Jinfeng Wang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9531369/publications.pdf

Version: 2024-02-01

471061 500791 2,803 29 17 28 h-index citations g-index papers 32 32 32 4188 docs citations times ranked citing authors all docs

| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 1 | CIRI: an efficient and unbiased algorithm for de novo circular RNA identification. Genome Biology, 2015, 16, 4. | 3.8 | 921 |
| 2 | Dysbiosis of maternal and neonatal microbiota associated with gestational diabetes mellitus. Gut, 2018, 67, 1614-1625. | 6.1 | 305 |
| 3 | Convergent Evolution of Rumen Microbiomes in High-Altitude Mammals. Current Biology, 2016, 26, 1873-1879. | 1.8 | 281 |
| 4 | Comprehensive identification of internal structure and alternative splicing events in circular RNAs. Nature Communications, 2016, 7, 12060. | 5.8 | 249 |
| 5 | Metagenomic sequencing reveals microbiota and its functional potential associated with periodontal disease. Scientific Reports, 2013, 3, 1843. | 1.6 | 207 |
| 6 | Large-Scale Comparative Analyses of Tick Genomes Elucidate Their Genetic Diversity and Vector Capacities. Cell, 2020, 182, 1328-1340.e13. | 13.5 | 145 |
| 7 | Phage–bacteria interaction network in human oral microbiome. Environmental Microbiology, 2016, 18, 2143-2158. | 1.8 | 87 |
| 8 | Translocation of vaginal microbiota is involved in impairment and protection of uterine health. Nature Communications, 2021, 12, 4191. | 5.8 | 70 |
| 9 | Deterministic transition of enterotypes shapes the infant gut microbiome at an early age. Genome Biology, 2021, 22, 243. | 3.8 | 65 |
| 10 | Molecular analysis of green-tide-forming macroalgae in the Yellow Sea. Aquatic Botany, 2010, 93, 25-31. | 0.8 | 63 |
| 11 | Composition-based classification of short metagenomic sequences elucidates the landscapes of taxonomic and functional enrichment of microorganisms. Nucleic Acids Research, 2013, 41, e3-e3. | 6.5 | 54 |
| 12 | Tracing the accumulation of in vivo human oral microbiota elucidates microbial community dynamics at the gateway to the GI tract. Gut, 2020, 69, 1355-1356. | 6.1 | 53 |
| 13 | MetaSort untangles metagenome assembly by reducing microbial community complexity. Nature Communications, 2017, 8, 14306. | 5.8 | 52 |
| 14 | Molecular phylogenetic analysis of attached Ulvaceae species and free-floating Enteromorpha from Qingdao coasts in 2007. Chinese Journal of Oceanology and Limnology, 2008, 26, 276-279. | 0.7 | 43 |
| 15 | Population-Genomic Insights into Variation in Prevotella intermedia and Prevotella nigrescens Isolates and Its Association with Periodontal Disease. Frontiers in Cellular and Infection Microbiology, 2017, 7, 409. | 1.8 | 31 |
| 16 | Genetic basis for the establishment of endosymbiosis in <i>Paramecium</i> . ISME Journal, 2019, 13, 1360-1369. | 4.4 | 30 |
| 17 | RiboFR-Seq: a novel approach to linking 16S rRNA amplicon profiles to metagenomes. Nucleic Acids Research, 2016, 44, e99-e99. | 6.5 | 24 |
| 18 | Gene transfer into conchospores of <i>Porphyra haitanensis </i> (Bangiales, Rhodophyta) by glass bead agitation. Phycologia, 2010, 49, 355-360. | 0.6 | 19 |

| # | Article | IF | CITATIONS |
|----|---|------------------|---------------------|
| 19 | Metatranscriptomic analysis of an <i>in vitro</i> biofilm model reveals strain-specific interactions among multiple bacterial species. Journal of Oral Microbiology, 2019, 11, 1599670. | 1.2 | 17 |
| 20 | Genetic transformation in Kappaphycus alvarezii using micro-particle bombardment: a potential strategy for germplasm improvement. Aquaculture International, 2010, 18, 1027-1034. | 1.1 | 16 |
| 21 | The oral microbiome of pregnant women facilitates gestational diabetes discrimination. Journal of Genetics and Genomics, 2021, 48, 32-39. | 1.7 | 16 |
| 22 | CRISPRs provide broad and robust protection to oral microbial flora of gingival health against bacteriophage challenge. Protein and Cell, 2015, 6, 541-545. | 4.8 | 14 |
| 23 | Early development patterns and morphogenesis of blades in four species of Porphyra (Bangiales,) Tj ETQq1 1 0.7 | 84314 rgB 1.5 | T <u>/Q</u> verlock |
| 24 | Ulva and Enteromorpha (Ulvaceae, Chlorophyta) from two sides of the Yellow Sea: analysis of nuclear rDNA ITS and plastid rbcL sequence data. Chinese Journal of Oceanology and Limnology, 2010, 28, 762-768. | 0.7 | 11 |
| 25 | The characterization of color mutations in Bangiaceae (Bangiales, Rhodophyta). Journal of Applied Phycology, 2008, 20, 499-504. | 1.5 | 6 |
| 26 | Haemaphysalis longicornis. Trends in Genetics, 2021, 37, 292-293. | 2.9 | 6 |
| 27 | Salivary Microbiome Variation in Early Childhood Caries of Children 3–6 Years of Age and Its Association With Iron Deficiency Anemia and Extrinsic Black Stain. Frontiers in Cellular and Infection Microbiology, 2021, 11, 628327. | 1.8 | 4 |
| 28 | Rapid methods for extracting high-quality DNA from shell-boring " <i>Conchocelisâ€</i> . Botanica Marina, 2010, 53, 63-68. | 0.6 | 1 |
| 29 | Reply to Evidence that microbes identified as tick-borne pathogens are nutritional endosymbionts. Cell, 2021, 184, 2261-2262. | 13.5 | O |