes reveal the evolution of genes and microRNAs after three rounds of whole genome duplication. <i>Communications Biology</i> , 2021, 4, 83.	4.4	31
10	SOX9-COL9A3â€œdependent regulation of choroid plexus epithelial polarity governs bloodâ€œcerebrospinal fluid barrier integrity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	10
11	Formation of artificial chromosomes in <i>Caenorhabditis elegans</i> and analyses of their segregation in mitosis, DNA sequence composition and holocentromere organization. <i>Nucleic Acids Research</i> , 2021, 49, 9174-9193.	14.5	13
12	Transcriptomic and proteomic analyses of venom glands from scorpions <i>Liocheles australasiae</i> , <i>Mesobuthus martensii</i> , and <i>Scorpio maurus palmatus</i> . <i>Peptides</i> , 2021, 146, 170643.	2.4	6
13	Ultrafast and scalable variant annotation and prioritization with big functional genomics data. <i>Genome Research</i> , 2020, 30, 1789-1801.	5.5	14
14	Reconstruction of ancient homeobox gene linkages inferred from a new high-quality assembly of the Hong Kong oyster (<i>Magallana hongkongensis</i>) genome. <i>BMC Genomics</i> , 2020, 21, 713.	2.8	24
15	Genome of the four-finger threadfin <i>Eleutheronema tetradactylum</i> (Perciforms: Polynemidae). <i>BMC Genomics</i> , 2020, 21, 726.	2.8	4
16	Proteomic Analysis of the Venom of Jellyfishes <i>Rhopilema esculentum</i> and <i>Sanderia malayensis</i> . <i>Marine Drugs</i> , 2020, 18, 655.	4.6	9
17	Micro-RNA Clusters Integrate Evolutionary Constraints on Expression and Target Affinities: The miR-6/5/4/286/3/309 Cluster in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 2955-2965.	8.9	2
18	Jellyfish genomes reveal distinct homeobox gene clusters and conservation of small RNA processing. <i>Nature Communications</i> , 2020, 11, 3051.	12.8	47

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19	Chromosomal-level reference genome of the incense tree <i>Aquilaria sinensis</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 971-979.	4.8	24
20	Genome-wide analysis of MicroRNA-messenger RNA interactome in ex-vivo gill filaments, <i>Anguilla japonica</i> . <i>BMC Genomics</i> , 2020, 21, 208.	2.8	7
21	A crustacean annotated transcriptome (CAT) database. <i>BMC Genomics</i> , 2020, 21, 32.	2.8	13
22	Millipede genomes reveal unique adaptations during myriapod evolution. <i>PLoS Biology</i> , 2020, 18, e3000636.	5.6	18
23	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
24	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
25	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
26	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
27	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
28	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
29	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
30	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
31	Muscle-generated BDNF is a sexually dimorphic myokine that controls metabolic flexibility. <i>Science Signaling</i> , 2019, 12, .	3.6	50
32	Discovery of microRNA-like RNAs during early fruiting body development in the model mushroom <i>Coprinopsis cinerea</i> . <i>PLoS ONE</i> , 2018, 13, e0198234.	2.5	28
33	Phenotypic and Genetic Diversity of the Culinary-Medicinal Winter Mushroom <i>Flammulina velutipes</i> (Agaricomycetes) in China. <i>International Journal of Medicinal Mushrooms</i> , 2018, 20, 517-536.	1.5	5
34	Adaptation to deep-sea chemosynthetic environments as revealed by mussel genomes. <i>Nature Ecology and Evolution</i> , 2017, 1, 121.	7.8	250
35	MicroRNAs regulate the sesquiterpenoid hormonal pathway in <i>Drosophila</i> and other arthropods. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171827.	2.6	20
36	Association Mapping Reveals Genetic Loci Associated with Important Agronomic Traits in <i>Lentinula edodes</i> , Shiitake Mushroom. <i>Frontiers in Microbiology</i> , 2017, 8, 237.	3.5	13

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37	Distribution and current infection status of <i>Biomphalaria straminea</i> in Hong Kong. <i>Parasites and Vectors</i> , 2017, 10, 351.	2.5	12
38	Genetic diversity and population structure of Chinese <i>Lentinula edodes</i> revealed by InDel and SSR markers. <i>Mycological Progress</i> , 2016, 15, 1.	1.4	25
39	Population genomic analysis uncovers environmental stress-driven selection and adaptation of <i>Lentinula edodes</i> population in China. <i>Scientific Reports</i> , 2016, 6, 36789.	3.3	23
40	Development of a food safety information database for Greater China. <i>Food Control</i> , 2016, 65, 54-62.	5.5	17
41	Next generation genome sequencing reveals phylogenetic clades with different level of virulence among <i>Salmonella Typhimurium</i> clinical human isolates in Hong Kong. <i>BMC Genomics</i> , 2015, 16, 688.	2.8	7
42	Rapid Change of Microbiota Diversity in the Gut but Not the Hepatopancreas During Gonadal Development of the New Shrimp Model <i>Neocaridina denticulata</i> . <i>Marine Biotechnology</i> , 2015, 17, 811-819.	2.4	61
43	Comparative genomic analysis of clinical and environmental strains provides insight into the pathogenicity and evolution of <i>Vibrio parahaemolyticus</i> . <i>BMC Genomics</i> , 2014, 15, 1135.	2.8	19
44	Human Proteins with Target Sites of Multiple Post-Translational Modification Types Are More Prone to Be Involved in Disease. <i>Journal of Proteome Research</i> , 2014, 13, 2735-2748.	3.7	31
45	Composition of Heterotrophic Flagellates in Coastal Waters of Different Trophic Status. <i>Current Microbiology</i> , 2013, 67, 351-355.	2.2	3
46	BSRD: a repository for bacterial small regulatory RNA. <i>Nucleic Acids Research</i> , 2013, 41, D233-D238.	14.5	104
47	Sputum Microbiota in Tuberculosis as Revealed by 16S rRNA Pyrosequencing. <i>PLoS ONE</i> , 2013, 8, e54574.	2.5	85
48	2011 German <i>Escherichia coli</i> O104:H4 outbreak: Alignment-free whole-genome phylogeny by feature frequency profiles. <i>Nature Precedings</i> , 2011, , .	0.1	1
49	A Proposal of Genomic Analytical Workflow in a Bacterial Pathogen Outbreak Investigation. <i>Nature Precedings</i> , 2011, , .	0.1	0