# Mauve: Multiple Alignment of Conserved Genomic Seq

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## Citation Report

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | A novel method for multiple alignment of sequences with repeated and shuffled elements. Genome Research, 2004, 14, 2336-2346. | 2.4 | 106 |
| 2 | Multiple alignment of rearranged genomes. , 0, , . |  | 4 |
| 3 | Identifying Evolutionarily Conserved Segments Among Multiple Divergent and Rearranged Genomes. Lecture Notes in Computer Science, 2005, , 72-84. | 1.0 | 1 |
| 4 | Genomics of enterobacteriaceae. , 2005, , . |  | 0 |
| 5 | Systematic determination of the mosaic structure of bacterial genomes: species backbone versus strain-specific loops. BMC Bioinformatics, 2005, 6, 171. | 1.2 | 46 |
| 6 | GATA: a graphic alignment tool for comparative sequence analysis. BMC Bioinformatics, 2005, 6, 9. | 1.2 | 70 |
| 7 | Current Awareness on Comparative and Functional Genomics. Comparative and Functional Genomics, 2005, 6, 97-112. | 2.0 | 0 |
| 8 | DNA Sequence and Comparative Genomics of pAPEC-O2-R, an Avian Pathogenic Escherichia coli Transmissible R Plasmid. Antimicrobial Agents and Chemotherapy, 2005, 49, 4681-4688. | 1.4 | 94 |
| 9 | Swine and Poultry Pathogens: the Complete Genome Sequences of Two Strains of Mycoplasma hyopneumoniae and a Strain of Mycoplasma synoviae. Journal of Bacteriology, 2005, 187, 5568-5577. | 1.0 | 289 |
| 10 | A Fast Algorithm Aligning Multiple Microbial Genomic Sequences. , 2005, 2006, 240-3. |  | 0 |
| 11 | ROBIN: a tool for genome rearrangement of block-interchanges. Bioinformatics, 2005, 21, 2780-2782. | 1.8 | 12 |
| 12 | Databases and software for the comparison of prokaryotic genomes. Microbiology (United Kingdom), 2005, 151, 2125-2132. | 0.7 | 29 |
| 13 | Genome-wide detection and analysis of homologous recombination among sequenced strains of Escherichia coli. Genome Biology, 2006, 7, R44. | 13.9 | 63 |
| 14 | Multiple sequence alignment for phylogenetic purposes. Australian Systematic Botany, 2006, 19, 479. | 0.3 | 131 |
| 15 | Understanding Microbial Metabolism. Annual Review of Microbiology, 2006, 60, 533-559. | 2.9 | 48 |
| 16 | GenomeDiagram: a python package for the visualization of large-scale genomic data. Bioinformatics, 2006, 22, 616-617. | 1.8 | 83 |
| 17 | Complete sequence of the large virulence plasmid pSFO157 of the sorbitol-fermenting enterohemorrhagic Escherichia coli O157:Hâˆ’ strain 3072/96. International Journal of Medical Microbiology, 2006, 296, 467-474. | 1.5 | 56 |
| 18 | Selection for Chromosome Architecture in Bacteria. Journal of Molecular Evolution, 2006, 62, 615-629. | 0.8 | 80 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 19 | M-GCAT: interactively and efficiently constructing large-scale multiple genome comparison frameworks in closely related species. BMC Bioinformatics, 2006, 7, 433. | 1.2 | 78 |
| 20 | inGeno â€“ an integrated genome and ortholog viewer for improved genome to genome comparisons. BMC Bioinformatics, 2006, 7, 461. | 1.2 | 8 |
| 21 | ASAP: a resource for annotating, curating, comparing, and disseminating genomic data. Nucleic Acids Research, 2006, 34, D41-D45. | 6.5 | 56 |
| 22 | SPRING: a tool for the analysis of genome rearrangement using reversals and block-interchanges. Nucleic Acids Research, 2006, 34, W696-W699. | 6.5 | 22 |
| 23 | The Evolutionary Origin of Xanthomonadales Genomes and the Nature of the Horizontal Gene Transfer Process. Molecular Biology and Evolution, 2006, 23, 2049-2057. | 3.5 | 44 |
| 24 | Evolution at the nucleotide level: the problem of multiple whole-genome alignment. Human Molecular Genetics, 2006, 15, R51-R56. | 1.4 | 51 |
| 25 | An Integrative Method for Accurate Comparative Genome Mapping. PLoS Computational Biology, 2006, 2, e75. | 1.5 | 25 |
| 26 | COMPAM :visualization of combining pairwise alignments for multiple genomes. Bioinformatics, 2006, 22, 242-244. | 1.8 | 7 |
| 27 | A bimodal pattern of relatedness between the Salmonella Paratyphi A and Typhi genomes: Convergence or divergence by homologous recombination?. Genome Research, 2006, 17, 61-68. | 2.4 | 112 |
| 28 | A novel strategy for the identification of genomic islands by comparative analysis of the contents and contexts of tRNA sites in closely related bacteria. Nucleic Acids Research, 2006, 34, e3-e3. | 6.5 | 67 |
| 29 | Exposing Phylogenetic Relationships by Genome Rearrangement. Advances in Computers, 2006, , 1-57. | 1.2 | 2 |
| 30 | Computation and Analysis of Genomic Multi-Sequence Alignments. Annual Review of Genomics and Human Genetics, 2007, 8, 193-213. | 2.5 | 30 |
| 31 | Inference of Bacterial Microevolution Using Multilocus Sequence Data. Genetics, 2007, 175, 1251-1266. | 1.2 | 616 |
| 32 | MobilomeFINDER: web-based tools for in silico and experimental discovery of bacterial genomic islands. Nucleic Acids Research, 2007, 35, W97-W104. | 6.5 | 74 |
| 33 | Enteropathogen Resource Integration Center (ERIC): bioinformatics support for research on biodefense-relevant enterobacteria. Nucleic Acids Research, 2007, 36, D519-D523. | 6.5 | 14 |
| 34 | Genome Analyses of Three Strains of Rhodobacter sphaeroides : Evidence of Rapid Evolution of Chromosome II. Journal of Bacteriology, 2007, 189, 1914-1921. | 1.0 | 81 |
| 35 | Los Alamos Hepatitis C Virus Sequence and Human Immunology Databases: An Expanding Resource for Antiviral Research. Antiviral Chemistry and Chemotherapy, 2007, 18, 113-123. | 0.3 | 10 |
| 36 | National Institute of Allergy and Infectious Diseases Bioinformatics Resource Centers: New Assets for Pathogen Informatics. Infection and Immunity, 2007, 75, 3212-3219. | 1.0 | 50 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 37 | Analyzing Patterns of Microbial Evolution Using the Mauve Genome Alignment System. Methods in Molecular Biology, 2007, 396, 135-152. | 0.4 | 51 |
| 38 | Living in a changing environment: Insights into host adaptation in Neisseria meningitidis from comparative genomics. International Journal of Medical Microbiology, 2007, 297, 601-613. | 1.5 | 21 |
| 39 | Analysis of invariant sequences in 266 complete genomes. Gene, 2007, 401, 172-180. | 1.0 | 10 |
| 40 | Genetic flux over time in the Salmonella lineage. Genome Biology, 2007, 8, R100. | 13.9 | 71 |
| 41 | Phylogenetic exploration of bacterial genomic rearrangements. Bioinformatics, 2007, 23, 1172-1174. | 1.8 | 7 |
| 42 | Evaluating Two Visualization Techniques for Genome Comparison. Proceedings / International Conference on Information Visualisation, 2007, , . | 0.0 | 5 |
| 43 | Yersinia pestis Evolution on a Small Timescale: Comparison of Whole Genome Sequences from North America. PLoS ONE, 2007, 2, e770. | 1.1 | 34 |
| 44 | Canonical Insertion-Deletion Markers for Rapid DNA Typing of<i>Francisella tularensis</i>. Emerging Infectious Diseases, 2007, 13, 1725-1732. | 2.0 | 45 |
| 45 | Mining the genomes of plant pathogenic bacteria: how not to drown in gigabases of sequence. Molecular Plant Pathology, 2007, 9, 071031023555001-???. | 2.0 | 2 |
| 46 | Multiple non-collinear TF-map alignments of promoter regions. BMC Bioinformatics, 2007, 8, 138. | 1.2 | 10 |
| 47 | Genomorama: genome visualization and analysis. BMC Bioinformatics, 2007, 8, 204. | 1.2 | 9 |
| 48 | Rapid evolutionary change of common bean (Phaseolus vulgaris L) plastome, and the genomic diversification of legume chloroplasts. BMC Genomics, 2007, 8, 228. | 1.2 | 95 |
| 49 | Subtle genetic changes enhance virulence of methicillin resistant and sensitive Staphylococcus aureus. BMC Microbiology, 2007, 7, 99. | 1.3 | 227 |
| 50 | The genome of Îµ15, a serotype-converting, Group E1 Salmonella enterica-specific bacteriophage. Virology, 2007, 369, 234-244. | 1.1 | 60 |
| 51 | Molecular Epidemiology, Evolution, and Ecology of <i>Francisella</i>. Annals of the New York Academy of Sciences, 2007, 1105, 30-66. | 1.8 | 331 |
| 52 | Chloroplast genomes of the diatoms Phaeodactylum tricornutum and Thalassiosira pseudonana: comparison with other plastid genomes of the red lineage. Molecular Genetics and Genomics, 2007, 277, 427-439. | 1.0 | 184 |
| 53 | Addressing chromosome evolution in the whole-genome sequence era. Chromosome Research, 2008, 16, 5-16. | 1.0 | 13 |
| 54 | Extensive Reorganization of the Plastid Genome of Trifolium subterraneum (Fabaceae) Is Associated with Numerous Repeated Sequences and Novel DNA Insertions. Journal of Molecular Evolution, 2008, 67, 696-704. | 0.8 | 217 |

| # | Article | IF | Citations |
|---|---|---|---|
| 55 | Comparison of complete sequences of potato rough dwarf virus and potato virus P and their relationships to other carlaviruses. Archives of Virology, 2008, 153, 1787-1789. | 0.9 | 6 |
| 56 | The genome of Streptomyces rimosus subsp. rimosus shows a novel structure compared to other Streptomyces using DNA/DNA microarray analysis. Antonie Van Leeuwenhoek, 2008, 94, 173-186. | 0.7 | 7 |
| 57 | A small trip in the untranquil world of genomes. Theoretical Computer Science, 2008, 395, 171-192. | 0.5 | 4 |
| 58 | Hindsight in the relative abundance, metabolic potential and genome dynamics of uncultivated marine archaea from comparative metagenomic analyses of bathypelagic plankton of different oceanic regions. ISME Journal, 2008, 2, 865-886. | 4.4 | 113 |
| 59 | The CACTA transposon <i>Bot1</i> played a major role in <i>Brassica</i> genome divergence and gene proliferation. Plant Journal, 2008, 56, 1030-1044. | 2.8 | 75 |
| 60 | SeqAn An efficient, generic C++ library for sequence analysis. BMC Bioinformatics, 2008, 9, 11. | 1.2 | 287 |
| 61 | Efficient computation of absent words in genomic sequences. BMC Bioinformatics, 2008, 9, 167. | 1.2 | 62 |
| 62 | PSAT: A web tool to compare genomic neighborhoods of multiple prokaryotic genomes. BMC Bioinformatics, 2008, 9, 170. | 1.2 | 30 |
| 63 | Precise detection of rearrangement breakpoints in mammalian chromosomes. BMC Bioinformatics, 2008, 9, 286. | 1.2 | 36 |
| 64 | Evaluation of genomic island predictors using a comparative genomics approach. BMC Bioinformatics, 2008, 9, 329. | 1.2 | 255 |
| 65 | MOSAIC: an online database dedicated to the comparative genomics of bacterial strains at the intra-species level. BMC Bioinformatics, 2008, 9, 498. | 1.2 | 19 |
| 66 | Genome classification by gene distribution: An overlapping subspace clustering approach. BMC Evolutionary Biology, 2008, 8, 116. | 3.2 | 10 |
| 67 | Comparative genomics-based investigation of resequencing targets in Vibrio fischeri: Focus on point miscalls and artefactual expansions. BMC Genomics, 2008, 9, 138. | 1.2 | 72 |
| 68 | Genome sequence and rapid evolution of the rice pathogen Xanthomonas oryzae pv. oryzae PXO99A. BMC Genomics, 2008, 9, 204. | 1.2 | 327 |
| 69 | Multiple genome alignment for identifying the core structure among moderately related microbial genomes. BMC Genomics, 2008, 9, 515. | 1.2 | 25 |
| 70 | Analysis of the genetic variation in Mycobacterium tuberculosis strains by multiple genome alignments. BMC Research Notes, 2008, 1, 110. | 0.6 | 34 |
| 71 | Extending the Bacillus cereus group genomics to putative food-borne pathogens of different toxicity. Chemico-Biological Interactions, 2008, 171, 236-249. | 1.7 | 140 |
| 72 | The genome and proteome of the Kluyvera bacteriophage Kvp1 â€“ another member of the T7-like Autographivirinae. Virology Journal, 2008, 5, 122. | 1.4 | 12 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 73 | Tools for simulating evolution of aligned genomic regions with integrated parameter estimation. Genome Biology, 2008, 9, R147. | 13.9 | 20 |
| 74 | Role of Recombination in the Evolution of the Model Plant Pathogen <i>Pseudomonas syringae</i> pv. tomato DC3000, a Very Atypical Tomato Strain. Applied and Environmental Microbiology, 2008, 74, 3171-3181. | 1.4 | 89 |
| 75 | Similar ectopic gene conversion frequencies in the backbone genome of pathogenic and nonpathogenic Escherichia coli strains. Genomics, 2008, 92, 168-172. | 1.3 | 3 |
| 76 | Genomic Comparison of Virulent <i>Rickettsia rickettsii</i> Sheila Smith and Avirulent <i>Rickettsia rickettsii</i> Iowa. Infection and Immunity, 2008, 76, 542-550. | 1.0 | 108 |
| 77 | Whole-genome comparison of disease and carriage strains provides insights into virulence evolution in <i>Neisseria meningitidis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3473-3478. | 3.3 | 159 |
| 78 | Evolution of the <i>iss</i> Gene in <i>Escherichia coli</i>. Applied and Environmental Microbiology, 2008, 74, 2360-2369. | 1.4 | 131 |
| 79 | Space Efficient Computation of Rare Maximal Exact Matches between Multiple Sequences. Journal of Computational Biology, 2008, 15, 357-377. | 0.8 | 12 |
| 80 | Whole-Genome Pyrosequencing of an Epidemic Multidrug-Resistant <i>Acinetobacter baumannii</i> Strain Belonging to the European Clone II Group. Antimicrobial Agents and Chemotherapy, 2008, 52, 2616-2625. | 1.4 | 240 |
| 81 | Dynamics of Genome Rearrangement in Bacterial Populations. PLoS Genetics, 2008, 4, e1000128. | 1.5 | 216 |
| 82 | Recent developments in the MAFFT multiple sequence alignment program. Briefings in Bioinformatics, 2008, 9, 286-298. | 3.2 | 3,115 |
| 83 | Inferring genomic flux in bacteria. Genome Research, 2009, 19, 306-317. | 2.4 | 35 |
| 84 | Newly introduced genomic prophage islands are critical determinants of in vivo competitiveness in the Liverpool Epidemic Strain of <i>Pseudomonas aeruginosa</i>. Genome Research, 2009, 19, 12-23. | 2.4 | 317 |
| 85 | Genome-wide nucleotide-level mammalian ancestor reconstruction. Genome Research, 2008, 18, 1829-1843. | 2.4 | 164 |
| 86 | The Complete Genome Sequence of<i>Escherichia coli</i>DH10B: Insights into the Biology of a Laboratory Workhorse. Journal of Bacteriology, 2008, 190, 2597-2606. | 1.0 | 331 |
| 87 | VisCHAINER: Visualizing Genome Comparison. , 2008, , . |  | 0 |
| 88 | Niche-Specificity and the Variable Fraction of the <i>Pectobacterium</i> Pan-Genome. Molecular Plant-Microbe Interactions, 2008, 21, 1549-1560. | 1.4 | 93 |
| 89 | CoCoNUT: an efficient system for the comparison and analysis of genomes. BMC Bioinformatics, 2008, 9, 476. | 1.2 | 23 |
| 90 | Rickettsia Phylogenomics: Unwinding the Intricacies of Obligate Intracellular Life. PLoS ONE, 2008, 3, e2018. | 1.1 | 175 |

| # | Article | IF | Citations |
|---|---|---|---|
| 91 | Assessing the Quality of Whole Genome Alignments in Bacteria. Advances in Bioinformatics, 2009, 2009, 1-8. | 5.7 | 4 |
| 92 | Tracing the Evolution of Competence in Haemophilus influenzae. PLoS ONE, 2009, 4, e5854. | 1.1 | 25 |
| 93 | The NlpD Lipoprotein Is a Novel Yersinia pestis Virulence Factor Essential for the Development of Plague. PLoS ONE, 2009, 4, e7023. | 1.1 | 79 |
| 94 | Genome Sequence of the Endosymbiont Rickettsia peacockii and Comparison with Virulent Rickettsia rickettsii: Identification of Virulence Factors. PLoS ONE, 2009, 4, e8361. | 1.1 | 113 |
| 95 | Genome Sequence of<i>Aggregatibacter actinomycetemcomitans</i>Serotype c Strain D11S-1. Journal of Bacteriology, 2009, 191, 7378-7379. | 1.0 | 34 |
| 96 | A Genomic Distance Based on MUM Indicates Discontinuity between Most Bacterial Species and Genera. Journal of Bacteriology, 2009, 191, 91-99. | 1.0 | 145 |
| 97 | Comparative Genomics Reveal Extensive Transposon-Mediated Genomic Plasticity and Diversity among Potential Effector Proteins within the Genus<i>Coxiella</i>. Infection and Immunity, 2009, 77, 642-656. | 1.0 | 197 |
| 98 | Pseudomonas Genome Database: facilitating user-friendly, comprehensive comparisons of microbial genomes. Nucleic Acids Research, 2009, 37, D483-D488. | 6.5 | 220 |
| 99 | Reordering contigs of draft genomes using the Mauve Aligner. Bioinformatics, 2009, 25, 2071-2073. | 1.8 | 532 |
| 100 | In Silico Prediction of Horizontal Gene Transfer Events in <i>Lactobacillus bulgaricus</i> and <i>Streptococcus thermophilus</i> Reveals Protocooperation in Yogurt Manufacturing. Applied and Environmental Microbiology, 2009, 75, 4120-4129. | 1.4 | 88 |
| 101 | Directed Evolution of Ionizing Radiation Resistance in <i>Escherichia coli</i>. Journal of Bacteriology, 2009, 191, 5240-5252. | 1.0 | 131 |
| 102 | Molecular Evolutionary Consequences of Niche Restriction in Francisella tularensis, a Facultative Intracellular Pathogen. PLoS Pathogens, 2009, 5, e1000472. | 2.1 | 127 |
| 103 | Organised Genome Dynamics in the Escherichia coli Species Results in Highly Diverse Adaptive Paths. PLoS Genetics, 2009, 5, e1000344. | 1.5 | 1,005 |
| 104 | Comparative Genomic Characterization of Francisella tularensis Strains Belonging to Low and High Virulence Subspecies. PLoS Pathogens, 2009, 5, e1000459. | 2.1 | 112 |
| 105 | Comparative ICE Genomics: Insights into the Evolution of the SXT/R391 Family of ICEs. PLoS Genetics, 2009, 5, e1000786. | 1.5 | 247 |
| 106 | Draft Genome Sequences of Yersinia pestis Isolates from Natural Foci of Endemic Plague in China. Journal of Bacteriology, 2009, 191, 7628-7629. | 1.0 | 16 |
| 107 | GR-Aligner: an algorithm for aligning pairwise genomic sequences containing rearrangement events. Bioinformatics, 2009, 25, 2188-2193. | 1.8 | 4 |
| 108 | Seevolution: visualizing chromosome evolution. Bioinformatics, 2009, 25, 960-961. | 1.8 | 5 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 109 | ABWGAT: anchor-based whole genome analysis tool. Bioinformatics, 2009, 25, 3319-3320. | 1.8 | 2 |
| 110 | Complete Genome of the Broad-Host-Range <i>Erwinia amylovora</i> Phage Î¦Ea21-4 and Its Relationship to <i>Salmonella</i> Phage Felix O1. Applied and Environmental Microbiology, 2009, 75, 2139-2147. | 1.4 | 61 |
| 111 | Analysis of Ten <i>Brucella</i> Genomes Reveals Evidence for Horizontal Gene Transfer Despite a Preferred Intracellular Lifestyle. Journal of Bacteriology, 2009, 191, 3569-3579. | 1.0 | 103 |
| 112 | Multiple whole-genome alignments without a reference organism. Genome Research, 2009, 19, 682-689. | 2.4 | 63 |
| 113 | CSA: An efficient algorithm to improve circular DNA multiple alignment. BMC Bioinformatics, 2009, 10, 230. | 1.2 | 37 |
| 114 | Context-driven discovery of gene cassettes in mobile integrons using a computational grammar. BMC Bioinformatics, 2009, 10, 281. | 1.2 | 17 |
| 115 | CASSIOPE: An expert system for conserved regions searches. BMC Bioinformatics, 2009, 10, 284. | 1.2 | 9 |
| 116 | Maximum independent sets of commuting and noninterfering inversions. BMC Bioinformatics, 2009, 10, S6. | 1.2 | 7 |
| 117 | Co-evolution of genomes and plasmids within Chlamydia trachomatis and the emergence in Sweden of a new variant strain. BMC Genomics, 2009, 10, 239. | 1.2 | 119 |
| 118 | Comparative genomic analyses of Streptococcus mutans provide insights into chromosomal shuffling and species-specific content. BMC Genomics, 2009, 10, 358. | 1.2 | 72 |
| 119 | Insertion sequence content reflects genome plasticity in strains of the root nodule actinobacterium Frankia. BMC Genomics, 2009, 10, 468. | 1.2 | 34 |
| 120 | Comparative analysis of two Neisseria gonorrhoeae genome sequences reveals evidence of mobilization of Correia Repeat Enclosed Elements and their role in regulation. BMC Genomics, 2009, 10, 70. | 1.2 | 29 |
| 121 | Contributions to selected phenotypic characteristics of large species- and lineage-specific genomic regions in Listeria monocytogenes. Food Microbiology, 2009, 26, 212-223. | 2.1 | 22 |
| 122 | A framework for phylogenetic sequence alignment. Plant Systematics and Evolution, 2009, 282, 127-149. | 0.3 | 45 |
| 123 | Plasmids captured in C. metallidurans CH34: defining the PromA family of broad-host-range plasmids. Antonie Van Leeuwenhoek, 2009, 96, 193-204. | 0.7 | 67 |
| 124 | Computational Biology Methods and Their Application to the Comparative Genomics of Endocellular Symbiotic Bacteria of Insects. Biological Procedures Online, 2009, 11, 52-78. | 1.4 | 6 |
| 125 | GO4genome: A Prokaryotic Phylogeny Based on Genome Organization. Journal of Molecular Evolution, 2009, 68, 550-562. | 0.8 | 4 |
| 126 | Comparative genomics-guided loop-mediated isothermal amplification for characterization of<i>Pseudomonas syringae</i>pv. phaseolicola. Journal of Applied Microbiology, 2009, 107, 717-726. | 1.4 | 13 |

| # | Article | IF | Citations |
|---|---|---|---|
| 127 | A single regulatory gene is sufficient to alter bacterial host range. Nature, 2009, 458, 215-218. | 13.7 | 177 |
| 128 | Genomic analysis of multiple Roseophage SIO1 strains. Environmental Microbiology, 2009, 11, 2863-2873. | 1.8 | 64 |
| 129 | Comparative analysis of the widespread and conserved PB1â€like viruses infecting <i>Pseudomonas aeruginosa</i>. Environmental Microbiology, 2009, 11, 2874-2883. | 1.8 | 85 |
| 130 | Genome analysis of Bacillus amyloliquefaciens FZB42 reveals its potential for biocontrol of plant pathogens. Journal of Biotechnology, 2009, 140, 27-37. | 1.9 | 372 |
| 131 | Comparative studies of Campylobacter jejuni genomic diversity reveal the importance of core and dispensable genes in the biology of this enigmatic food-borne pathogen. Current Opinion in Biotechnology, 2009, 20, 158-165. | 3.3 | 19 |
| 132 | Genome flexibility in Neisseria meningitidis. Vaccine, 2009, 27, B103-B111. | 1.7 | 47 |
| 133 | The genome and proteome of a virulent Escherichia coli O157:H7 bacteriophage closely resembling Salmonella phage Felix O1. Virology Journal, 2009, 6, 41. | 1.4 | 34 |
| 134 | Brucella. , 2009, , 1-64. |  | 5 |
| 135 | Cytogenetics and Molecular Data in Snakes: A Phylogenetic Approach. Cytogenetic and Genome Research, 2009, 127, 128-142. | 0.6 | 43 |
| 136 | Decoding Synteny Blocks and Large-Scale Duplications in Mammalian and Plant Genomes. Lecture Notes in Computer Science, 2009, , 220-232. | 1.0 | 9 |
| 137 | A Novel Heuristic for Local Multiple Alignment of Interspersed DNA Repeats. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 180-189. | 1.9 | 14 |
| 138 | MizBee: A Multiscale Synteny Browser. IEEE Transactions on Visualization and Computer Graphics, 2009, 15, 897-904. | 2.9 | 127 |
| 139 | 3D Genome Tuner: Compare Multiple Circular Genomes in a 3D Context. Genomics, Proteomics and Bioinformatics, 2009, 7, 143-146. | 3.0 | 1 |
| 140 | Multiple Alignment of DNA Sequences with MAFFT. Methods in Molecular Biology, 2009, 537, 39-64. | 0.4 | 1,145 |
| 141 | Genomic Sequencing Reveals Regulatory Mutations and Recombinational Events in the Widely Used MC4100 Lineage of<i>Escherichia coli</i>K-12. Journal of Bacteriology, 2009, 191, 4025-4029. | 1.0 | 98 |
| 142 | Chromosomal diversity in Lactococcus lactis and the origin of dairy starter cultures. Genome Biology and Evolution, 2010, 2, 729-44. | 1.1 | 90 |
| 143 | The Sequence of a 1.8-Mb Bacterial Linear Plasmid Reveals a Rich Evolutionary Reservoir of Secondary Metabolic Pathways. Genome Biology and Evolution, 2010, 2, 212-224. | 1.1 | 193 |
| 145 | Complete Genome Sequence of the Fire Blight Pathogen <i>Erwinia amylovora</i> CFBP 1430 and Comparison to Other <i>Erwinia</i> spp.. Molecular Plant-Microbe Interactions, 2010, 23, 384-393. | 1.4 | 156 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 147 | Comparative genomics of green sulfur bacteria. Photosynthesis Research, 2010, 104, 137-152. | 1.6 | 12 |
| 148 | Comparative genomics of pAKD4, the prototype IncP-1Î´ plasmid with a complete backbone. Plasmid, 2010, 63, 98-107. | 0.4 | 20 |
| 149 | Improving de novo sequence assembly using machine learning and comparative genomics for overlap correction. BMC Bioinformatics, 2010, 11, 33. | 1.2 | 16 |
| 150 | MS4 - Multi-Scale Selector of Sequence Signatures: An alignment-free method for classification of biological sequences. BMC Bioinformatics, 2010, 11, 406. | 1.2 | 8 |
| 151 | Automatic detection of anchor points for multiple sequence alignment. BMC Bioinformatics, 2010, 11, 445. | 1.2 | 6 |
| 152 | Pan-genome sequence analysis using Panseq: an online tool for the rapid analysis of core and accessory genomic regions. BMC Bioinformatics, 2010, 11, 461. | 1.2 | 249 |
| 153 | BIGSdb: Scalable analysis of bacterial genome variation at the population level. BMC Bioinformatics, 2010, 11, 595. | 1.2 | 2,074 |
| 154 | High-throughput genome sequencing of two Listeria monocytogenes clinical isolates during a large foodborne outbreak. BMC Genomics, 2010, 11, 120. | 1.2 | 306 |
| 155 | Legionella pneumophila pangenome reveals strain-specific virulence factors. BMC Genomics, 2010, 11, 181. | 1.2 | 161 |
| 156 | Complete genome sequence of the fire blight pathogen Erwinia pyrifoliae DSM 12163T and comparative genomic insights into plant pathogenicity. BMC Genomics, 2010, 11, 2. | 1.2 | 57 |
| 157 | A scenario of mitochondrial genome evolution in maize based on rearrangement events. BMC Genomics, 2010, 11, 233. | 1.2 | 44 |
| 158 | Genome comparison of the epiphytic bacteria Erwinia billingiae and E. tasmaniensis with the pear pathogen E. pyrifoliae. BMC Genomics, 2010, 11, 393. | 1.2 | 92 |
| 159 | Markedly different genome arrangements between serotype a strains and serotypes b or c strains of Aggregatibacter actinomycetemcomitans. BMC Genomics, 2010, 11, 489. | 1.2 | 17 |
| 160 | Comparative genomics of the bacterial genus Listeria: Genome evolution is characterized by limited gene acquisition and limited gene loss. BMC Genomics, 2010, 11, 688. | 1.2 | 174 |
| 161 | Analysis of genomic differences among Clostridium botulinum type A1 strains. BMC Genomics, 2010, 11, 725. | 1.2 | 21 |
| 162 | Genetic and phenotypic diversity in Burkholderia: contributions by prophage and phage-like elements. BMC Microbiology, 2010, 10, 202. | 1.3 | 45 |
| 163 | Characterization of JG024, a pseudomonas aeruginosa PB1-like broad host range phage under simulated infection conditions. BMC Microbiology, 2010, 10, 301. | 1.3 | 81 |
| 164 | A highly conserved gene island of three genes on chromosome 3B of hexaploid wheat: diverse gene function and genomic structure maintained in a tightly linked block. BMC Plant Biology, 2010, 10, 98. | 1.6 | 16 |

| # | Article | IF | Citations |
|---|---|---|---|
| 166 | Global gene expression profile of <i>Orientia tsutsugamushi</i>. Proteomics, 2010, 10, 1699-1715. | 1.3 | 26 |
| 167 | ANALYSES OF THE COMPLETE CHLOROPLAST GENOME SEQUENCES OF TWO MEMBERS OF THE PELAGOPHYCEAE: <i>AUREOCOCCUS ANOPHAGEFFERENS</i> CCMP1984 AND <i>AUREOUMBRA LAGUNENSIS</i> CCMP1507<sup>1</sup>. Journal of Phycology, 2010, 46, 602-615. | 1.0 | 32 |
| 168 | Visualizing genomes: techniques and challenges. Nature Methods, 2010, 7, S5-S15. | 9.0 | 146 |
| 169 | Detecting genomic islands using bioinformatics approaches. Nature Reviews Microbiology, 2010, 8, 373-382. | 13.6 | 257 |
| 170 | Annotation and overview of the <i>Pseudomonas savastanoi</i> pv. savastanoi NCPPB 3335 draft genome reveals the virulence gene complement of a tumourâ€inducing pathogen of woody hosts. Environmental Microbiology, 2010, 12, 1604-1620. | 1.8 | 80 |
| 171 | AnÃ¡lisis comparativo de seis genomas del complejo Mycobacterium tuberculosis. Biomedica, 2010, 30, 23. | 0.3 | 2 |
| 172 | Complete Genome Sequence of the Multiresistant Taxonomic Outlier Pseudomonas aeruginosa PA7. PLoS ONE, 2010, 5, e8842. | 1.1 | 236 |
| 173 | Shewanella spp. Genomic Evolution for a Cold Marine Lifestyle and In-Situ Explosive Biodegradation. PLoS ONE, 2010, 5, e9109. | 1.1 | 76 |
| 174 | Sequencing and Genetic Variation of Multidrug Resistance Plasmids in Klebsiella pneumoniae. PLoS ONE, 2010, 5, e10141. | 1.1 | 52 |
| 175 | The Complete Plastid Genomes of the Two â€˜Dinotomsâ€™ Durinskia baltica and Kryptoperidinium foliaceum. PLoS ONE, 2010, 5, e10711. | 1.1 | 89 |
| 176 | Conjugative Botulinum Neurotoxin-Encoding Plasmids in Clostridium botulinum. PLoS ONE, 2010, 5, e11087. | 1.1 | 48 |
| 177 | Murasaki: A Fast, Parallelizable Algorithm to Find Anchors from Multiple Genomes. PLoS ONE, 2010, 5, e12651. | 1.1 | 30 |
| 178 | Identification of Mendel's White Flower Character. PLoS ONE, 2010, 5, e13230. | 1.1 | 135 |
| 179 | Population Genetic Analysis of Propionibacterium acnes Identifies a Subpopulation and Epidemic Clones Associated with Acne. PLoS ONE, 2010, 5, e12277. | 1.1 | 233 |
| 180 | Host-Interactive Genes in Amerindian<i>Helicobacter pylori</i>Diverge from Their Old World Homologs and Mediate Inflammatory Responses. Journal of Bacteriology, 2010, 192, 3078-3092. | 1.0 | 50 |
| 181 | Inference of Homologous Recombination in Bacteria Using Whole-Genome Sequences. Genetics, 2010, 186, 1435-1449. | 1.2 | 155 |
| 182 | Comparative Genomic Characterization of <i>Actinobacillus pleuropneumoniae</i>. Journal of Bacteriology, 2010, 192, 5625-5636. | 1.0 | 59 |
| 183 | Evolutionary dynamics of <i>Clostridium difficile</i> over short and long time scales. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7527-7532. | 3.3 | 346 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 184 | Differential Gene Retention in Plastids of Common Recent Origin. Molecular Biology and Evolution, 2010, 27, 1530-1537. | 3.5 | 102 |
| 187 | The Genetic Basis of Laboratory Adaptation in <i>Caulobacter crescentus</i>. Journal of Bacteriology, 2010, 192, 3678-3688. | 1.0 | 166 |
| 188 | Virulence Factors Encoded by Legionella longbeachae Identified on the Basis of the Genome Sequence Analysis of Clinical Isolate D-4968. Journal of Bacteriology, 2010, 192, 1030-1044. | 1.0 | 58 |
| 189 | A computational genomics pipeline for prokaryotic sequencing projects. Bioinformatics, 2010, 26, 1819-1826. | 1.8 | 71 |
| 190 | genoPlotR: comparative gene and genome visualization in R. Bioinformatics, 2010, 26, 2334-2335. | 1.8 | 651 |
| 191 | A milieu of regulatory elements in the epidermal differentiation complex syntenic block: implications for atopic dermatitis and psoriasis. Human Molecular Genetics, 2010, 19, 1453-1460. | 1.4 | 92 |
| 192 | Different Phylogenomic Approaches to Resolve the Evolutionary Relationships among Model Fish Species. Molecular Biology and Evolution, 2010, 27, 2757-2774. | 3.5 | 18 |
| 193 | Cassis: detection of genomic rearrangement breakpoints. Bioinformatics, 2010, 26, 1897-1898. | 1.8 | 22 |
| 194 | A Novel Technique for Detecting Putative Horizontal Gene Transfer in the Sequence Space. Journal of Computational Biology, 2010, 17, 1535-1548. | 0.8 | 2 |
| 195 | The Chloroplast Genome Sequence of Mungbean (Vigna radiata) Determined by High-throughput Pyrosequencing: Structural Organization and Phylogenetic Relationships. DNA Research, 2010, 17, 11-22. | 1.5 | 198 |
| 196 | Emergence of a New Multidrug-Resistant Serotype X Variant in an Epidemic Clone of Shigella flexneri. Journal of Clinical Microbiology, 2010, 48, 419-426. | 1.8 | 104 |
| 197 | mGenomeSubtractor: a web-based tool for parallel in silico subtractive hybridization analysis of multiple bacterial genomes. Nucleic Acids Research, 2010, 38, W194-W200. | 6.5 | 74 |
| 198 | Analysis of the Legionella longbeachae Genome and Transcriptome Uncovers Unique Strategies to Cause Legionnaires' Disease. PLoS Genetics, 2010, 6, e1000851. | 1.5 | 143 |
| 199 | Evolution of an X-Linked Primate-Specific Micro RNA Cluster. Molecular Biology and Evolution, 2010, 27, 671-683. | 3.5 | 64 |
| 200 | SNPS IN THE HIV-1 TATA BOX AND THE AIDS PANDEMIC. Journal of Bioinformatics and Computational Biology, 2010, 08, 607-625. | 0.3 | 19 |
| 201 | The solution space of genome sequence alignment and LIS graph decomposition. , 2010, , . |  | 0 |
| 202 | Comparative Analysis of Plasmids in the Genus Listeria. PLoS ONE, 2010, 5, e12511. | 1.1 | 110 |
| 203 | Complete Genomic Sequence of Bacteriophage Felix O1. Viruses, 2010, 2, 710-730. | 1.5 | 72 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 204 | Complex prokaryotic genome structure: rapid evolution of chromosome II. Genome, 2010, 53, 675-687. | 0.9 | 18 |
| 205 | DRIMM-Synteny: decomposing genomes into evolutionary conserved segments. Bioinformatics, 2010, 26, 2509-2516. | 1.8 | 78 |
| 206 | Genomic differences between the food-grade Staphylococcus carnosus and pathogenic staphylococcal species. International Journal of Medical Microbiology, 2010, 300, 104-108. | 1.5 | 22 |
| 207 | Genomic and transcriptomic studies in Mycobacterium avium subspecies paratuberculosis. Veterinary Immunology and Immunopathology, 2010, 138, 303-311. | 0.5 | 8 |
| 208 | Identification of lytic bacteriophage MmP1, assigned to a new member of T7-like phages infecting Morganella morganii. Genomics, 2010, 96, 167-172. | 1.3 | 19 |
| 209 | Genomic Databases and Resources at the National Center for Biotechnology Information. Methods in Molecular Biology, 2010, 609, 17-44. | 0.4 | 17 |
| 210 | Structure and dynamics of the pan-genome of Streptococcus pneumoniae and closely related species. Genome Biology, 2010, 11, R107. | 3.8 | 321 |
| 211 | Small variable segments constitute a major type of diversity of bacterial genomes at the species level. Genome Biology, 2010, 11, R45. | 13.9 | 17 |
| 212 | Genomic characterization of the Yersinia genus. Genome Biology, 2010, 11, R1. | 13.9 | 103 |
| 213 | Multilocus Sequence Typing of <i>Clostridium difficile</i>. Journal of Clinical Microbiology, 2010, 48, 770-778. | 1.8 | 399 |
| 214 | Visual comparison for information visualization. Information Visualization, 2011, 10, 289-309. | 1.2 | 417 |
| 215 | Evolution and Spread of a Multidrug-Resistant Proteus mirabilis Clone with Chromosomal AmpC-Type Cephalosporinases in Europe. Antimicrobial Agents and Chemotherapy, 2011, 55, 2735-2742. | 1.4 | 52 |
| 217 | Recent Trends in Molecular Phylogenetic Analysis: Where to Next?. Journal of Heredity, 2011, 102, 130-138. | 1.0 | 85 |
| 218 | Pathogen comparative genomics in the next-generation sequencing era: genome alignments, pangenomics and metagenomics. Briefings in Functional Genomics, 2011, 10, 322-333. | 1.3 | 41 |
| 219 | Development and evaluation of a loop-mediated isothermal amplification assay for rapid detection and identification of<i>Pectobacterium atrosepticum</i>. Canadian Journal of Plant Pathology, 2011, 33, 447-457. | 0.8 | 26 |
| 220 | Characterization of the complete chloroplast genome of Hevea brasiliensis reveals genome rearrangement, RNA editing sites and phylogenetic relationships. Gene, 2011, 475, 104-112. | 1.0 | 92 |
| 221 | Identifying and characterizing a member of the RhopH1/Clag family in Plasmodium vivax. Gene, 2011, 481, 17-23. | 1.0 | 7 |
| 222 | Short communication: The complete genome sequence of Bifidobacterium animalis subspecies animalis ATCC 25527T and comparative analysis of growth in milk with B. animalis subspecies lactis DSM 10140T. Journal of Dairy Science, 2011, 94, 5864-5870. | 1.4 | 10 |

| # | Article | IF | Citations |
|---|---|---|---|
| 223 | Sequence Surveyor: Leveraging Overview for Scalable Genomic Alignment Visualization. IEEE Transactions on Visualization and Computer Graphics, 2011, 17, 2392-2401. | 2.9 | 38 |
| 224 | PoPoolation: A Toolbox for Population Genetic Analysis of Next Generation Sequencing Data from Pooled Individuals. PLoS ONE, 2011, 6, e15925. | 1.1 | 556 |
| 225 | Using Genomic Sequencing for Classical Genetics in E. coli K12. PLoS ONE, 2011, 6, e16717. | 1.1 | 56 |
| 226 | Sequencing and Comparative Genome Analysis of Two Pathogenic Streptococcus gallolyticus Subspecies: Genome Plasticity, Adaptation and Virulence. PLoS ONE, 2011, 6, e20519. | 1.1 | 41 |
| 227 | Microbial Diversity in the Midguts of Field and Lab-Reared Populations of the European Corn Borer Ostrinia nubilalis. PLoS ONE, 2011, 6, e21751. | 1.1 | 71 |
| 228 | Evolutionary Genomics of a Temperate Bacteriophage in an Obligate Intracellular Bacteria (Wolbachia). PLoS ONE, 2011, 6, e24984. | 1.1 | 45 |
| 229 | Structural and Content Diversity of Mitochondrial Genome in Beet: A Comparative Genomic Analysis. Genome Biology and Evolution, 2011, 3, 723-736. | 1.1 | 67 |
| 230 | Chloroplast genome sequences from total DNA for plant identification. Plant Biotechnology Journal, 2011, 9, 328-333. | 4.1 | 316 |
| 231 | Rickettsial evolution in the light of comparative genomics. Biological Reviews, 2011, 86, 379-405. | 4.7 | 219 |
| 232 | Adherence and motility characteristics of clinical Acinetobacter baumannii isolates. FEMS Microbiology Letters, 2011, 323, 44-51. | 0.7 | 168 |
| 233 | Comparative genomics and phylogeny of the IncI1 plasmids: A common plasmid type among porcine enterotoxigenic Escherichia coli. Plasmid, 2011, 66, 144-151. | 0.4 | 66 |
| 234 | Everything at once: Comparative analysis of the genomes of bacterial pathogens. Veterinary Microbiology, 2011, 153, 13-26. | 0.8 | 12 |
| 235 | Horizontal gene transfer in Histophilus somni and its role in the evolution of pathogenic strain 2336, as determined by comparative genomic analyses. BMC Genomics, 2011, 12, 570. | 1.2 | 34 |
| 236 | Closely related Campylobacter jejuni strains from different sources reveal a generalist rather than a specialist lifestyle. BMC Genomics, 2011, 12, 584. | 1.2 | 101 |
| 237 | Complete genome sequence of the lytic Pseudomonas fluorescens phage Ï•IBB-PF7A. Virology Journal, 2011, 8, 142. | 1.4 | 11 |
| 238 | The evolution of chloroplast genes and genomes in ferns. Plant Molecular Biology, 2011, 76, 251-261. | 2.0 | 87 |
| 239 | Complete genomic sequence of the Lactobacillus temperate phage LF1. Archives of Virology, 2011, 156, 1909-1912. | 0.9 | 11 |
| 240 | Interplay of recombination and selection in the genomes of Chlamydia trachomatis. Biology Direct, 2011, 6, 28. | 1.9 | 70 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 241 | nocoRNAc: Characterization of non-coding RNAs in prokaryotes. BMC Bioinformatics, 2011, 12, 40. | 1.2 | 39 |
| 242 | The rise and fall of breakpoint reuse depending on genome resolution. BMC Bioinformatics, 2011, 12, S1. | 1.2 | 19 |
| 243 | Genomic lineages of Rhizobium etli revealed by the extent of nucleotide polymorphisms and low recombination. BMC Evolutionary Biology, 2011, 11, 305. | 3.2 | 40 |
| 244 | Mycoplasma mycoides, from "mycoides Small Colony" to "capri". A microevolutionary perspective. BMC Genomics, 2011, 12, 114. | 1.2 | 64 |
| 245 | Investigation of the human pathogen Acinetobacter baumannii under iron limiting conditions. BMC Genomics, 2011, 12, 126. | 1.2 | 215 |
| 246 | Shotgun sequencing of Yersinia enterocolitica strain W22703 (biotype 2, serotype O:9): genomic evidence for oscillation between invertebrates and mammals. BMC Genomics, 2011, 12, 168. | 1.2 | 33 |
| 247 | Characterization and genome sequencing of two Propionibacterium acnes phages displaying pseudolysogeny. BMC Genomics, 2011, 12, 198. | 1.2 | 34 |
| 248 | Comparative genome analysis and genome-guided physiological analysis of Roseobacter litoralis. BMC Genomics, 2011, 12, 324. | 1.2 | 54 |
| 249 | Complete genome and comparative analysis of Streptococcus gallolyticus subsp. gallolyticus, an emerging pathogen of infective endocarditis. BMC Genomics, 2011, 12, 400. | 1.2 | 41 |
| 250 | BLAST Ring Image Generator (BRIG): simple prokaryote genome comparisons. BMC Genomics, 2011, 12, 402. | 1.2 | 2,691 |
| 251 | Attenuation of virulence in an apicomplexan hemoparasite results in reduced genome diversity at the population level. BMC Genomics, 2011, 12, 410. | 1.2 | 31 |
| 252 | Within-species lateral genetic transfer and the evolution of transcriptional regulation in Escherichia coli and Shigella. BMC Genomics, 2011, 12, 532. | 1.2 | 28 |
| 253 | Sequence of the hyperplastic genome of the naturally competent Thermus scotoductus SA-01. BMC Genomics, 2011, 12, 577. | 1.2 | 49 |
| 254 | Sequencing and Characterization of Pseudomonas aeruginosa phage JG004. BMC Microbiology, 2011, 11, 102. | 1.3 | 60 |
| 255 | Hypervirulent Chlamydia trachomatis Clinical Strain Is a Recombinant between Lymphogranuloma Venereum (L <sub>2</sub> ) and D Lineages. MBio, 2011, 2, e00045-11. | 1.8 | 100 |
| 256 | Using inversion signatures to generate draft genome sequence scaffolds. , 2011, , . | | 1 |
| 257 | Evidence-Based Annotation of Transcripts and Proteins in the Sulfate-Reducing Bacterium Desulfovibrio vulgaris Hildenborough. Journal of Bacteriology, 2011, 193, 5716-5727. | 1.0 | 28 |
| 258 | Genome of Multidrug-Resistant Uropathogenic Escherichia coli Strain NA114 from India. Journal of Bacteriology, 2011, 193, 4272-4273. | 1.0 | 63 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 259 | Mauve Assembly Metrics. Bioinformatics, 2011, 27, 2756-2757. | 1.8 | 108 |
| 260 | Comparative Genomic Analysis of Acinetobacter oleivorans DR1 To Determine Strain-Specific Genomic Regions and Gentisate Biodegradation. Applied and Environmental Microbiology, 2011, 77, 7418-7424. | 1.4 | 27 |
| 261 | Using Single-Nucleotide Polymorphisms To Discriminate Disease-Associated from Carried Genomes of Neisseria meningitidis. Journal of Bacteriology, 2011, 193, 3633-3641. | 1.0 | 5 |
| 262 | Genome Sequence of Vibrio rotiferianus Strain DAT722. Journal of Bacteriology, 2011, 193, 3381-3382. | 1.0 | 16 |
| 263 | Complete Genome Sequence of the Nicotine-Degrading Pseudomonas putida Strain S16. Journal of Bacteriology, 2011, 193, 5541-5542. | 1.0 | 60 |
| 264 | Major Families of Multiresistant Plasmids from Geographically and Epidemiologically Diverse Staphylococci. G3: Genes, Genomes, Genetics, 2011, 1, 581-591. | 0.8 | 92 |
| 265 | An alternative approach to multiple genome comparison. Nucleic Acids Research, 2011, 39, e101-e101. | 6.5 | 3 |
| 266 | Pan-genome of the dominant human gut-associated archaeon, <i>Methanobrevibacter smithii</i> , studied in twins. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4599-4606. | 3.3 | 221 |
| 267 | Long-Range and Targeted Ectopic Recombination between the Two Homeologous Chromosomes 11 and 12 in Oryza Species. Molecular Biology and Evolution, 2011, 28, 3139-3150. | 3.5 | 23 |
| 268 | Whole-Genome Sequence of Streptococcus pseudopneumoniae Isolate IS7493. Journal of Bacteriology, 2011, 193, 6102-6103. | 1.0 | 20 |
| 269 | Genome of a Novel Isolate of Paracoccus denitrificans Capable of Degrading N , N -Dimethylformamide. Journal of Bacteriology, 2011, 193, 5598-5599. | 1.0 | 42 |
| 270 | Complete Genome Sequence of Bacillus subtilis BSn5, an Endophytic Bacterium of Amorphophallus konjac with Antimicrobial Activity for the Plant Pathogen Erwinia carotovora subsp. carotovora. Journal of Bacteriology, 2011, 193, 2070-2071. | 1.0 | 97 |
| 271 | Birth and death of genes linked to chromosomal inversion. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1501-1506. | 3.3 | 62 |
| 272 | Complete Genome Sequences of Brucella melitensis Strains M28 and M5-90, with Different Virulence Backgrounds. Journal of Bacteriology, 2011, 193, 2904-2905. | 1.0 | 20 |
| 273 | ORIGINAL RESEARCH: Comparative constraint-based model development for thermophilic hydrogen production. Industrial Biotechnology, 2011, 7, 63-82. | 0.5 | 4 |
| 274 | Complete Genome Sequence of the Bacterium Porphyromonas gingivalis TDC60, Which Causes Periodontal Disease. Journal of Bacteriology, 2011, 193, 4259-4260. | 1.0 | 54 |
| 275 | <i>Neisseria meningitidis</i> is structured in clades associated with restriction modification systems that modulate homologous recombination. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4494-4499. | 3.3 | 198 |
| 276 | SyMAP v3.4: a turnkey synteny system with application to plant genomes. Nucleic Acids Research, 2011, 39, e68-e68. | 6.5 | 304 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 277 | Genome Sequences of Three Acinetobacter baumannii Strains Assigned to the Multilocus Sequence Typing Genotypes ST2, ST25, and ST78. Journal of Bacteriology, 2011, 193, 2359-2360. | 1.0 | 28 |
| 278 | Mutation of a Broadly Conserved Operon (RL3499-RL3502) from Rhizobium leguminosarum Biovar viciae Causes Defects in Cell Morphology and Envelope Integrity. Journal of Bacteriology, 2011, 193, 2684-2694. | 1.0 | 24 |
| 279 | The<i>tib</i>Adherence Locus of Enterotoxigenic<i>Escherichia coli</i>Is Regulated by Cyclic AMP Receptor Protein. Journal of Bacteriology, 2011, 193, 1369-1376. | 1.0 | 10 |
| 280 | Broad-Host-Range Plasmids from Agricultural Soils Have IncP-1 Backbones with Diverse Accessory Genes. Applied and Environmental Microbiology, 2011, 77, 7975-7983. | 1.4 | 96 |
| 281 | The pleitropic regulator AdpAch is required for natamycin biosynthesis and morphological differentiation in Streptomyces chattanoogensis. Microbiology (United Kingdom), 2011, 157, 1300-1311. | 0.7 | 48 |
| 282 | Complete Genome Sequence of Bacillus amyloliquefaciens TA208, a Strain for Industrial Production of Guanosine and Ribavirin. Journal of Bacteriology, 2011, 193, 3142-3143. | 1.0 | 16 |
| 283 | A Theoretical Model for Whole Genome Alignment. Journal of Computational Biology, 2011, 18, 705-728. | 0.8 | 2 |
| 284 | Quantifying Nonvertical Inheritance in the Evolution of Legionella pneumophila. Molecular Biology and Evolution, 2011, 28, 985-1001. | 3.5 | 47 |
| 285 | Neisseria Base: a comparative genomics database for Neisseria meningitidis. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar035. | 1.4 | 9 |
| 286 | Conserved small RNAs govern replication and incompatibility of a diverse new plasmid family from marine bacteria. Nucleic Acids Research, 2011, 39, 1004-1013. | 6.5 | 40 |
| 287 | Computational inference of grammars for larger-than-gene structures from annotated gene sequences. Bioinformatics, 2011, 27, 791-796. | 1.8 | 6 |
| 288 | Recombination and Population Structure in Salmonella enterica. PLoS Genetics, 2011, 7, e1002191. | 1.5 | 135 |
| 289 | Cactus: Algorithms for genome multiple sequence alignment. Genome Research, 2011, 21, 1512-1528. | 2.4 | 245 |
| 290 | Transformation of Natural Genetic Variation into Haemophilus Influenzae Genomes. PLoS Pathogens, 2011, 7, e1002151. | 2.1 | 75 |
| 291 | Mugsy: fast multiple alignment of closely related whole genomes. Bioinformatics, 2011, 27, 334-342. | 1.8 | 444 |
| 293 | A Novel Computational Method Identifies Intra- and Inter-Species Recombination Events in Staphylococcus aureus and Streptococcus pneumoniae. PLoS Computational Biology, 2012, 8, e1002668. | 1.5 | 9 |
| 294 | Whole Genome Sequencing Reveals Local Transmission Patterns of Mycobacterium bovis in Sympatric Cattle and Badger Populations. PLoS Pathogens, 2012, 8, e1003008. | 2.1 | 173 |
| 295 | Genome Sequence of a Serotype b Non-JP2 Aggregatibacter actinomycetemcomitans Strain, ANH9381, from a Periodontally Healthy Individual. Journal of Bacteriology, 2012, 194, 1837-1837. | 1.0 | 6 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 296 | i-ADHoRe 3.0â€"fast and sensitive detection of genomic homology in extremely large data sets. Nucleic Acids Research, 2012, 40, e11-e11. | 6.5 | 192 |
| 297 | Draft Genome Sequence of Corynebacterium diphtheriae Biovar Intermedius NCTC 5011. Journal of Bacteriology, 2012, 194, 4738-4738. | 1.0 | 19 |
| 298 | Genome-Wide Survey of Mutual Homologous Recombination in a Highly Sexual Bacterial Species. Genome Biology and Evolution, 2012, 4, 628-640. | 1.1 | 34 |
| 299 | Using Sybil for interactive comparative genomics of microbes on the web. Bioinformatics, 2012, 28, 160-166. | 1.8 | 53 |
| 300 | Single-cell sequencing provides clues about the host interactions of segmented filamentous bacteria (SFB). Genome Research, 2012, 22, 1107-1119. | 2.4 | 108 |
| 301 | Characterization of the ELPhiS Prophage from Salmonella enterica Serovar Enteritidis Strain LK5. Applied and Environmental Microbiology, 2012, 78, 1785-1793. | 1.4 | 23 |
| 302 | After the bottleneck: Genome-wide diversification of the <i>Mycobacterium tuberculosis</i> complex by mutation, recombination, and natural selection. Genome Research, 2012, 22, 721-734. | 2.4 | 141 |
| 303 | Insight into the Transmission Biology and Species-Specific Functional Capabilities of Tsetse (Diptera:) Tj ETQq1 1 0.784314 rgBT /Overlo | 1.8 | 105 |
| 304 | Using Comparative Genomics for Inquiry-Based Learning to Dissect Virulence of Escherichia coli O157:H7 and Yersinia pestis. CBE Life Sciences Education, 2012, 11, 81-93. | 1.1 | 15 |
| 305 | GenomeRing: alignment visualization based on SuperGenome coordinates. Bioinformatics, 2012, 28, i7-i15. | 1.8 | 41 |
| 306 | Comparative chloroplast genomics between <i>Euglena viridis</i> and <i>Euglena gracilis</i> (Euglenophyta). Phycologia, 2012, 51, 711-718. | 0.6 | 21 |
| 307 | Complete DNA Sequence Analysis of Enterohemorrhagic Escherichia coli Plasmid pO157_2 in Î²-Glucuronidase-Positive E. coli O157:H7 Reveals a Novel Evolutionary Path. Journal of Bacteriology, 2012, 194, 3457-3463. | 1.0 | 31 |
| 308 | Genomic characterization of the <i>Bacillus cereus</i> sensu lato species: Backdrop to the evolution of <i>Bacillus anthracis</i>. Genome Research, 2012, 22, 1512-1524. | 2.4 | 148 |
| 309 | Transcriptional Analysis of a Dehalococcoides-Containing Microbial Consortium Reveals Prophage Activation. Applied and Environmental Microbiology, 2012, 78, 1178-1186. | 1.4 | 34 |
| 310 | FSL J1-208, a Virulent Uncommon Phylogenetic Lineage IV Listeria monocytogenes Strain with a Small Chromosome Size and a Putative Virulence Plasmid Carrying Internalin-Like Genes. Applied and Environmental Microbiology, 2012, 78, 1876-1889. | 1.4 | 43 |
| 311 | Impact of Loci Nature on Estimating Recombination and Mutation Rates in Chlamydia trachomatis. G3: Genes, Genomes, Genetics, 2012, 2, 761-768. | 0.8 | 12 |
| 312 | Whole-Genome Sequence of the Human Pathogen Legionella pneumophila Serogroup 12 Strain 570-CO-H. Journal of Bacteriology, 2012, 194, 1613-1614. | 1.0 | 21 |
| 313 | Genomic analysis of Pseudomonas putida: genes in a genome island are crucial for nicotine degradation. Scientific Reports, 2012, 2, 377. | 1.6 | 69 |

| # | Article | IF | Citations |
|---|---|---|---|
| 314 | Evolutionary Dynamics of Small RNAs in 27 Escherichia coli and Shigella Genomes. Genome Biology and Evolution, 2012, 4, 330-345. | 1.1 | 43 |
| 315 | Polyclonality of Concurrent Natural Populations of Alteromonas macleodii. Genome Biology and Evolution, 2012, 4, 1360-1374. | 1.1 | 57 |
| 316 | Role of IncP-1Î² Plasmids pWDL7:: <i>rfp</i> and pNB8c in Chloroaniline Catabolism as Determined by Genomic and Functional Analyses. Applied and Environmental Microbiology, 2012, 78, 828-838. | 1.4 | 45 |
| 317 | Complete Mitochondrial and Plastid Genomes of the Green Microalga Trebouxiophyceae sp. Strain MX-AZ01 Isolated from a Highly Acidic Geothermal Lake. Eukaryotic Cell, 2012, 11, 1417-1418. | 3.4 | 20 |
| 318 | Genome Sequence of the Persistent Salmonella enterica subsp. enterica Serotype Senftenberg Strain SS209. Journal of Bacteriology, 2012, 194, 2385-2386. | 1.0 | 8 |
| 319 | Genome Sequence of the Invasive Salmonella enterica subsp. enterica Serotype Enteritidis Strain LA5. Journal of Bacteriology, 2012, 194, 2387-2388. | 1.0 | 12 |
| 320 | Draft Genome Sequence of Lactobacillus gigeriorum CRBIP 24.85 <sup>T</sup> , Isolated from a Chicken Crop. Journal of Bacteriology, 2012, 194, 5973-5973. | 1.0 | 0 |
| 321 | Complete Genome Sequence of the Serotype k Streptococcus mutans Strain LJ23. Journal of Bacteriology, 2012, 194, 2754-2755. | 1.0 | 20 |
| 322 | Genome Sequence of the Moderately Halotolerant, Arsenite-Oxidizing Bacterium Pseudomonas stutzeri TS44. Journal of Bacteriology, 2012, 194, 4473-4474. | 1.0 | 22 |
| 323 | Non-contiguous finished genome sequence and description of Paenibacillus senegalensis sp. nov.. Standards in Genomic Sciences, 2012, 7, 70-81. | 1.5 | 66 |
| 324 | Phylogeny rather than ecology or lifestyle biases the construction of <i>Escherichia coli</i> â€" <i>Shigella</i> genetic exchange communities. Open Biology, 2012, 2, 120112. | 1.5 | 42 |
| 325 | Whole-Genome Sequences of Bacillus subtilis and Close Relatives. Journal of Bacteriology, 2012, 194, 2378-2379. | 1.0 | 52 |
| 326 | Phylogenetic Analysis of Non-O157 Shiga Toxin-Producing Escherichia coli Strains by Whole-Genome Sequencing. Journal of Clinical Microbiology, 2012, 50, 4123-4127. | 1.8 | 39 |
| 327 | Mitochondrial genome variability within the Candida parapsilosis species complex. Mitochondrion, 2012, 12, 514-519. | 1.6 | 20 |
| 328 | Comparative analysis of mitochondrial genomes of Rhizophagus irregularis â€" syn. Glomus irregulare â€" reveals a polymorphism induced by variability generating elements. New Phytologist, 2012, 196, 1217-1227. | 3.5 | 66 |
| 329 | Sequencing papaya X and Y <sup>h</sup> chromosomes reveals molecular basis of incipient sex chromosome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13710-13715. | 3.3 | 264 |
| 330 | Evolution of the Chloroplast Genome in Photosynthetic Euglenoids: A Comparison of Eutreptia viridis and Euglena gracilis (Euglenophyta). Protist, 2012, 163, 832-843. | 0.6 | 33 |
| 331 | Pneumococcal genome sequencing tracks a vaccine escape variant formed through a multi-fragment recombination event. Nature Genetics, 2012, 44, 352-355. | 9.4 | 144 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 332 | Gene-RiViT: A visualization tool for comparative analysis of gene neighborhoods in prokaryotes. , 2012, , . |  | 3 |
| 333 | Horizontal Transfer of PAH Catabolism Genes in <i>Mycobacterium</i>: Evidence from Comparative Genomics and Isolated Pyrene-Degrading Bacteria. Environmental Science &amp; Technology, 2012, 46, 99-106. | 4.6 | 71 |
| 334 | Miniature Inverted-Repeat Transposable Elements (MITEs) Have Been Accumulated through Amplification Bursts and Play Important Roles in Gene Expression and Species Diversity in Oryza sativa. Molecular Biology and Evolution, 2012, 29, 1005-1017. | 3.5 | 191 |
| 335 | Complete cpDNA genome sequence of Smilax china and phylogenetic placement of Liliales â€" Influences of gene partitions and taxon sampling. Molecular Phylogenetics and Evolution, 2012, 64, 545-562. | 1.2 | 49 |
| 336 | Tracking a Hospital Outbreak of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> with Whole-Genome Sequencing. Science Translational Medicine, 2012, 4, 148ra116. | 5.8 | 781 |
| 337 | Transforming clinical microbiology with bacterial genome sequencing. Nature Reviews Genetics, 2012, 13, 601-612. | 7.7 | 684 |
| 338 | Mapping single molecule sequencing reads using basic local alignment with successive refinement (BLASR): application and theory. BMC Bioinformatics, 2012, 13, 238. | 1.2 | 1,075 |
| 339 | Genomic and Phylogenetic Characterization of Brazilian Yellow Fever Virus Strains. Journal of Virology, 2012, 86, 13263-13271. | 1.5 | 41 |
| 340 | Prokaryote Genome Fluidity: Toward a System Approach of the Mobilome. Methods in Molecular Biology, 2012, 804, 57-80. | 0.4 | 41 |
| 341 | Population Genomics of Chlamydia trachomatis: Insights on Drift, Selection, Recombination, and Population Structure. Molecular Biology and Evolution, 2012, 29, 3933-3946. | 3.5 | 94 |
| 342 | Rapid detection and antimicrobial resistance gene profiling of Yersinia pestis using pyrosequencing technology. Journal of Microbiological Methods, 2012, 90, 228-234. | 0.7 | 21 |
| 343 | Development of species-, strain- and antibiotic biosynthesis-specific quantitative PCR assays for Pantoea agglomerans as tools for biocontrol monitoring. Journal of Microbiological Methods, 2012, 90, 315-320. | 0.7 | 24 |
| 344 | Comparative analysis of the Hrp pathogenicity island of Rubus- and Spiraeoideae-infecting Erwinia amylovora strains identifies the IT region as a remnant of an integrative conjugative element. Gene, 2012, 504, 6-12. | 1.0 | 16 |
| 345 | <i>Phaeobacter gallaeciensis</i> genomes from globally opposite locations reveal high similarity of adaptation to surface life. ISME Journal, 2012, 6, 2229-2244. | 4.4 | 143 |
| 346 | SIS: a program to generate draft genome sequence scaffolds for prokaryotes. BMC Bioinformatics, 2012, 13, 96. | 1.2 | 29 |
| 347 | A phylogenomic analysis of Escherichia coli / Shigella group: implications of genomic features associated with pathogenicity and ecological adaptation. BMC Evolutionary Biology, 2012, 12, 174. | 3.2 | 72 |
| 348 | A genome-wide study of recombination rate variation in Bartonella henselae. BMC Evolutionary Biology, 2012, 12, 65. | 3.2 | 18 |
| 349 | A comparative genomics perspective on the genetic content of the alkaliphilic haloarchaeon Natrialba magadii ATCC 43099T. BMC Genomics, 2012, 13, 165. | 1.2 | 36 |

| # | Article | IF | Citations |
|---|---|---|---|
| 350 | Mitochondrial genome evolution in species belonging to the Phialocephala fortinii s.l. - Acephala applanata species complex. BMC Genomics, 2012, 13, 166. | 1.2 | 49 |
| 351 | Impact of homologous and non-homologous recombination in the genomic evolution of Escherichia coli. BMC Genomics, 2012, 13, 256. | 1.2 | 141 |
| 352 | High resolution clustering of Salmonella enterica serovar Montevideo strains using a next-generation sequencing approach. BMC Genomics, 2012, 13, 32. | 1.2 | 140 |
| 353 | Genetic changes during a laboratory adaptive evolution process that allowed fast growth in glucose to an Escherichia coli strain lacking the major glucose transport system. BMC Genomics, 2012, 13, 385. | 1.2 | 45 |
| 354 | Comparative genomic analysis of Geobacter sulfurreducens KN400, a strain with enhanced capacity for extracellular electron transfer and electricity production. BMC Genomics, 2012, 13, 471. | 1.2 | 36 |
| 355 | Sequencing of the core MHC region of black grouse (Tetrao tetrix) and comparative genomics of the galliform MHC. BMC Genomics, 2012, 13, 553. | 1.2 | 29 |
| 356 | Genome sequencing of ovine isolates of Mycobacterium avium subspecies paratuberculosis offers insights into host association. BMC Genomics, 2012, 13, 89. | 1.2 | 54 |
| 357 | Complete genome sequence of Enterococcus faecium strain TX16 and comparative genomic analysis of Enterococcus faecium genomes. BMC Microbiology, 2012, 12, 135. | 1.3 | 126 |
| 358 | Investigations into genome diversity of Haemophilus influenzae using whole genome sequencing of clinical isolates and laboratory transformants. BMC Microbiology, 2012, 12, 273. | 1.3 | 39 |
| 359 | Genomes-based phylogeny of the genus Xanthomonas. BMC Microbiology, 2012, 12, 43. | 1.3 | 71 |
| 360 | Endemic bacteriophages: a cautionary tale for evaluation of bacteriophage therapy and other interventions for infection control in animals. Virology Journal, 2012, 9, 207. | 1.4 | 24 |
| 361 | The highly dynamic CRISPR1 system of <i>Streptococcus agalactiae</i> controls the diversity of its mobilome. Molecular Microbiology, 2012, 85, 1057-1071. | 1.2 | 153 |
| 362 | Condition-Dependent Transcriptome Reveals High-Level Regulatory Architecture in <i>Bacillus subtilis</i>. Science, 2012, 335, 1103-1106. | 6.0 | 809 |
| 363 | Evolution of Multipartite Genomes in Prokaryotes. , 2012, , 301-323. |  | 5 |
| 364 | Replacing and Additive Horizontal Gene Transfer in Streptococcus. Molecular Biology and Evolution, 2012, 29, 3309-3320. | 3.5 | 33 |
| 365 | Fighting Outbreaks with Bacterial Genomics: Case Review and Workflow Proposal. Public Health Genomics, 2012, 15, 341-351. | 0.6 | 10 |
| 366 | High-throughput bacterial genome sequencing: an embarrassment of choice, a world of opportunity. Nature Reviews Microbiology, 2012, 10, 599-606. | 13.6 | 367 |
| 367 | Comparison of genome diversity of Brucella spp. field isolates using Universal Bio-signature Detection Array and whole genome sequencing reveals limitations of current diagnostic methods. Gene, 2012, 509, 142-148. | 1.0 | 9 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 368 | Whole-Genome Alignment. Methods in Molecular Biology, 2012, 855, 237-257. | 0.4 | 27 |
| 370 | A multiplex real-time PCR assay for the detection and differentiation of Francisella tularensis subspecies. Journal of Medical Microbiology, 2012, 61, 1525-1531. | 0.7 | 17 |
| 371 | Bacteriophages with the Ability to Degrade Uropathogenic Escherichia Coli Biofilms. Viruses, 2012, 4, 471-487. | 1.5 | 94 |
| 372 | Multiple genome comparison based on overlap regions of pairwise local alignments. BMC Bioinformatics, 2012, 13, S7. | 1.2 | 6 |
| 373 | Whole genome sequencing of the fish pathogen Francisella noatunensis subsp. orientalis Toba04 gives novel insights into Francisella evolution and pathogenecity. BMC Genomics, 2012, 13, 598. | 1.2 | 31 |
| 374 | Genetic structure of community acquired methicillin-resistant Staphylococcus aureus USA300. BMC Genomics, 2012, 13, 508. | 1.2 | 24 |
| 375 | New Insights into the Bacterial Fitness-Associated Mechanisms Revealed by the Characterization of Large Plasmids of an Avian Pathogenic E. coli. PLoS ONE, 2012, 7, e29481. | 1.1 | 24 |
| 376 | The Highly Virulent 2006 Norwegian EHEC O103:H25 Outbreak Strain Is Related to the 2011 German O104:H4 Outbreak Strain. PLoS ONE, 2012, 7, e31413. | 1.1 | 29 |
| 377 | A Novel Escherichia coli O157:H7 Clone Causing a Major Hemolytic Uremic Syndrome Outbreak in China. PLoS ONE, 2012, 7, e36144. | 1.1 | 61 |
| 378 | Optimizing Read Mapping to Reference Genomes to Determine Composition and Species Prevalence in Microbial Communities. PLoS ONE, 2012, 7, e36427. | 1.1 | 48 |
| 379 | The Molecular Mechanism of Action of the CR6261-Azichromycin Combination Found through Computational Analysis. PLoS ONE, 2012, 7, e37790. | 1.1 | 1 |
| 380 | Comparative Geno-Plasticity Analysis of Mycoplasma bovis HB0801 (Chinese Isolate). PLoS ONE, 2012, 7, e38239. | 1.1 | 71 |
| 381 | Molecular Characterization of Podoviral Bacteriophages Virulent for Clostridium perfringens and Their Comparison with Members of the Picovirinae. PLoS ONE, 2012, 7, e38283. | 1.1 | 37 |
| 382 | Identification and Characterization of Novel Salmonella Mobile Elements Involved in the Dissemination of Genes Linked to Virulence and Transmission. PLoS ONE, 2012, 7, e41247. | 1.1 | 61 |
| 383 | An Integrated Pipeline for de Novo Assembly of Microbial Genomes. PLoS ONE, 2012, 7, e42304. | 1.1 | 436 |
| 384 | Tertiary Endosymbiosis in Two Dinotoms Has Generated Little Change in the Mitochondrial Genomes of Their Dinoflagellate Hosts and Diatom Endosymbionts. PLoS ONE, 2012, 7, e43763. | 1.1 | 47 |
| 385 | Survey of Endosymbionts in the Diaphorina citri Metagenome and Assembly of a Wolbachia wDi Draft Genome. PLoS ONE, 2012, 7, e50067. | 1.1 | 77 |
| 386 | Conveniently Pre-Tagged and Pre-Packaged: Extended Molecular Identification and Metagenomics Using Complete Metazoan Mitochondrial Genomes. PLoS ONE, 2012, 7, e51263. | 1.1 | 14 |

| # | Article | IF | Citations |
|---|---|---|---|
| 387 | Lineage-specific Virulence Determinants of<i>Haemophilus influenzae</i>Biogroup aegyptius. Emerging Infectious Diseases, 2012, 18, 449-457. | 2.0 | 22 |
| 388 | Case Study of Sequence Capture Enrichment Technology: Identification of Variation Underpinning Developmental Syndromes in an Amniote Model. Genes, 2012, 3, 233-247. | 1.0 | 7 |
| 389 | In Silico Characterization and Molecular Evolutionary Analysis of a Novel Superfamily of Fungal Effector Proteins. Molecular Biology and Evolution, 2012, 29, 3371-3384. | 3.5 | 90 |
| 390 | Insights into salt tolerance from the genome of <i>Thellungiella salsuginea</i>. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12219-12224. | 3.3 | 272 |
| 391 | Chloroplast genome sequence confirms distinctness of Australian and Asian wild rice. Ecology and Evolution, 2012, 2, 211-217. | 0.8 | 84 |
| 392 | Nucleosomes Suppress Spontaneous Mutations Base-Specifically in Eukaryotes. Science, 2012, 335, 1235-1238. | 6.0 | 90 |
| 393 | The Draft Genome Sequence of Corynebacterium diphtheriae bv. mitis NCTC 3529 Reveals Significant Diversity between the Primary Disease-Causing Biovars. Journal of Bacteriology, 2012, 194, 3269-3269. | 1.0 | 16 |
| 394 | Accurate Identification of Candida parapsilosis (Sensu Lato) by Use of Mitochondrial DNA and Real-Time PCR. Journal of Clinical Microbiology, 2012, 50, 2310-2314. | 1.8 | 28 |
| 395 | Whole genome shotgun sequencing of one Colombian clinical isolate of Mycobacterium tuberculosis reveals DosR regulon gene deletions. FEMS Microbiology Letters, 2012, 330, 113-120. | 0.7 | 20 |
| 396 | Comparative genomic analysis of Salmonella enterica subsp. enterica serovar Weltevreden foodborne strains with other serovars. International Journal of Food Microbiology, 2012, 155, 247-256. | 2.1 | 16 |
| 397 | Alignment of multiple complete genomes suggests that gene rearrangements may contribute towards the speciation of Mycobacteria. Infection, Genetics and Evolution, 2012, 12, 819-826. | 1.0 | 16 |
| 398 | Expansion of the IncX plasmid family for improved identification and typing of novel plasmids in drug-resistant Enterobacteriaceae. Plasmid, 2012, 68, 43-50. | 0.4 | 260 |
| 399 | Lipopolysaccharide biosynthesis genes discriminate between <i>Rubusâ€•</i> and Spiraeoideaeâ€•infective genotypes of <i>Erwinia amylovora</i>. Molecular Plant Pathology, 2012, 13, 975-984. | 2.0 | 16 |
| 400 | The metagenome of the marine anammox bacterium â€˜<i>Candidatus</i> Scalindua profundaâ€™ illustrates the versatility of this globally important nitrogen cycle bacterium. Environmental Microbiology, 2013, 15, 1275-1289. | 1.8 | 246 |
| 401 | Comparative genome characterization of Achromobacter members reveals potential genetic determinants facilitating the adaptation to a pathogenic lifestyle. Applied Microbiology and Biotechnology, 2013, 97, 6413-6425. | 1.7 | 45 |
| 402 | Dissection of a major <scp>QTL</scp> for seed colour and fibre content in <i>Brassica napus</i> reveals colocalization with candidate genes for phenylpropanoid biosynthesis and flavonoid deposition. Plant Breeding, 2013, 132, 382-389. | 1.0 | 46 |
| 403 | Tool for rapid annotation of microbial SNPs (TRAMS): a simple program for rapid annotation of genomic variation in prokaryotes. Antonie Van Leeuwenhoek, 2013, 104, 431-434. | 0.7 | 15 |
| 404 | Genomic characterization provides new insight into Salmonella phage diversity. BMC Genomics, 2013, 14, 481. | 1.2 | 80 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 405 | Comparative genomics of Salmonella enterica serovars Derby and Mbandaka, two prevalent serovars associated with different livestock species in the UK. BMC Genomics, 2013, 14, 365. | 1.2 | 45 |
| 406 | Reductive evolution in Streptococcus agalactiae and the emergence of a host adapted lineage. BMC Genomics, 2013, 14, 252. | 1.2 | 81 |
| 407 | Comparative genomic analyses of Mycoplasma hyopneumoniae pathogenic 168 strain and its high-passaged attenuated strain. BMC Genomics, 2013, 14, 80. | 1.2 | 49 |
| 408 | High quality de novo sequencing and assembly of the Saccharomyces arboricolus genome. BMC Genomics, 2013, 14, 69. | 1.2 | 87 |
| 409 | Comparative genome analysis of Spiroplasma melliferumIPMB4A, a honeybee-associated bacterium. BMC Genomics, 2013, 14, 22. | 1.2 | 118 |
| 410 | Draft genome sequence of the male-killing Wolbachia strain wBol1 reveals recent horizontal gene transfers from diverse sources. BMC Genomics, 2013, 14, 20. | 1.2 | 65 |
| 411 | Comparative genome analysis of an avirulent and two virulent strains of avian Pasteurella multocida reveals candidate genes involved in fitness and pathogenicity. BMC Microbiology, 2013, 13, 106. | 1.3 | 40 |
| 412 | â€œMarseilleviridaeâ€: a new family of giant viruses infecting amoebae. Archives of Virology, 2013, 158, 915-920. | 0.9 | 106 |
| 413 | Long-term strain improvements accumulate mutations in regulatory elements responsible for hyper-production of cellulolytic enzymes. Scientific Reports, 2013, 3, 1569. | 1.6 | 104 |
| 414 | Genome Sequencing of Giardia lamblia Genotypes A2 and B Isolates (DH and GS) and Comparative Analysis with the Genomes of Genotypes A1 and E (WB and Pig). Genome Biology and Evolution, 2013, 5, 2498-2511. | 1.1 | 83 |
| 415 | Truncation and Sequence Shuffling of Segment 6 Generate Replication-Competent Neuraminidase-Negative Influenza H5N1 Viruses. Journal of Virology, 2013, 87, 13556-13568. | 1.5 | 10 |
| 416 | An alignment-free test for recombination. Bioinformatics, 2013, 29, 3121-3127. | 1.8 | 8 |
| 417 | Genome sequencing and comparative genomics of honey bee microsporidia, Nosema apis reveal novel insights into host-parasite interactions. BMC Genomics, 2013, 14, 451. | 1.2 | 61 |
| 418 | Comparative analysis of the complete genome of an epidemic hospital sequence type 203 clone of vancomycin-resistant Enterococcus faecium. BMC Genomics, 2013, 14, 595. | 1.2 | 50 |
| 419 | Comparative genomics of actinomycetes with a focus on natural product biosynthetic genes. BMC Genomics, 2013, 14, 611. | 1.2 | 175 |
| 420 | inTB - a data integration platform for molecular and clinical epidemiological analysis of tuberculosis. BMC Bioinformatics, 2013, 14, 264. | 1.2 | 7 |
| 421 | Microbes, metagenomes and marine mammals: enabling the next generation of scientist to enter the genomic era. BMC Genomics, 2013, 14, 600. | 1.2 | 27 |
| 422 | Comparative genomics of Campylobacter concisus isolates reveals genetic diversity and provides insights into disease association. BMC Genomics, 2013, 14, 585. | 1.2 | 39 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 423 | Genetic variability of mutans streptococci revealed by wide whole-genome sequencing. BMC Genomics, 2013, 14, 430. | 1.2 | 31 |
| 424 | Two Rapidly Evolving Genes Contribute to Male Fitness in Drosophila. Journal of Molecular Evolution, 2013, 77, 246-259. | 0.8 | 6 |
| 425 | Streptococcal collagenâ€like protein A and general stress protein 24 are immunomodulating virulence factors of group A Streptococcus. FASEB Journal, 2013, 27, 2633-2643. | 0.2 | 18 |
| 426 | Comparison of Genomes of Brucella melitensis M28 and the B. melitensis M5-90 Derivative Vaccine Strain Highlights the Translation Elongation Factor Tu Gene <i>tuf2</i> as an Attenuation-Related Gene. Infection and Immunity, 2013, 81, 2812-2818. | 1.0 | 18 |
| 427 | The evolutionary landscape of the Mycobacterium tuberculosis genome. Gene, 2013, 518, 187-193. | 1.0 | 8 |
| 428 | Intraspecific comparative genomics of Candida albicans mitochondria reveals non-coding regions under neutral evolution. Infection, Genetics and Evolution, 2013, 14, 302-312. | 1.0 | 19 |
| 429 | Real-Time Sequencing To Decipher the Molecular Mechanism of Resistance of a Clinical Pan-Drug-Resistant Acinetobacter baumannii Isolate from Marseille, France. Antimicrobial Agents and Chemotherapy, 2013, 57, 592-596. | 1.4 | 70 |
| 430 | Bioinformatics for microbial genotyping of equine encephalitis viruses, orthopoxviruses, and hantaviruses. Journal of Virological Methods, 2013, 193, 112-120. | 1.0 | 3 |
| 431 | Complete genome sequence of the endosymbiont Blattabacterium from the cockroach Nauphoeta cinerea (Blattodea: Blaberidae). Genomics, 2013, 102, 479-483. | 1.3 | 20 |
| 432 | The IncF plasmid pRSB225 isolated from a municipal wastewater treatment plantâ€™s on-site preflooder combining antibiotic resistance and putative virulence functions is highly related to virulence plasmids identified in pathogenic E. coli isolates. Plasmid, 2013, 69, 127-137. | 0.4 | 35 |
| 433 | Evaluation of whole-genome sequencing as a genotyping tool for Campylobacter jejuni in comparison with pulsed-field gel electrophoresis and flaA typing. Poultry Science, 2013, 92, 573-580. | 1.5 | 25 |
| 434 | Bioinformatics Approaches in Studying Microbial Diversity. , 2013, , 119-140. |  | 1 |
| 435 | Identification and characterization of a periplasmic trilactone esterase, <scp>Cee</scp>, revealed unique features of ferric enterobactin acquisition in <i><scp>C</scp>ampylobacter</i>. Molecular Microbiology, 2013, 87, 594-608. | 1.2 | 42 |
| 436 | Tracing Patterns of Chloroplast Evolution in Euglenoids: Contributions from <i>Colacium vesiculosum</i> and <i>Strombomonas acuminata</i> (Euglenophyta). Journal of Eukaryotic Microbiology, 2013, 60, 214-221. | 0.8 | 25 |
| 437 | Genomeâ€assisted development of nuclear intergenic sequence markers for entomopathogenic fungi of the <i><scp>M</scp>etarhizium anisopliae</i> species complex. Molecular Ecology Resources, 2013, 13, 210-217. | 2.2 | 56 |
| 438 | Organellar genome, nuclear ribosomal DNA repeat unit, and microsatellites isolated from a small-scale of 454 GS FLX sequencing on two mosses. Molecular Phylogenetics and Evolution, 2013, 66, 1089-1094. | 1.2 | 23 |
| 439 | High-Resolution Transcriptome Maps Reveal Strain-Specific Regulatory Features of Multiple Campylobacter jejuni Isolates. PLoS Genetics, 2013, 9, e1003495. | 1.5 | 260 |
| 440 | Genome-Wide Comparison of Medieval and Modern <i>Mycobacterium leprae</i>. Science, 2013, 341, 179-183. | 6.0 | 313 |

| # | Article | IF | Citations |
|---|---|---|---|
| 441 | Whole genome sequencing identifies zoonotic transmission of MRSA isolates with the novel <i>mecA</i> homologue <i>mecC</i>. EMBO Molecular Medicine, 2013, 5, 509-515. | 3.3 | 192 |
| 442 | Comprehensive discovery and characterization of small RNAs in Corynebacterium glutamicumATCC 13032. BMC Genomics, 2013, 14, 714. | 1.2 | 61 |
| 443 | STAR: ultrafast universal RNA-seq aligner. Bioinformatics, 2013, 29, 15-21. | 1.8 | 35,376 |
| 444 | Genome Sequence of the Group III Clostridium botulinum Strain Eklund-C. Genome Announcements, 2013, 1, e0004413. | 0.8 | 5 |
| 445 | Draft Genome Sequence of Vibrio mimicus Strain CAIM 602 T. Genome Announcements, 2013, 1, e0008413. | 0.8 | 4 |
| 446 | Draft Genome Sequence of MKD8, a Conjugal Recipient Mycobacterium smegmatis Strain. Genome Announcements, 2013, 1, e0014813. | 0.8 | 8 |
| 447 | Genome Sequence of Salmonella bongori Strain N268-08, a Rare Clinical Isolate. Genome Announcements, 2013, 1, . | 0.8 | 2 |
| 448 | Draft Genome Sequence of Lactobacillus hominis Strain CRBIP 24.179 T , Isolated from Human Intestine. Genome Announcements, 2013, 1, . | 0.8 | 1 |
| 449 | A Conserved Apomixis-Specific Polymorphism Is Correlated with Exclusive Exonuclease Expression in Premeiotic Ovules of Apomictic Boechera Species. Plant Physiology, 2013, 163, 1660-1672. | 2.3 | 71 |
| 450 | The Conserved Chimeric Transcript UPGRADE2 Is Associated with Unreduced Pollen Formation and Is Exclusively Found in Apomictic Boechera Species. Plant Physiology, 2013, 163, 1640-1659. | 2.3 | 31 |
| 451 | Complete Sequence of pOZ176, a 500-Kilobase IncP-2 Plasmid Encoding IMP-9-Mediated Carbapenem Resistance, from Outbreak Isolate Pseudomonas aeruginosa 96. Antimicrobial Agents and Chemotherapy, 2013, 57, 3775-3782. | 1.4 | 73 |
| 452 | Genome Sequence of an Epidemic Isolate of Mycobacterium abscessus subsp. bolletii from Rio de Janeiro, Brazil. Genome Announcements, 2013, 1, . | 0.8 | 9 |
| 453 | Draft Genome Sequence of Geobacillus thermoleovorans Strain B23. Genome Announcements, 2013, 1, . | 0.8 | 7 |
| 454 | Comparative Analysis of Chlamydia psittaci Genomes Reveals the Recent Emergence of a Pathogenic Lineage with a Broad Host Range. MBio, 2013, 4, . | 1.8 | 90 |
| 455 | Deciphering the Cryptic Genome: Genome-wide Analyses of the Rice Pathogen Fusarium fujikuroi Reveal Complex Regulation of Secondary Metabolism and Novel Metabolites. PLoS Pathogens, 2013, 9, e1003475. | 2.1 | 406 |
| 456 | The Subtelomeric khipu Satellite Repeat from Phaseolus vulgaris: Lessons Learned from the Genome Analysis of the Andean Genotype G19833. Frontiers in Plant Science, 2013, 4, 109. | 1.7 | 39 |
| 457 | De Novo ORFs in Drosophila Are Important to Organismal Fitness and Evolved Rapidly from Previously Non-coding Sequences. PLoS Genetics, 2013, 9, e1003860. | 1.5 | 124 |
| 458 | Whole Genome Sequencing versus Traditional Genotyping for Investigation of a Mycobacterium tuberculosis Outbreak: A Longitudinal Molecular Epidemiological Study. PLoS Medicine, 2013, 10, e1001387. | 3.9 | 425 |

| # | Article | IF | Citations |
|---|---|---|---|
| 459 | Replicon-Dependent Bacterial Genome Evolution: The Case of Sinorhizobium meliloti. Genome Biology and Evolution, 2013, 5, 542-558. | 1.1 | 94 |
| 460 | Characterization of the Genome of the Dairy Lactobacillus helveticus Bacteriophage Î¦AQ113. Applied and Environmental Microbiology, 2013, 79, 4712-4718. | 1.4 | 24 |
| 461 | Genomic Evolution of the Pathogenic Wolbachia Strain, wMelPop. Genome Biology and Evolution, 2013, 5, 2189-2204. | 1.1 | 96 |
| 462 | Genomic Diversity of â€œDeep Ecotypeâ€•Alteromonas macleodii Isolates: Evidence for Pan-Mediterranean Clonal Frames. Genome Biology and Evolution, 2013, 5, 1220-1232. | 1.1 | 71 |
| 463 | Progressive genomeâ€wide introgression in agricultural <i>Campylobacter coli</i>. Molecular Ecology, 2013, 22, 1051-1064. | 2.0 | 128 |
| 464 | Whole-Genome Draft Sequences of 26 Enterohemorrhagic Escherichia coli O157:H7 Strains. Genome Announcements, 2013, 1, e0013412. | 0.8 | 31 |
| 465 | Comparative genomics of Japanese<i>Erwinia pyrifoliae</i>strain Ejp617 with closely related erwinias. Genome, 2013, 56, 83-90. | 0.9 | 5 |
| 466 | Nucleotide sequence alignment using sparse coding and belief propagation. , 2013, 2013, 588-91. |  | 1 |
| 467 | H-NS Plays a Role in Expression of Acinetobacter baumannii Virulence Features. Infection and Immunity, 2013, 81, 2574-2583. | 1.0 | 100 |
| 468 | Genome Sequencing Identifies Two Nearly Unchanged Strains of Persistent Listeria monocytogenes Isolated at Two Different Fish Processing Plants Sampled 6 Years Apart. Applied and Environmental Microbiology, 2013, 79, 2944-2951. | 1.4 | 110 |
| 469 | Non-contiguous finished genome sequence and description of Clostridium dakarense sp. nov.. Standards in Genomic Sciences, 2013, 9, 14-27. | 1.5 | 45 |
| 470 | Non-contiguous finished genome sequence and description of Nosocomiicoccus massiliensis sp. nov.. Standards in Genomic Sciences, 2013, 9, 205-219. | 1.5 | 18 |
| 471 | Non-contiguous finished genome sequence and description of Holdemania massiliensis sp. nov.. Standards in Genomic Sciences, 2013, 9, 395-409. | 1.5 | 25 |
| 472 | Non contiguous-finished genome sequence and description of Peptoniphilus grossensis sp. nov.. Standards in Genomic Sciences, 2012, 7, 320-330. | 1.5 | 34 |
| 473 | Non contiguous-finished genome sequence and description of Peptoniphilus senegalensis sp. nov.. Standards in Genomic Sciences, 2013, 7, 370-381. | 1.5 | 38 |
| 474 | Non contiguous-finished genome sequence and description of Enorma massiliensis gen. nov., sp. nov., a new member of the Family Coriobacteriaceae. Standards in Genomic Sciences, 2013, 8, 290-305. | 1.5 | 37 |
| 475 | Non contiguous-finished genome sequence and description of Bacillus massiliosenegalensis sp. nov.. Standards in Genomic Sciences, 2013, 8, 264-278. | 1.5 | 33 |
| 476 | Non contiguous-finished genome sequence and description of Dielma fastidiosa gen. nov., sp. nov., a new member of the Family Erysipelotrichaceae. Standards in Genomic Sciences, 2013, 8, 336-351. | 1.5 | 52 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 477 | Non-contiguous finished genome sequence and description of Kallipyga massiliensis gen. nov., sp. nov., a new member of the family Clostridiales Incertae Sedis XI. Standards in Genomic Sciences, 2013, 8, 500-515. | 1.5 | 23 |
| 478 | Genome sequence and description of Timonella senegalensis gen. nov., sp. nov., a new member of the suborder Micrococcinae. Standards in Genomic Sciences, 2013, 8, 318-335. | 1.5 | 32 |
| 479 | Non-contiguous finished genome sequence and description of Bacillus massilioanorexius sp. nov.. Standards in Genomic Sciences, 2013, 8, 465-479. | 1.5 | 24 |
| 480 | Large-scale multiple sequence alignment visualization through gradient vector flow analysis. , 2013, , . |  | 4 |
| 481 | Comparative Genomics of Multiple Strains of Pseudomonas cannabina pv. alisalensis, a Potential Model Pathogen of Both Monocots and Dicots. PLoS ONE, 2013, 8, e59366. | 1.1 | 34 |
| 482 | On the Evolutionary History, Population Genetics and Diversity among Isolates of Salmonella Enteritidis PFGE Pattern JEGX01.0004. PLoS ONE, 2013, 8, e55254. | 1.1 | 146 |
| 483 | Comparative Genomic Analysis of Mycobacterium tuberculosis Drug Resistant Strains from Russia. PLoS ONE, 2013, 8, e56577. | 1.1 | 42 |
| 484 | Evolution of Red Algal Plastid Genomes: Ancient Architectures, Introns, Horizontal Gene Transfer, and Taxonomic Utility of Plastid Markers. PLoS ONE, 2013, 8, e59001. | 1.1 | 112 |
| 485 | Genome Sequence of Lactobacillus pentosus KCA1: Vaginal Isolate from a Healthy Premenopausal Woman. PLoS ONE, 2013, 8, e59239. | 1.1 | 50 |
| 486 | Defining the Sequence Elements and Candidate Genes for the Coloboma Mutation. PLoS ONE, 2013, 8, e60267. | 1.1 | 4 |
| 487 | Adaptability and Persistence of the Emerging Pathogen Bordetella petrii. PLoS ONE, 2013, 8, e65102. | 1.1 | 17 |
| 488 | The Plastid Genome of the Red Macroalga Grateloupia taiwanensis (Halymeniaceae). PLoS ONE, 2013, 8, e68246. | 1.1 | 26 |
| 489 | TCW: Transcriptome Computational Workbench. PLoS ONE, 2013, 8, e69401. | 1.1 | 17 |
| 490 | Genome Annotation of Burkholderia sp. SJ98 with Special Focus on Chemotaxis Genes. PLoS ONE, 2013, 8, e70624. | 1.1 | 9 |
| 491 | Comparative Genome Analysis of Mycobacterium avium Revealed Genetic Diversity in Strains that Cause Pulmonary and Disseminated Disease. PLoS ONE, 2013, 8, e71831. | 1.1 | 75 |
| 492 | Normal Mutation Rate Variants Arise in a Mutator (Mut S) Escherichia coli Population. PLoS ONE, 2013, 8, e72963. | 1.1 | 37 |
| 493 | Virulence Potential and Genome-Wide Characterization of Drug Resistant Streptococcus pneumoniae Clones Selected In Vivo by the 7-Valent Pneumococcal Conjugate Vaccine. PLoS ONE, 2013, 8, e74867. | 1.1 | 13 |
| 494 | Comparative Genomic Analyses of Streptococcus pseudopneumoniae Provide Insight into Virulence and Commensalism Dynamics. PLoS ONE, 2013, 8, e65670. | 1.1 | 21 |

| # | Article | IF | Citations |
|---|---|---|---|
| 495 | Complete Genome Analysis of Three Acinetobacter baumannii Clinical Isolates in China for Insight into the Diversification of Drug Resistance Elements. PLoS ONE, 2013, 8, e66584. | 1.1 | 107 |
| 496 | Evolutionary Genomics and Adaptive Evolution of the Hedgehog Gene Family (Shh, Ihh and Dhh) in Vertebrates. PLoS ONE, 2014, 9, e74132. | 1.1 | 27 |
| 497 | Genomics of Sponge-Associated Streptomyces spp. Closely Related to Streptomyces albus J1074: Insights into Marine Adaptation and Secondary Metabolite Biosynthesis Potential. PLoS ONE, 2014, 9, e96719. | 1.1 | 51 |
| 498 | Marinobacter salarius sp. nov. and Marinobacter similis sp. nov., Isolated from Sea Water. PLoS ONE, 2014, 9, e106514. | 1.1 | 39 |
| 499 | New Insights into Dehalococcoides mccartyi Metabolism from a Reconstructed Metabolic Network-Based Systems-Level Analysis of D. mccartyi Transcriptomes. PLoS ONE, 2014, 9, e94808. | 1.1 | 14 |
| 500 | Genomes of Two New Ammonia-Oxidizing Archaea Enriched from Deep Marine Sediments. PLoS ONE, 2014, 9, e96449. | 1.1 | 32 |
| 501 | The 203 kbp Mitochondrial Genome of the Phytopathogenic Fungus Sclerotinia borealis Reveals Multiple Invasions of Introns and Genomic Duplications. PLoS ONE, 2014, 9, e107536. | 1.1 | 93 |
| 502 | Conserved Gene Order and Expanded Inverted Repeats Characterize Plastid Genomes of Thalassiosirales. PLoS ONE, 2014, 9, e107854. | 1.1 | 44 |
| 503 | Exploring the Genes of Yerba Mate (Ilex paraguariensis A. St.-Hil.) by NGS and De Novo Transcriptome Assembly. PLoS ONE, 2014, 9, e109835. | 1.1 | 19 |
| 504 | Local Similarity Search to Find Gene Indicators in Mitochondrial Genomes. Biology, 2014, 3, 220-242. | 1.3 | 1 |
| 505 | Complete Genome Sequence of Klebsiella pneumoniae Strain ATCC 43816 KPPR1, a Rifampin-Resistant Mutant Commonly Used in Animal, Genetic, and Molecular Biology Studies. Genome Announcements, 2014, 2, . | 0.8 | 52 |
| 506 | Inference of the Properties of the Recombination Process from Whole Bacterial Genomes. Genetics, 2014, 196, 253-265. | 1.2 | 41 |
| 507 | Whole-Genome Sequencing for Rapid and Accurate Identification of Bacterial Transmission Pathways. Methods in Microbiology, 2014, 41, 123-152. | 0.4 | 4 |
| 508 | Genetic distance in the whole-genome perspective on Listeria monocytogenes strains F2-382 and NIHS-28 that show similar subtyping results. BMC Microbiology, 2014, 14, 309. | 1.3 | 3 |
| 509 | Phylogenetic Analyses on the Diversity of Aspergillus fumigatus Sensu Lato Based on Five Orthologous Loci. Mycopathologia, 2014, 178, 163-176. | 1.3 | 9 |
| 510 | Comparative analysis of surface-exposed virulence factors of Acinetobacter baumannii. BMC Genomics, 2014, 15, 1020. | 1.2 | 149 |
| 511 | Genome organisation of the Acinetobacter lytic phage ZZ1 and comparison with other T4-like Acinetobacter phages. BMC Genomics, 2014, 15, 793. | 1.2 | 14 |
| 512 | Complete genome sequence of bacteriophage vB_YenP_AP5 which infects Yersinia enterocoliticaof serotype O:3. Virology Journal, 2014, 11, 188. | 1.4 | 20 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 513 | Genome analysis of Campylobacter jejuni strains isolated from a waterborne outbreak. BMC Genomics, 2014, 15, 768. | 1.2 | 40 |
| 514 | Insights into the history of a bacterial group II intron remnant from the genomes of the nitrogen-fixing symbionts Sinorhizobium meliloti and Sinorhizobium medicae. Heredity, 2014, 113, 306-315. | 1.2 | 13 |
| 515 | Potential impact on kidney infection: a whole-genome analysis of <i>Leptospira santarosai</i> serovar Shermani. Emerging Microbes and Infections, 2014, 3, 1-11. | 3.0 | 12 |
| 516 | Annotation of a hybrid partial genome of the coffee rust (Hemileia vastatrix) contributes to the gene repertoire catalog of the Pucciniales. Frontiers in Plant Science, 2014, 5, 594. | 1.7 | 34 |
| 517 | Draft Genome Sequences of the Onion Center Rot Pathogen Pantoea ananatis PA4 and Maize Brown Stalk Rot Pathogen <i>P. ananatis</i> BD442. Genome Announcements, 2014, 2, . | 0.8 | 7 |
| 518 | Gene Arrangement Convergence, Diverse Intron Content, and Genetic Code Modifications in Mitochondrial Genomes of Sphaeropleales (Chlorophyta). Genome Biology and Evolution, 2014, 6, 2170-2180. | 1.1 | 37 |
| 519 | Evolution and Comparative Genomics of Campylobacter jejuni ST-677 Clonal Complex. Genome Biology and Evolution, 2014, 6, 2424-2438. | 1.1 | 21 |
| 520 | Comparative Genomic Analysis of N2-Fixing and Non-N2-Fixing Paenibacillus spp.: Organization, Evolution and Expression of the Nitrogen Fixation Genes. PLoS Genetics, 2014, 10, e1004231. | 1.5 | 117 |
| 521 | Bacterial gene neighborhood investigation environment: A large-scale genome visualization for big displays. , 2014, , . |  | 1 |
| 522 | Symbionts Commonly Provide Broad Spectrum Resistance to Viruses in Insects: A Comparative Analysis of Wolbachia Strains. PLoS Pathogens, 2014, 10, e1004369. | 2.1 | 226 |
| 523 | Whole-Genome Sequencing of the Nonproteolytic Bacillus anthracis V770-NP1-R Strain Reveals Multiple Mutations in Peptidase Loci. Genome Announcements, 2014, 2, . | 0.8 | 7 |
| 524 | Genome Sequence of a Presumptive Mannheimia haemolytica Strain with an A1/A6-Cross-Reactive Serotype from a White-Tailed Deer (Odocoileus virginianus). Genome Announcements, 2014, 2, . | 0.8 | 2 |
| 525 | Draft Genome Sequence of a Multidrug-Resistant Acinetobacter baumannii PKAB07 Clinical Strain from India Belonging to Sequence Type 195. Genome Announcements, 2014, 2, . | 0.8 | 6 |
| 526 | Whole-Genome Sequencing of Streptomycin-Resistant Mycobacterium tuberculosis Isolate VRFCWCF MRTB 180 Reveals Novel and Potential Mutations for Resistance. Genome Announcements, 2014, 2, . | 0.8 | 2 |
| 527 | Finished Genome Sequence of the Laboratory Strain Escherichia coli K-12 RV308 (ATCC 31608). Genome Announcements, 2014, 2, . | 0.8 | 2 |
| 528 | The mitochondrial and chloroplast genomes of the haptophyte Chrysochromulina tobin contain unique repeat structures and gene profiles. BMC Genomics, 2014, 15, 604. | 1.2 | 30 |
| 529 | Alignathon: a competitive assessment of whole-genome alignment methods. Genome Research, 2014, 24, 2077-2089. | 2.4 | 102 |
| 530 | Complete Genome Sequences of Bacillus subtilis subsp. <i>subtilis</i> Laboratory Strains JH642 (AG174) and AG1839. Genome Announcements, 2014, 2, . | 0.8 | 45 |

| # | Article | IF | Citations |
|---|---|---|---|
| 531 | A Shared Population of Epidemic Methicillin-Resistant Staphylococcus aureus 15 Circulates in Humans and Companion Animals. MBio, 2014, 5, e00985-13. | 1.8 | 95 |
| 532 | Finished Genome Sequence of Escherichia coli K-12 Strain HMS174 (ATCC 47011). Genome Announcements, 2014, 2, . | 0.8 | 4 |
| 533 | Genomic insights into the rapid emergence and evolution of MDR in <i>Staphylococcus pseudintermedius</i>. Journal of Antimicrobial Chemotherapy, 2015, 70, 997-1007. | 1.3 | 77 |
| 534 | A novel plasmid pEA68 of Erwinia amylovora and the description of a new family of plasmids. Archives of Microbiology, 2014, 196, 891-899. | 1.0 | 9 |
| 535 | Revolutionizing Prokaryotic Systematics Through Next-Generation Sequencing. Methods in Microbiology, 2014, , 75-101. | 0.4 | 7 |
| 536 | Nextâ€Gen phylogeography of rainforest trees: exploring landscapeâ€level cp<scp>DNA</scp> variation from wholeâ€genome sequencing. Molecular Ecology Resources, 2014, 14, 199-208. | 2.2 | 34 |
| 537 | Complete genome sequence of the bacteriophage YMC/09/04/R1988 MRSA BP: a lytic phage from a methicillin-resistantStaphylococcus aureusisolate. FEMS Microbiology Letters, 2014, 359, 144-146. | 0.7 | 7 |
| 538 | The marine bacterium<i>Marinobacter hydrocarbonoclasticus</i>SP17 degrades a wide range of lipids and hydrocarbons through the formation of oleolytic biofilms with distinct gene expression profiles. FEMS Microbiology Ecology, 2014, 90, 816-831. | 1.3 | 56 |
| 539 | Uncovering a Glycosyltransferase Provides Insights into the Glycosylation Step during Macrolactin and Bacillaene Biosynthesis. ChemBioChem, 2014, 15, 2747-2753. | 1.3 | 19 |
| 540 | Population Structure of KPC-Producing Klebsiella pneumoniae Isolates from Midwestern U.S. Hospitals. Antimicrobial Agents and Chemotherapy, 2014, 58, 4961-4965. | 1.4 | 78 |
| 541 | Genetic Diversity of <i>Salmonella</i> Pathogenicity Islands SPI-5 and SPI-6 in <i>Salmonella</i> Newport. Foodborne Pathogens and Disease, 2014, 11, 798-807. | 0.8 | 13 |
| 542 | Genome skimming by shotgun sequencing helps resolve the phylogeny of a pantropical tree family. Molecular Ecology Resources, 2014, 14, 966-975. | 2.2 | 102 |
| 543 | Origin and Evolution of European Community-Acquired Methicillin-Resistant Staphylococcus aureus. MBio, 2014, 5, e01044-14. | 1.8 | 112 |
| 544 | Strategy for Genome Sequencing Analysis and Assembly for Comparative Genomics of Pseudomonas Genomes. Methods in Molecular Biology, 2014, 1149, 565-577. | 0.4 | 3 |
| 545 | Widespread expression of conserved small RNAs in small symbiont genomes. ISME Journal, 2014, 8, 2490-2502. | 4.4 | 47 |
| 546 | Evidence for a single loss of mineralized teeth in the common avian ancestor. Science, 2014, 346, 1254390. | 6.0 | 99 |
| 547 | An <i>In Vitro</i> Deletion in <i>ribE</i> Encoding Lumazine Synthase Contributes to Nitrofurantoin Resistance in Escherichia coli. Antimicrobial Agents and Chemotherapy, 2014, 58, 7225-7233. | 1.4 | 32 |
| 548 | Comparative genomics reveals insights into avian genome evolution and adaptation. Science, 2014, 346, 1311-1320. | 6.0 | 895 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 549 | Diversity and genomic insights into the uncultured <scp><i>C</i></scp><i>hloroflexi</i> from the human microbiota. Environmental Microbiology, 2014, 16, 2635-2643. | 1.8 | 55 |
| 550 | Genomeâ€guided insights into the versatile metabolic capabilities of the mercaptosuccinateâ€utilizing <scp>Î²</scp>â€proteobacterium <scp><i>V</i></scp><i>ariovorax paradoxus</i> strain <scp>B</scp>4. Environmental Microbiology, 2014, 16, 3370-3386. | 1.8 | 13 |
| 551 | NextGen sequencing reveals short double crossovers contribute disproportionately to genetic diversity in Toxoplasma gondii. BMC Genomics, 2014, 15, 1168. | 1.2 | 17 |
| 552 | Genome sequence of Erinnyis ello granulovirus (ErelGV), a natural cassava hornworm pesticide and the first sequenced sphingid-infecting betabaculovirus. BMC Genomics, 2014, 15, 856. | 1.2 | 23 |
| 553 | Comparative genomics of the major fungal agents of human and animal Sporotrichosis: Sporothrix schenckii and Sporothrix brasiliensis. BMC Genomics, 2014, 15, 943. | 1.2 | 121 |
| 554 | Intraspecies comparison of Streptomyces pratensis genomes reveals high levels of recombination and gene conservation between strains of disparate geographic origin. BMC Genomics, 2014, 15, 970. | 1.2 | 46 |
| 555 | Comparative analyses of Legionella species identifies genetic features of strains causing Legionnairesâ€™ disease. Genome Biology, 2014, 15, 505. | 3.8 | 82 |
| 556 | The Harvest suite for rapid core-genome alignment and visualization of thousands of intraspecific microbial genomes. Genome Biology, 2014, 15, 524. | 3.8 | 1,428 |
| 557 | Widespread differences in cortex DNA methylation of the â€œlanguage geneâ€<i>CNTNAP2</i>between humans and chimpanzees. Epigenetics, 2014, 9, 533-545. | 1.3 | 30 |
| 558 | Mining the Pseudomonas Genome. Methods in Molecular Biology, 2014, 1149, 417-432. | 0.4 | 4 |
| 559 | Phytoplasma Genomes: Evolution Through Mutually Complementary Mechanisms, Gene Loss and Horizontal Acquisition. , 2014, , 235-271. |  | 22 |
| 560 | Genome Sequencing of a Mung Bean Plant Growth Promoting Strain ofP. aeruginosawith Biocontrol Ability. International Journal of Genomics, 2014, 2014, 1-10. | 0.8 | 12 |
| 561 | Novel Three-Component Rieske Non-Heme Iron Oxygenase System Catalyzing the <i>N</i> -Dealkylation of Chloroacetanilide Herbicides in Sphingomonads DC-6 and DC-2. Applied and Environmental Microbiology, 2014, 80, 5078-5085. | 1.4 | 90 |
| 562 | Using Arabidopsis-Related Model Species (ARMS): Growth, Genetic Transformation, and Comparative Genomics. Methods in Molecular Biology, 2014, 1062, 27-51. | 0.4 | 8 |
| 563 | Comparative Analysis of the Full Genome of Helicobacter pylori Isolate Sahul64 Identifies Genes of High Divergence. Journal of Bacteriology, 2014, 196, 1073-1083. | 1.0 | 25 |
| 564 | Assembly and analysis of a male sterile rubber tree mitochondrial genome reveals DNA rearrangement events and a novel transcript. BMC Plant Biology, 2014, 14, 45. | 1.6 | 53 |
| 565 | Previously Undescribed Plasmids Recovered from Activated Sludge Confer Tetracycline Resistance and Phenotypic Changes to Acinetobacter oleivorans DR1. Microbial Ecology, 2014, 67, 369-379. | 1.4 | 12 |
| 566 | CodaChrome: a tool for the visualization of proteome conservation across all fully sequenced bacterial genomes. BMC Genomics, 2014, 15, 65. | 1.2 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 567 | Comparative analysis of the complete genome of KPC-2-producing Klebsiella pneumoniae Kp13 reveals remarkable genome plasticity and a wide repertoire of virulence and resistance mechanisms. BMC Genomics, 2014, 15, 54. | 1.2 | 109 |
| 568 | Genomic comparison of sporeforming bacilli isolated from milk. BMC Genomics, 2014, 15, 26. | 1.2 | 27 |
| 569 | Narrow-Host-Range Bacteriophages That Infect Rhizobium etli Associate with Distinct Genomic Types. Applied and Environmental Microbiology, 2014, 80, 446-454. | 1.4 | 59 |
| 570 | Genomic analysis ofPseudomonas aeruginosaPA96, the host of carbapenem resistance plasmid pOZ176. FEMS Microbiology Letters, 2014, 356, 212-216. | 0.7 | 9 |
| 571 | Characterization of <i>Euglenaformis</i> gen. nov. and the chloroplast genome of <i>Euglenaformis</i> [<i>Euglena</i>] <i>proxima</i> (Euglenophyta). Phycologia, 2014, 53, 66-73. | 0.6 | 36 |
| 572 | To settle or to move? The interplay between two classes of cyclic lipopeptides in the biocontrol strain <scp><i>P</i></scp><i>seudomonas</i>â€…<scp>CMR</scp>12a. Environmental Microbiology, 2014, 16, 2282-2300. | 1.8 | 78 |
| 573 | Genetic Characteristics and Pathogenic Mechanisms of Periodontal Pathogens. Advances in Dental Research, 2014, 26, 15-22. | 3.6 | 34 |
| 574 | Origin and Evolution of B Chromosomes in the Cichlid Fish Astatotilapia latifasciata Based on Integrated Genomic Analyses. Molecular Biology and Evolution, 2014, 31, 2061-2072. | 3.5 | 112 |
| 575 | Microevolution of <i>Renibacterium salmoninarum</i>: evidence for intercontinental dissemination associated with fish movements. ISME Journal, 2014, 8, 746-756. | 4.4 | 32 |
| 576 | Genomic analysis of three sponge-associated Arthrobacter Antarctic strains, inhibiting the growth of Burkholderia cepacia complex bacteria by synthesizing volatile organic compounds. Microbiological Research, 2014, 169, 593-601. | 2.5 | 38 |
| 577 | A single nucleotide in the promoter region modulates the expression of the Â-lactamase OXA-61 in Campylobacter jejuni. Journal of Antimicrobial Chemotherapy, 2014, 69, 1215-1223. | 1.3 | 57 |
| 578 | Streptococcus pneumoniae Arginine Synthesis Genes Promote Growth and Virulence in Pneumococcal Meningitis. Journal of Infectious Diseases, 2014, 209, 1781-1791. | 1.9 | 23 |
| 579 | A lack of genetic basis for biovar differentiation in clinically important Corynebacterium diphtheriae from whole genome sequencing. Infection, Genetics and Evolution, 2014, 21, 54-57. | 1.0 | 43 |
| 580 | Complete genome sequence of Courdo11 virus, a member of the family Mimiviridae. Virus Genes, 2014, 48, 218-223. | 0.7 | 21 |
| 581 | Î±-Acetolactate synthase of Lactococcus lactis contributes to pH homeostasis in acid stress conditions. International Journal of Food Microbiology, 2014, 188, 99-107. | 2.1 | 38 |
| 582 | Streptococcus agalactiae clones infecting humans were selected and fixed through the extensive use of tetracycline. Nature Communications, 2014, 5, 4544. | 5.8 | 208 |
| 583 | Genomic analysis of a phage and prophage from a Bacillus thuringiensis strain. Journal of General Virology, 2014, 95, 751-761. | 1.3 | 9 |
| 584 | The genome of the<i>Erwinia amylovora</i>phage PhiEaH1 reveals greater diversity and broadens the applicability of phages for the treatment of fire blight. FEMS Microbiology Letters, 2014, 350, 25-27. | 0.7 | 31 |

| # | Article | IF | Citations |
|---|---|---|---|
| 585 | The Vibrio cholerae type VI secretion system employs diverse effector modules for intraspecific competition. Nature Communications, 2014, 5, 3549. | 5.8 | 211 |
| 586 | Comparative genomic analyses reveal a lack of a substantial signature of host adaptation inRhodococcus equi(â€˜Prescottella equiâ€™). Pathogens and Disease, 2014, 71, 352-356. | 0.8 | 11 |
| 587 | Spontaneously Induced Prophages in Lactobacillus gasseri Contribute to Horizontal Gene Transfer. Applied and Environmental Microbiology, 2014, 80, 3508-3517. | 1.4 | 62 |
| 588 | Genomic Insights into the Evolutionary Origin of Xanthomonas axonopodis pv. citri and Its Ecological Relatives. Applied and Environmental Microbiology, 2014, 80, 6266-6279. | 1.4 | 36 |
| 589 | Complete genome sequence of the Gram-negative probiotic Escherichia coli strain Nissle 1917. Journal of Biotechnology, 2014, 187, 106-107. | 1.9 | 76 |
| 590 | Nextâ€generation sequencing, <scp>FISH</scp> mapping and syntenyâ€based modeling reveal mechanisms of decreasing dysploidy in <i><scp>C</scp>ucumis</i>. Plant Journal, 2014, 77, 16-30. | 2.8 | 90 |
| 591 | High diversity of beta-lactamases in the General Hospital Vienna verified by whole genome sequencing and statistical analysis. Infection, Genetics and Evolution, 2014, 27, 408-417. | 1.0 | 9 |
| 592 | Prevalence and mapping of a plasmid encoding a type IV secretion system in Acinetobacter baumannii. Genomics, 2014, 104, 215-223. | 1.3 | 23 |
| 593 | Unveiling viralâ€“host interactions within the â€˜microbial dark matterâ€™. Nature Communications, 2014, 5, 4542. | 5.8 | 69 |
| 594 | Recombination drives genome evolution in outbreak-related Legionella pneumophila isolates. Nature Genetics, 2014, 46, 1205-1211. | 9.4 | 76 |
| 595 | Mitochondrial Phylogenomics of Early Land Plants: Mitigating the Effects of Saturation, Compositional Heterogeneity, and Codon-Usage Bias. Systematic Biology, 2014, 63, 862-878. | 2.7 | 108 |
| 596 | Chromosomal Rearrangement Features of Yersinia pestis Strains from Natural Plague Foci in China. American Journal of Tropical Medicine and Hygiene, 2014, 91, 722-728. | 0.6 | 4 |
| 597 | Evolution of Resistance to a Last-Resort Antibiotic in Staphylococcus aureus via Bacterial Competition. Cell, 2014, 158, 1060-1071. | 13.5 | 178 |
| 598 | Whole genome phylogeny of Prochlorococcus marinus group of cyanobacteria: genome alignment and overlapping gene approach. Interdisciplinary Sciences, Computational Life Sciences, 2014, 6, 149-157. | 2.2 | 5 |
| 599 | Analysis of the Pantoea ananatis pan-genome reveals factors underlying its ability to colonize and interact with plant, insect and vertebrate hosts. BMC Genomics, 2014, 15, 404. | 1.2 | 127 |
| 600 | Comparative genomic analysis of Mycobacterium tuberculosis clinical isolates. BMC Genomics, 2014, 15, 469. | 1.2 | 33 |
| 601 | Genomes of Alteromonas australica,a world apart. BMC Genomics, 2014, 15, 483. | 1.2 | 45 |
| 602 | Complete nucleotide sequence of pRS218, a large virulence plasmid, that augments pathogenic potential of meningitis-associated Escherichia coli strain RS218. BMC Microbiology, 2014, 14, 203. | 1.3 | 34 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 603 | Immunoglobulin A Coating Identifies Colitogenic Bacteria in Inflammatory Bowel Disease. Cell, 2014, 158, 1000-1010. | 13.5 | 982 |
| 604 | In silico identification of potential virulence genes in 1,3-propanediol producer Klebsiella pneumonia. Journal of Biotechnology, 2014, 189, 9-14. | 1.9 | 11 |
| 605 | An algebraic view of bacterial genome evolution. Journal of Mathematical Biology, 2014, 69, 1693-1718. | 0.8 | 12 |
| 606 | Genomic characterization of a Helicobacter pylori isolate from a patient with gastric cancer in China. Gut Pathogens, 2014, 6, 5. | 1.6 | 6 |
| 607 | Genetic Diversity and Evolution of Salmonella enterica Serovar Enteritidis Strains with Different Phage Types. Journal of Clinical Microbiology, 2014, 52, 1490-1500. | 1.8 | 26 |
| 608 | AOBA: Recognizing Object Behavior in Pervasive Urban Management. IEEE Transactions on Knowledge and Data Engineering, 2014, 26, 2625-2638. | 4.0 | 2 |
| 609 | Nitrogen-Fixing Rhizobial Strains Isolated from Common Bean Seeds: Phylogeny, Physiology, and Genome Analysis. Applied and Environmental Microbiology, 2014, 80, 5644-5654. | 1.4 | 48 |
| 610 | New Insights into Dissemination and Variation of the Health Care-Associated Pathogen Acinetobacter baumannii from Genomic Analysis. MBio, 2014, 5, e00963-13. | 1.8 | 184 |
| 611 | A Survey Sequence Comparison of Saccharum Genotypes Reveals Allelic Diversity Differences. Tropical Plant Biology, 2014, 7, 71-83. | 1.0 | 14 |
| 612 | Superinfection exclusion reveals heteroimmunity between Pseudomonas aeruginosa temperate phages. Journal of Microbiology, 2014, 52, 515-520. | 1.3 | 3 |
| 613 | Genome alignment with graph data structures: a comparison. BMC Bioinformatics, 2014, 15, 99. | 1.2 | 32 |
| 614 | Genomic and metabolic comparison with Dickeya dadantii 3937 reveals the emerging Dickeya solani potato pathogen to display distinctive metabolic activities and T5SS/T6SS-related toxin repertoire. BMC Genomics, 2014, 15, 283. | 1.2 | 61 |
| 615 | A high resolution map of mammalian X chromosome fragile regions assessed by large-scale comparative genomics. Mammalian Genome, 2014, 25, 618-635. | 1.0 | 5 |
| 616 | Abundant and Diverse Clustered Regularly Interspaced Short Palindromic Repeat Spacers in Clostridium difficile Strains and Prophages Target Multiple Phage Types within This Pathogen. MBio, 2014, 5, e01045-13. | 1.8 | 67 |
| 617 | Mitochondrial Genome Sequences and Comparative Genomics of <i>Achlya hypogyna</i> and <i>Thraustotheca clavata</i>. Journal of Eukaryotic Microbiology, 2014, 61, 146-154. | 0.8 | 12 |
| 618 | Genomic Heterogeneity and Ecological Speciation within One Subspecies of Bacillus subtilis. Applied and Environmental Microbiology, 2014, 80, 4842-4853. | 1.4 | 44 |
| 619 | Draft genome sequences of Terra1 and Terra2 viruses, new members of the family Mimiviridae isolated from soil. Virology, 2014, 452-453, 125-132. | 1.1 | 22 |
| 620 | Comparative genomics of oral isolates of Streptococcus mutans by in silico genome subtraction does not reveal accessory DNA associated with severe early childhood caries. Infection, Genetics and Evolution, 2014, 21, 269-278. | 1.0 | 18 |

| # | Article | IF | Citations |
|---|---|---|---|
| 621 | A Novel Angular Dioxygenase Gene Cluster Encoding 3-Phenoxybenzoate 1â€²,2â€²-Dioxygenase in Sphingobium wenxiniae JZ-1. Applied and Environmental Microbiology, 2014, 80, 3811-3818. | 1.4 | 30 |
| 622 | Functional type 2 photosynthetic reaction centers found in the rare bacterial phylum Gemmatimonadetes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7795-7800. | 3.3 | 220 |
| 623 | The mitochondrial genome of the red alga Kappaphycus striatus (â€œGreen Sacolâ€•variety): Complete nucleotide sequence, genome structure and organization, and comparative analysis. Marine Genomics, 2014, 18, 155-161. | 0.4 | 20 |
| 624 | Non-contiguous finished genome sequence and description of Clostridium saudii sp. nov. Standards in Genomic Sciences, 2014, 9, 8. | 1.5 | 15 |
| 625 | Identifying Pathogenicity Islands in Bacterial Pathogenomics Using Computational Approaches. Pathogens, 2014, 3, 36-56. | 1.2 | 78 |
| 626 | Genomic characterization of Ï•RS603, a filamentous bacteriophage that is infectious to the phytopathogen <i>Ralstonia solanacearum</i>. Microbiology and Immunology, 2014, 58, 697-700. | 0.7 | 18 |
| 627 | The Mitochondrial Genome of Grateloupia taiwanensis (Halymeniaceae, Rhodophyta) and Comparative Mitochondrial Genomics of Red Algae. Biological Bulletin, 2014, 227, 191-200. | 0.7 | 11 |
| 628 | Whole Genome Sequence of Polyresistant Mycobacterium tuberculosis CWCFVRF PRTB 19 Sputum Isolate from Chennai, India, Closely Clustering with East African Indian 5 Genogroup. Genome Announcements, 2014, 2, . | 0.8 | 2 |
| 629 | Draft Genome Sequence of Multidrug-Resistant Mycobacterium tuberculosis Strain CWCFVRF MDRTB 670, Isolated from the Sputum of a Patient from Chennai, India, with Clinically Suspected Tuberculosis. Genome Announcements, 2014, 2, . | 0.8 | 4 |
| 630 | Draft genome sequence of Gluconobacter thailandicus NBRC 3257. Standards in Genomic Sciences, 2014, 9, 614-623. | 1.5 | 12 |
| 631 | Non-contiguous finished genome sequence and description of Collinsella massiliensis sp. nov.. Standards in Genomic Sciences, 2014, 9, 1144-1158. | 1.5 | 13 |
| 632 | Non-contiguous finished genome sequence and description of Corynebacterium jeddahense sp. nov.. Standards in Genomic Sciences, 2014, 9, 987-1002. | 1.5 | 11 |
| 633 | Genome sequence and description of Nesterenkonia massiliensis sp. nov. strain NP1T. Standards in Genomic Sciences, 2014, 9, 866-882. | 1.5 | 18 |
| 634 | Non-contiguous finished genome sequence and description of Alistipes ihumii sp. nov.. Standards in Genomic Sciences, 2014, 9, 1221-1235. | 1.5 | 48 |
| 635 | Non contiguous-finished genome sequence and description of Enorma timonensis sp. nov.. Standards in Genomic Sciences, 2014, 9, 970-986. | 1.5 | 10 |
| 636 | Genome sequence and description of Bacteroides timonensis sp. nov.. Standards in Genomic Sciences, 2014, 9, 1181-1197. | 1.5 | 10 |
| 637 | Non contiguous-finished genome sequence and description of Clostridium jeddahense sp. nov.. Standards in Genomic Sciences, 2014, 9, 1003-1019. | 1.5 | 26 |
| 638 | Genomic analysis of Skermanella stibiiresistens type strain SB22T. Standards in Genomic Sciences, 2014, 9, 1211-1220. | 1.5 | 14 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 639 | Complete Genome Sequence of the Multiresistant Acinetobacter baumannii Strain AbH12O-A2, Isolated during a Large Outbreak in Spain. Genome Announcements, 2014, 2, . | 0.8 | 19 |
| 640 | Identification and characterization of accessory genomes in bacterial species based on genome comparison and metagenomic recruitment. , 2014, , . | | 0 |
| 641 | Noncontiguous finished genome sequence and description of Paenibacillus antibioticophila sp.Ânov. GD11T, the type strain ofÂPaenibacillus antibioticophila. New Microbes and New Infections, 2015, 8, 137-147. | 0.8 | 5 |
| 642 | Noncontiguous finished genome sequence and description of Weeksella massiliensis sp. nov.. New Microbes and New Infections, 2015, 8, 89-98. | 0.8 | 12 |
| 643 | Comparative genomics of Pseudomonas fluorescens subclade III strains from human lungs. BMC Genomics, 2015, 16, 1032. | 1.2 | 15 |
| 644 | Clostridium polynesiense sp. nov., a new member of the human gut microbiota in French Polynesia. Anaerobe, 2015, 36, 79-87. | 1.0 | 4 |
| 645 | Supergroup C <i>Wolbachia</i> , mutualist symbionts of filarial nematodes, have a distinct genome structure. Open Biology, 2015, 5, 150099. | 1.5 | 38 |
| 646 | Genomic analysis of a ginger pathogen Bacillus pumilus providing the understanding to the pathogenesis and the novel control strategy. Scientific Reports, 2015, 5, 10259. | 1.6 | 29 |
| 647 | Comparative genomics Lactobacillus reuteri from sourdough reveals adaptation of an intestinal symbiont to food fermentations. Scientific Reports, 2015, 5, 18234. | 1.6 | 65 |
| 648 | Four novel algal virus genomes discovered from Yellowstone Lake metagenomes. Scientific Reports, 2015, 5, 15131. | 1.6 | 44 |
| 649 | The post-vaccine microevolution of invasive Streptococcus pneumoniae. Scientific Reports, 2015, 5, 14952. | 1.6 | 36 |
| 650 | Revisiting the reference genomes of human pathogenic Cryptosporidium species: reannotation of C. parvum Iowa and a new C. hominis reference. Scientific Reports, 2015, 5, 16324. | 1.6 | 44 |
| 651 | Phylogeny Inference of Closely Related Bacterial Genomes: Combining the Features of Both Overlapping Genes and Collinear Genomic Regions. Evolutionary Bioinformatics, 2015, 11s2, EBO.S33491. | 0.6 | 3 |
| 652 | BactoGeNIE: a large-scale comparative genome visualization for big displays. BMC Bioinformatics, 2015, 16, S6. | 1.2 | 10 |
| 653 | A platform for leveraging next generation sequencing for routine microbiology and public health use. Health Information Science and Systems, 2015, 3, S7. | 3.4 | 7 |
| 654 | Deep sequencing analysis of the heterogeneity of seed and commercial lots of the bacillus Calmette-GuÃ©rin (BCG) tuberculosis vaccine substrain Tokyo-172. Scientific Reports, 2015, 5, 17827. | 1.6 | 10 |
| 655 | Noncontiguous finished genome sequence and description of Necropsobacter massiliensis sp. nov.. New Microbes and New Infections, 2015, 8, 41-50. | 0.8 | 8 |
| 656 | Genome analysis and in vivo virulence of porcine extraintestinal pathogenic Escherichia coli strain PCN033. BMC Genomics, 2015, 16, 717. | 1.2 | 63 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 657 | Genome analysis of Daldinia eschscholtzii strains UM 1400 and UM 1020, wood-decaying fungi isolated from human hosts. BMC Genomics, 2015, 16, 966. | 1.2 | 16 |
| 658 | Non contiguous-finished genome sequence and description of Bacillus jeddahensis sp. nov.. Standards in Genomic Sciences, 2015, 10, 47. | 1.5 | 22 |
| 659 | Draft genome sequence of Cellulomonas carbonis T26T and comparative analysis of six Cellulomonas genomes. Standards in Genomic Sciences, 2015, 10, 104. | 1.5 | 5 |
| 660 | Draft Genome Sequence of <i>Halostagnicola</i> sp. A56, an Extremely Halophilic Archaeon Isolated from the Andaman Islands. Genome Announcements, 2015, 3, . | 0.8 | 3 |
| 661 | Draft Genome Sequence of <i>Pedobacter</i> sp. Strain Hv1, an Isolate from Medicinal Leech Mucosal Castings. Genome Announcements, 2015, 3, . | 0.8 | 0 |
| 662 | Fatty acid kinase A is an important determinant of biofilm formation in Staphylococcus aureus USA300. BMC Genomics, 2015, 16, 861. | 1.2 | 26 |
| 663 | The genome of Dasychira pudibunda nucleopolyhedrovirus (DapuNPV) reveals novel genetic connection between baculoviruses infecting moths of the Lymantriidae family. BMC Genomics, 2015, 16, 759. | 1.2 | 11 |
| 664 | Comparison of Xenorhabdus bovienii bacterial strain genomes reveals diversity in symbiotic functions. BMC Genomics, 2015, 16, 889. | 1.2 | 22 |
| 665 | Comparative genome analysis identifies two large deletions in the genome of highly-passaged attenuated Streptococcus agalactiae strain YM001 compared to the parental pathogenic strain HN016. BMC Genomics, 2015, 16, 897. | 1.2 | 21 |
| 666 | Phylogenetic patterns of gene rearrangements in four mitochondrial genomes from the green algal family Hydrodictyaceae (Sphaeropleales, Chlorophyceae). BMC Genomics, 2015, 16, 826. | 1.2 | 11 |
| 667 | Exploring the genomic traits of fungus-feeding bacterial genus Collimonas. BMC Genomics, 2015, 16, 1103. | 1.2 | 57 |
| 668 | Brachyspira suanatina sp. nov., an enteropathogenic intestinal spirochaete isolated from pigs and mallards: genomic and phenotypic characteristics. BMC Microbiology, 2015, 15, 208. | 1.3 | 39 |
| 669 | Non-contiguous finished genome sequence and description of Clostridium ihumii sp. nov.. Standards in Genomic Sciences, 2015, 10, 63. | 1.5 | 11 |
| 670 | Draft genome sequence of Halomonas meridiana R1t3 isolated from the surface microbiota of the Caribbean Elkhorn coral Acropora palmata. Standards in Genomic Sciences, 2015, 10, 75. | 1.5 | 19 |
| 671 | Genomic information of the arsenic-resistant bacterium Lysobacter arseniciresistens type strain ZS79T and comparison of Lysobacter draft genomes. Standards in Genomic Sciences, 2015, 10, 88. | 1.5 | 6 |
| 672 | Chloroplast Genome Evolution in the Euglenaceae. Journal of Eukaryotic Microbiology, 2015, 62, 773-785. | 0.8 | 35 |
| 673 | A quantitative hybridization approach using 17 <scp>DNA</scp> markers for identification and clustering analysis of <i>Ralstonia solanacearum</i>. Plant Pathology, 2015, 64, 1270-1283. | 1.2 | 2 |
| 674 | Draft Genome Sequences of Two South African Bacillus anthracis Strains. Genome Announcements, 2015, 3, . | 0.8 | 6 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 675 | Draft Genome Sequences of the Fish Pathogen Vibrio harveyi Strains VH2 and VH5. Genome Announcements, 2015, 3, . | 0.8 | 6 |
| 676 | Phage Î¦Pan70, a Putative Temperate Phage, Controls Pseudomonas aeruginosa in Planktonic, Biofilm and Burn Mouse Model Assays. Viruses, 2015, 7, 4602-4623. | 1.5 | 42 |
| 677 | Characterization of enteropathogenic and Shiga toxin-producing Escherichia coli in cattle and deer in a shared agroecosystem. Frontiers in Cellular and Infection Microbiology, 2015, 5, 29. | 1.8 | 43 |
| 678 | Genomic Resources of Three Pulsatilla Species Reveal Evolutionary Hotspots, Species-Specific Sites and Variable Plastid Structure in the Family Ranunculaceae. International Journal of Molecular Sciences, 2015, 16, 22258-22279. | 1.8 | 25 |
| 679 | Best practices for evaluating single nucleotide variant calling methods for microbial genomics. Frontiers in Genetics, 2015, 6, 235. | 1.1 | 160 |
| 680 | Unravelling the genome of long chain N-acylhomoserine lactone-producing Acinetobacter sp. strain GG2 and identification of its quorum sensing synthase gene. Frontiers in Microbiology, 2015, 6, 240. | 1.5 | 16 |
| 681 | Whole-genome comparative analysis of virulence genes unveils similarities and differences between endophytes and other symbiotic bacteria. Frontiers in Microbiology, 2015, 6, 419. | 1.5 | 31 |
| 682 | Genomic comparison of closely related Giant Viruses supports an accordion-like model of evolution. Frontiers in Microbiology, 2015, 6, 593. | 1.5 | 41 |
| 683 | Genome sequencing reveals a new lineage associated with lablab bean and genetic exchange between Xanthomonas axonopodis pv. phaseoli and Xanthomonas fuscans subsp. fuscans. Frontiers in Microbiology, 2015, 6, 1080. | 1.5 | 29 |
| 684 | A New Zamilon-like Virophage Partial Genome Assembled from a Bioreactor Metagenome. Frontiers in Microbiology, 2015, 6, 1308. | 1.5 | 20 |
| 685 | A Census of Nuclear Cyanobacterial Recruits in the Plant Kingdom. PLoS ONE, 2015, 10, e0120527. | 1.1 | 1 |
| 686 | Comparative Genomics of a Helicobacter pylori Isolate from a Chinese Yunnan Naxi Ethnic Aborigine Suggests High Genetic Divergence and Phage Insertion. PLoS ONE, 2015, 10, e0120659. | 1.1 | 9 |
| 687 | Genome-Guided Analysis of Physiological Capacities of Tepidanaerobacter acetatoxydans Provides Insights into Environmental Adaptations and Syntrophic Acetate Oxidation. PLoS ONE, 2015, 10, e0121237. | 1.1 | 28 |
| 688 | Comparative Genome Analyses of Serratia marcescens FS14 Reveals Its High Antagonistic Potential. PLoS ONE, 2015, 10, e0123061. | 1.1 | 51 |
| 689 | The Plastid Genome of the Cryptomonad Teleaulax amphioxeia. PLoS ONE, 2015, 10, e0129284. | 1.1 | 30 |
| 690 | Novel recA-Independent Horizontal Gene Transfer in Escherichia coli K-12. PLoS ONE, 2015, 10, e0130813. | 1.1 | 12 |
| 691 | Genome Sequence Analysis of the Naphthenic Acid Degrading and Metal Resistant Bacterium Cupriavidus gilardii CR3. PLoS ONE, 2015, 10, e0132881. | 1.1 | 44 |
| 692 | Comparative Transcriptome Analysis Reveals Cool Virulence Factors of Ralstonia solanacearum Race 3 Biovar 2. PLoS ONE, 2015, 10, e0139090. | 1.1 | 43 |

| # | Article | IF | Citations |
|---|---|---|---|
| 693 | Deciphering the conserved genetic loci implicated in plant disease control through comparative genomics of Bacillus amyloliquefaciens subsp. plantarum. Frontiers in Plant Science, 2015, 6, 631. | 1.7 | 52 |
| 694 | An Effective Big Data Supervised Imbalanced Classification Approach for Ortholog Detection in Related Yeast Species. BioMed Research International, 2015, 2015, 1-12. | 0.9 | 17 |
| 695 | Population structure of<i>Neisseria gonorrhoeae</i>based on whole genome data and its relationship with antibiotic resistance. PeerJ, 2015, 3, e806. | 0.9 | 67 |
| 696 | Targeting DnaN for tuberculosis therapy using novel griselimycins. Science, 2015, 348, 1106-1112. | 6.0 | 262 |
| 697 | Detection and Genomic Characterization of Motility in Lactobacillus curvatus: Confirmation of Motility in a Species outside the Lactobacillus salivarius Clade. Applied and Environmental Microbiology, 2015, 81, 1297-1308. | 1.4 | 67 |
| 698 | Genome sequencing reveals novel deletions associated with secondary resistance to pyrazinamide in MDR<i>Mycobacterium tuberculosis</i>. Journal of Antimicrobial Chemotherapy, 2015, 70, 2511-2514. | 1.3 | 21 |
| 699 | Mechanisms of solvent resistance mediated by interplay of cellular factors in<i>Pseudomonas putida</i>. FEMS Microbiology Reviews, 2015, 39, 555-566. | 3.9 | 143 |
| 700 | dipSPAdes: Assembler for Highly Polymorphic Diploid Genomes. Journal of Computational Biology, 2015, 22, 528-545. | 0.8 | 69 |
| 701 | The genomes of closely related Pantoea ananatis maize seed endophytes having different effects on the host plant differ in secretion system genes and mobile genetic elements. Frontiers in Microbiology, 2015, 6, 440. | 1.5 | 85 |
| 702 | Next-generation sequencing approach for connecting secondary metabolites to biosynthetic gene clusters in fungi. Frontiers in Microbiology, 2015, 5, 774. | 1.5 | 80 |
| 703 | Full genome SNP-based phylogenetic analysis reveals the origin and global spread of Brucella melitensis. BMC Genomics, 2015, 16, 93. | 1.2 | 72 |
| 704 | Comparative genomic analysis reveals occurrence of genetic recombination in virulent Cryptosporidium hominis subtypes and telomeric gene duplications in Cryptosporidium parvum. BMC Genomics, 2015, 16, 320. | 1.2 | 74 |
| 705 | Comprehensive insights inthe Mycobacterium aviumsubsp.paratuberculosisgenome using new WGS data of sheep strain JIII-386 from Germany. Genome Biology and Evolution, 2015, 7, evv154. | 1.1 | 31 |
| 706 | Structure, evolution and functional inference on the Mildew Locus O (MLO) gene family in three cultivated Cucurbitaceae spp.. BMC Genomics, 2015, 16, 1112. | 1.2 | 45 |
| 707 | As Clear as Mud? Determining the Diversity and Prevalence of Prophages in the Draft Genomes of Estuarine Isolates of<i>Clostridium difficile</i>. Genome Biology and Evolution, 2015, 7, 1842-1855. | 1.1 | 20 |
| 708 | Distinctive Genome Reduction Rates Revealed by Genomic Analyses of Two<i>Coxiella-</i>Like Endosymbionts in Ticks. Genome Biology and Evolution, 2015, 7, 1779-1796. | 1.1 | 140 |
| 709 | Draft Genome Sequence of Isolate Staphylococcus aureus LHSKBClinical, Isolated from an Infected Hip. Genome Announcements, 2015, 3, . | 0.8 | 2 |
| 710 | Draft Genome Sequences of Two Clinical Isolates of Mycobacterium tuberculosis from Sputum of Kazakh Patients. Genome Announcements, 2015, 3, . | 0.8 | 4 |

| # | Article | IF | Citations |
|---|---|---|---|
| 711 | Draft Genome Sequence of Stenotrophomonas maltophilia Strain UV74 Reveals Extensive Variability within Its Genomic Group. Genome Announcements, 2015, 3, . | 0.8 | 5 |
| 712 | Draft Genome Sequences of Vibrio alginolyticus Strains V1 and V2, Opportunistic Marine Pathogens. Genome Announcements, 2015, 3, . | 0.8 | 20 |
| 713 | Draft Genome Sequence of the Biofilm-Hyperproducing Acinetobacter baumannii Clinical Strain MAR002. Genome Announcements, 2015, 3, . | 0.8 | 6 |
| 714 | Genome Sequence and Annotation of a Human Infection Isolate of Escherichia coli O26:H11 Involved in a Raw Milk Cheese Outbreak. Genome Announcements, 2015, 3, . | 0.8 | 10 |
| 715 | Population genomics reveals additive and replacing horizontal gene transfers in the emerging pathogen Dickeya solani. BMC Genomics, 2015, 16, 788. | 1.2 | 63 |
| 716 | <i>Chlamydiaceae</i>Genomics Reveals Interspecies Admixture and the Recent Evolution of<i>Chlamydia abortus</i>Infecting Lower Mammalian Species and Humans. Genome Biology and Evolution, 2015, 7, 3070-3084. | 1.1 | 30 |
| 717 | Rise of Microbial Culturomics: Noncontiguous Finished Genome Sequence and Description ofBeduini massiliensisgen. nov., sp. nov.. OMICS A Journal of Integrative Biology, 2015, 19, 766-776. | 1.0 | 15 |
| 719 | Draft Genome Sequence of the Commercial Biocontrol Strain Pantoea agglomerans P10c. Genome Announcements, 2015, 3, . | 0.8 | 29 |
| 720 | The Bacillus cereus Group. , 2015, , 1041-1078. |  | 5 |
| 721 | Phylogenomics characterization of a highly virulent Edwardsiella strain ET080813T encoding two distinct T3SS and three T6SS gene clusters: Propose a novel species as Edwardsiella anguillarum sp. nov.. Systematic and Applied Microbiology, 2015, 38, 36-47. | 1.2 | 126 |
| 722 | Comparative Analysis of Asteraceae Chloroplast Genomes: Structural Organization, RNA Editing and Evolution. Plant Molecular Biology Reporter, 2015, 33, 1526-1538. | 1.0 | 65 |
| 723 | Genome assembly and annotation of a Drosophila simulans strain from Madagascar. Molecular Ecology Resources, 2015, 15, 372-381. | 2.2 | 46 |
| 724 | Ecology and genomic features of infection with Mycobacterium avium subspecies paratuberculosis in Egypt. Microbiology (United Kingdom), 2015, 161, 807-818. | 0.7 | 27 |
| 725 | Complete genome sequence of a filamentous bacteriophage, RS611, that infects the phytopathogen Ralstonia solanacearum. Archives of Virology, 2015, 160, 865-867. | 0.9 | 7 |
| 726 | <tt>andi</tt>: Fast and accurate estimation of evolutionary distances between closely related genomes. Bioinformatics, 2015, 31, 1169-1175. | 1.8 | 89 |
| 727 | Polymerase chain reaction-based serotyping of pathogenic bacteria in food. Journal of Microbiological Methods, 2015, 110, 18-26. | 0.7 | 25 |
| 728 | Identification and monitoring of nitrification and denitrification genes in Klebsiella pneumoniae EGD-HP19-C for its ability to perform heterotrophic nitrification and aerobic denitrification. Functional and Integrative Genomics, 2015, 15, 63-76. | 1.4 | 77 |
| 729 | Is Sequence Alignment an Art or a Science?. Systematic Botany, 2015, 40, 14-26. | 0.2 | 25 |

| # | Article | IF | Citations |
|---|---|---|---|
| 730 | Molecular and serological in-herd prevalence of Anaplasma marginale infection in Texas cattle. Preventive Veterinary Medicine, 2015, 119, 1-9. | 0.7 | 34 |
| 731 | Genomic and phenotypic differentiation among <i>Methanosarcina mazei</i> populations from Columbia River sediment. ISME Journal, 2015, 9, 2191-2205. | 4.4 | 42 |
| 732 | The broad-host-range plasmid pSFA231 isolated from petroleum-contaminated sediment represents a new member of the PromA plasmid family. Frontiers in Microbiology, 2014, 5, 777. | 1.5 | 32 |
| 733 | Gene Amplification and Sequencing for Bacterial Identification. Methods in Microbiology, 2015, 42, 433-464. | 0.4 | 10 |
| 734 | Genomic Tools for the Study of Azospirillum and Other Plant Growth-Promoting Rhizobacteria. , 2015, , 83-97. |  | 1 |
| 735 | Exploring Vertical Transmission of Bifidobacteria from Mother to Child. Applied and Environmental Microbiology, 2015, 81, 7078-7087. | 1.4 | 191 |
| 736 | Genetic profiles of Propionibacterium acnes and identification of a unique transposon with novel insertion sequences in sarcoid and non-sarcoid isolates. Scientific Reports, 2015, 5, 9832. | 1.6 | 12 |
| 737 | Genome-Assisted Development of a Diagnostic Protocol for Distinguishing High Virulence Pseudomonas syringae pv. tomato Strains. Plant Disease, 2015, 99, 527-534. | 0.7 | 10 |
| 738 | In silico identification of AMPylating enzymes and study of their divergent evolution. Scientific Reports, 2015, 5, 10804. | 1.6 | 32 |
| 739 | Characterization of Three<i>Mycobacterium</i>spp. with Potential Use in Bioremediation by Genome Sequencing and Comparative Genomics. Genome Biology and Evolution, 2015, 7, 1871-1886. | 1.1 | 17 |
| 740 | Exceptional reduction of the plastid genome of saguaro cactus (<i>Carnegiea gigantea</i>): Loss of the <i>ndh</i> gene suite and inverted repeat. American Journal of Botany, 2015, 102, 1115-1127. | 0.8 | 137 |
| 741 | Worldwide Population Structure, Long-Term Demography, and Local Adaptation of <i>Helicobacter pylori</i>. Genetics, 2015, 200, 947-963. | 1.2 | 65 |
| 742 | Differential RNA-seq (dRNA-seq) for annotation of transcriptional start sites and small RNAs in Helicobacter pylori. Methods, 2015, 86, 89-101. | 1.9 | 47 |
| 743 | Whole-Genome Sequence Analysis and Genome-Wide Virulence Gene Identification of Riemerella anatipestifer Strain Yb2. Applied and Environmental Microbiology, 2015, 81, 5093-5102. | 1.4 | 35 |
| 744 | Proteny: discovering and visualizing statistically significant syntenic clusters at the proteome level. Bioinformatics, 2015, 31, 3437-3444. | 1.8 | 6 |
| 745 | Genome Sequence of the Drosophila melanogaster Male-Killing Spiroplasma Strain MSRO Endosymbiont. MBio, 2015, 6, . | 1.8 | 60 |
| 746 | A naturally occurring prfA truncation in a Listeria monocytogenes field strain contributes to reduced replication and cell-to-cell spread. Veterinary Microbiology, 2015, 179, 91-101. | 0.8 | 37 |
| 747 | Genomic Avenue to Avian Colisepticemia. MBio, 2015, 6, . | 1.8 | 59 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 748 | Complete Genome Sequence of Bifidobacterium longum GT15: Identification and Characterization of Unique and Global Regulatory Genes. Microbial Ecology, 2015, 70, 819-834. | 1.4 | 19 |
| 749 | Ecophysiological diversity of a novel member of the genus Alteromonas, and description of Alteromonas mediterranea sp. nov.. Antonie Van Leeuwenhoek, 2015, 107, 119-132. | 0.7 | 44 |
| 750 | The genome sequence of Pseudoplusia includens single nucleopolyhedrovirus and an analysis of p26 gene evolution in the baculoviruses. BMC Genomics, 2015, 16, 127. | 1.2 | 22 |
| 751 | The Alternaria genomes database: a comprehensive resource for a fungal genus comprised of saprophytes, plant pathogens, and allergenic species. BMC Genomics, 2015, 16, 239. | 1.2 | 105 |
| 752 | Comparative genome analysis of Pediococcus damnosus LMG 28219, a strain well-adapted to the beer environment. BMC Genomics, 2015, 16, 267. | 1.2 | 26 |
| 753 | Genome sequencing and comparative genomics provides insights on the evolutionary dynamics and pathogenic potential of different H-serotypes of Shiga toxin-producing Escherichia coli O104. BMC Microbiology, 2015, 15, 83. | 1.3 | 24 |
| 754 | Complete plastome sequence of Thalictrum coreanum (Ranunculaceae) and transfer of the rpl32 gene to the nucleus in the ancestor of the subfamily Thalictroideae. BMC Plant Biology, 2015, 15, 40. | 1.6 | 71 |
| 755 | Bioinformatic analysis of phage AB3, a phiKMV-like virus infecting Acinetobacter baumannii. Genetics and Molecular Research, 2015, 14, 190-198. | 0.3 | 7 |
| 756 | Single-molecule sequencing reveals the molecular basis of multidrug-resistance in ST772 methicillin-resistant Staphylococcus aureus. BMC Genomics, 2015, 16, 388. | 1.2 | 24 |
| 757 | IonGAP: integrative bacterial genome analysis for Ion Torrent sequence data. Bioinformatics, 2015, 31, 2870-2873. | 1.8 | 12 |
| 758 | Identifying a potential receptor for the antibacterial peptide of sponge Axinella donnani endosymbiont. Gene, 2015, 566, 166-174. | 1.0 | 3 |
| 759 | Sequencing and characterizing the genome of Estrella lausannensis as an undergraduate project: training students and biological insights. Frontiers in Microbiology, 2015, 6, 101. | 1.5 | 32 |
| 760 | Characterization of a new ViI-like Erwinia amylovora bacteriophage phiEa2809. FEMS Microbiology Letters, 2015, 362, . | 0.7 | 18 |
| 761 | Origin and domestication of papaya Y<sup>h</sup> chromosome. Genome Research, 2015, 25, 524-533. | 2.4 | 87 |
| 762 | Use of Whole-Genome Phylogeny and Comparisons for Development of a Multiplex PCR Assay To Identify Sequence Type 36 Vibrio parahaemolyticus. Journal of Clinical Microbiology, 2015, 53, 1864-1872. | 1.8 | 21 |
| 763 | The Pathogen of the Great Barrier Reef Sponge Rhopaloeides odorabile Is a New Strain of Pseudoalteromonas agarivorans Containing Abundant and Diverse Virulence-Related Genes. Marine Biotechnology, 2015, 17, 463-478. | 1.1 | 51 |
| 764 | Genomic characterization of Italian Clostridium botulinum group I strains. Infection, Genetics and Evolution, 2015, 36, 62-71. | 1.0 | 24 |
| 765 | The lanthipeptides of Bacillus methylotrophicus and their association with genomic islands. Systematic and Applied Microbiology, 2015, 38, 525-533. | 1.2 | 10 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 766 | Whole-Genome Sequences of Eight Campylobacter jejuni Isolates from Wild Birds. Genome Announcements, 2015, 3, . | 0.8 | 6 |
| 767 | Nanoarchaeota, Their Sulfolobales Host, and Nanoarchaeota Virus Distribution across Yellowstone National Park Hot Springs. Applied and Environmental Microbiology, 2015, 81, 7860-7868. | 1.4 | 63 |
| 768 | Genome sequence and comparative analysis of a putative entomopathogenic Serratia isolated from Caenorhabditis briggsae. BMC Genomics, 2015, 16, 531. | 1.2 | 27 |
| 769 | Virgibacillus senegalensis sp. nov., a new moderately halophilic bacterium isolated from human gut. New Microbes and New Infections, 2015, 8, 116-126. | 0.8 | 12 |
| 770 | Isolation and characterization of a native avirulent strain of Streptococcus suis serotype 2: a perspective for vaccine development. Scientific Reports, 2015, 5, 9835. | 1.6 | 19 |
| 771 | Lifestyle Evolution in Cyanobacterial Symbionts of Sponges. MBio, 2015, 6, e00391-15. | 1.8 | 103 |
| 772 | Hypermutator Salmonella Heidelberg induces an early cell death in epithelial cells. Veterinary Microbiology, 2015, 180, 65-74. | 0.8 | 4 |
| 773 | Genome Sequencing of Multiple Isolates Highlights Subtelomeric Genomic Diversity within<i>Fusarium fujikuroi</i>. Genome Biology and Evolution, 2015, 7, 3062-3069. | 1.1 | 36 |
| 774 | Multiple Genetic Mutations Associated with Polymyxin Resistance in Acinetobacter baumannii. Antimicrobial Agents and Chemotherapy, 2015, 59, 7899-7902. | 1.4 | 35 |
| 775 | Burkholderia kirstenboschensis sp. nov. nodulates papilionoid legumes indigenous to South Africa. Systematic and Applied Microbiology, 2015, 38, 545-554. | 1.2 | 68 |
| 776 | YOC, A new strategy for pairwise alignment of collinear genomes. BMC Bioinformatics, 2015, 16, 111. | 1.2 | 8 |
| 777 | The chloroplast genomes of Bryopsis plumosa and Tydemania expeditiones (Bryopsidales,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf | 1.2 | 63 |
| 778 | Draft Genome Sequence of the Streptococcus pneumoniae Avery Strain A66. Genome Announcements, 2015, 3, . | 0.8 | 10 |
| 779 | Buying in to bioinformatics: an introduction to commercial sequence analysis software. Briefings in Bioinformatics, 2015, 16, 700-709. | 3.2 | 36 |
| 780 | Whole-Genome Sequencing Identifies Emergence of a Quinolone Resistance Mutation in a Case of Stenotrophomonas maltophilia Bacteremia. Antimicrobial Agents and Chemotherapy, 2015, 59, 7117-7120. | 1.4 | 24 |
| 781 | Bordetella pertussisevolution in the (functional) genomics era. Pathogens and Disease, 2015, 73, ftv064. | 0.8 | 25 |
| 782 | It Is Not All about Single Nucleotide Polymorphisms: Comparison of Mobile Genetic Elements and Deletions in Listeria monocytogenes Genomes Links Cases of Hospital-Acquired Listeriosis to the Environmental Source. Journal of Clinical Microbiology, 2015, 53, 3492-3500. | 1.8 | 24 |
| 783 | A protocol for targeted enrichment of intronâ€containing sequence markers for recent radiations: A phylogenomic example from <i>Heuchera</i> (Saxifragaceae). Applications in Plant Sciences, 2015, 3, 1500039. | 0.8 | 99 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 784 | Comparative Genomics of Environmental and Clinical<i>Stenotrophomonas maltophilia</i>Strains with Different Antibiotic Resistance Profiles. Genome Biology and Evolution, 2015, 7, 2484-2505. | 1.1 | 90 |
| 785 | Draft Genome Sequence of Thermus sp. Isolate 2.9, Obtained from a Hot Water Spring Located in Salta, Argentina. Genome Announcements, 2015, 3, . | 0.8 | 6 |
| 786 | An Exploration into Fern Genome Space. Genome Biology and Evolution, 2015, 7, 2533-2544. | 1.1 | 85 |
| 787 | Genomic Epidemiology of Clostridium botulinum Isolates from Temporally Related Cases of Infant Botulism in New South Wales, Australia. Journal of Clinical Microbiology, 2015, 53, 2846-2853. | 1.8 | 9 |
| 788 | Sinorhizobium meliloti Phage Î¦M9 Defines a New Group of T4 Superfamily Phages with Unusual Genomic Features but a Common T=16 Capsid. Journal of Virology, 2015, 89, 10945-10958. | 1.5 | 29 |
| 789 | A single nucleotide change in<i>mutY</i>increases the emergence of antibiotic-resistant<i>Campylobacter jejuni</i>mutants. Journal of Antimicrobial Chemotherapy, 2015, 70, 2739-2748. | 1.3 | 13 |
| 790 | Complete Genome Sequence of the Nonpathogenic Soil-Dwelling Bacterium Clostridium sporogenes Strain NCIMB 10696. Genome Announcements, 2015, 3, . | 0.8 | 4 |
| 791 | Draft genomic sequence of a selenite-reducing bacterium, Paenirhodobacter enshiensis DW2-9T. Standards in Genomic Sciences, 2015, 10, 38. | 1.5 | 4 |
| 792 | Mutations and genomic islands can explain the strain dependency of sugar utilization in 21 strains of Propionibacterium freudenreichii. BMC Genomics, 2015, 16, 296. | 1.2 | 30 |
| 793 | Transcriptional profiles of Haloferax mediterranei based on nitrogen availability. Journal of Biotechnology, 2015, 193, 100-107. | 1.9 | 19 |
| 794 | Environmental Surveillance for Toxigenic Vibrio cholerae in Surface Waters of Haiti. American Journal of Tropical Medicine and Hygiene, 2015, 92, 118-125. | 0.6 | 20 |
| 795 | Bacteriophage Resistance Mechanisms in the Fish Pathogen Flavobacterium psychrophilum: Linking Genomic Mutations to Changes in Bacterial Virulence Factors. Applied and Environmental Microbiology, 2015, 81, 1157-1167. | 1.4 | 95 |
| 796 | Genomic analyses of Clostridium perfringens isolates from five toxinotypes. Research in Microbiology, 2015, 166, 255-263. | 1.0 | 71 |
| 797 | Ten years of pan-genome analyses. Current Opinion in Microbiology, 2015, 23, 148-154. | 2.3 | 498 |
| 798 | Integration of genomic and proteomic analyses in the classification of the Siphoviridae family. Virology, 2015, 477, 144-154. | 1.1 | 52 |
| 799 | Molecular methods for serovar determination of Salmonella. Critical Reviews in Microbiology, 2015, 41, 309-325. | 2.7 | 76 |
| 800 | <scp>POY</scp> version 5: phylogenetic analysis using dynamic homologies under multiple optimality criteria. Cladistics, 2015, 31, 189-196. | 1.5 | 74 |
| 801 | Genomic and Transcriptomic Analyses of Colistin-Resistant Clinical Isolates of Klebsiella pneumoniae Reveal Multiple Pathways of Resistance. Antimicrobial Agents and Chemotherapy, 2015, 59, 536-543. | 1.4 | 185 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 802 | Effects of Actin-Like Proteins Encoded by Two Bacillus pumilus Phages on Unstable Lysogeny, Revealed by Genomic Analysis. Applied and Environmental Microbiology, 2015, 81, 339-350. | 1.4 | 21 |
| 803 | Genomic overview of the phytopathogen Pectobacterium wasabiae strain RNS 08.42.1A suggests horizontal acquisition of quorum-sensing genes. Genetica, 2015, 143, 241-252. | 0.5 | 7 |
| 804 | Insights into structural variations and genome rearrangements in prokaryotic genomes. Bioinformatics, 2015, 31, 1-9. | 1.8 | 58 |
| 805 | Complete genome of the multidrug-resistant Acinetobacter baumannii strain KBN10P02143 isolated from Korea. Memorias Do Instituto Oswaldo Cruz, 2016, 111, 355-358. | 0.8 | 4 |
| 807 | The Complete Genome of Brucella Suis 019 Provides Insights on Cross-Species Infection. Genes, 2016, 7, 7. | 1.0 | 13 |
| 808 | Genetic Characterization and Comparative Genome Analysis of<i>Brucella melitensis</i>Isolates from India. International Journal of Genomics, 2016, 2016, 1-13. | 0.8 | 12 |
| 809 | A Brazilian Marseillevirus Is the Founding Member of a Lineage in Family Marseilleviridae. Viruses, 2016, 8, 76. | 1.5 | 74 |
| 810 | TP53 copy number expansion is associated with the evolution of increased body size and an enhanced DNA damage response in elephants. ELife, 2016, 5, . | 2.8 | 191 |
| 811 | Evolution and Diversity of the Antimicrobial Resistance Associated Mobilome in Streptococcus suis: A Probable Mobile Genetic Elements Reservoir for Other Streptococci. Frontiers in Cellular and Infection Microbiology, 2016, 6, 118. | 1.8 | 75 |
| 812 | Comparative Genomics of Two ST 195 Carbapenem-Resistant Acinetobacter baumannii with Different Susceptibility to Polymyxin Revealed Underlying Resistance Mechanism. Frontiers in Microbiology, 2015, 6, 1445. | 1.5 | 40 |
| 813 | Recombination Does Not Hinder Formation or Detection of Ecological Species of Synechococcus Inhabiting a Hot Spring Cyanobacterial Mat. Frontiers in Microbiology, 2015, 6, 1540. | 1.5 | 16 |
| 814 | Novel Virophages Discovered in a Freshwater Lake in China. Frontiers in Microbiology, 2016, 7, 5. | 1.5 | 48 |
| 815 | Comparative Genomic Analysis of the ICESa2603 Family ICEs and Spread of erm(B)- and tet(O)-Carrying Transferable 89K-Subtype ICEs in Swine and Bovine Isolates in China. Frontiers in Microbiology, 2016, 7, 55. | 1.5 | 38 |
| 816 | Microevolution Analysis of Bacillus coahuilensis Unveils Differences in Phosphorus Acquisition Strategies and Their Regulation. Frontiers in Microbiology, 2016, 7, 58. | 1.5 | 17 |
| 817 | Multiple ESBL-Producing Escherichia coli Sequence Types Carrying Quinolone and Aminoglycoside Resistance Genes Circulating in Companion and Domestic Farm Animals in Mwanza, Tanzania, Harbor Commonly Occurring Plasmids. Frontiers in Microbiology, 2016, 7, 142. | 1.5 | 63 |
| 818 | Genetic Evidence for O-Specific Antigen as Receptor of Pseudomonas aeruginosa Phage K8 and Its Genomic Analysis. Frontiers in Microbiology, 2016, 7, 252. | 1.5 | 22 |
| 819 | Genomic Insights into a New Citrobacter koseri Strain Revealed Gene Exchanges with the Virulence-Associated Yersinia pestis pPCP1 Plasmid. Frontiers in Microbiology, 2016, 7, 340. | 1.5 | 13 |
| 820 | Integrating DNA Methylation and Gene Expression Data in the Development of the Soybean-Bradyrhizobium N2-Fixing Symbiosis. Frontiers in Microbiology, 2016, 7, 518. | 1.5 | 32 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 822 | Genome and Transcriptome Sequences Reveal the Specific Parasitism of the Nematophagous Purpureocillium lilacinum 36-1. Frontiers in Microbiology, 2016, 7, 1084. | 1.5 | 33 |
| 823 | Identification of Novel Genomic Islands in Liverpool Epidemic Strain of Pseudomonas aeruginosa Using Segmentation and Clustering. Frontiers in Microbiology, 2016, 7, 1210. | 1.5 | 57 |
| 824 | Production of the Bioactive Compounds Violacein and Indolmycin Is Conditional in a maeA Mutant of Pseudoalteromonas luteoviolacea S4054 Lacking the Malic Enzyme. Frontiers in Microbiology, 2016, 7, 1461. | 1.5 | 18 |
| 825 | Co-diversification of Enterococcus faecium Core Genomes and PBP5: Evidences of pbp5 Horizontal Transfer. Frontiers in Microbiology, 2016, 7, 1581. | 1.5 | 34 |
| 826 | Comparative Functional Genomic Analysis of Two Vibrio Phages Reveals Complex Metabolic Interactions with the Host Cell. Frontiers in Microbiology, 2016, 7, 1807. | 1.5 | 16 |
| 827 | Intraclonal Genome Stability of the Metallo-Î²-lactamase SPM-1-producing Pseudomonas aeruginosa ST277, an Endemic Clone Disseminated in Brazilian Hospitals. Frontiers in Microbiology, 2016, 7, 1946. | 1.5 | 37 |
| 828 | Comparative Genomic Analysis of Two Serotype 1/2b Listeria monocytogenes Isolates from Analogous Environmental Niches Demonstrates the Influence of Hypervariable Hotspots in Defining Pathogenesis. Frontiers in Nutrition, 2016, 3, 54. | 1.6 | 4 |
| 829 | Comparative Analysis of the Chloroplast Genomic Information of Cunninghamia lanceolata (Lamb.) Hook with Sibling Species from the Genera Cryptomeria D. Don, Taiwania Hayata, and Calocedrus Kurz. International Journal of Molecular Sciences, 2016, 17, 1084. | 1.8 | 23 |
| 830 | H-NS Facilitates Sequence Diversification of Horizontally Transferred DNAs during Their Integration in Host Chromosomes. PLoS Genetics, 2016, 12, e1005796. | 1.5 | 25 |
| 831 | Comparative Genome Analysis Provides Insights into the Pathogenicity of Flavobacterium psychrophilum. PLoS ONE, 2016, 11, e0152515. | 1.1 | 41 |
| 832 | Mutation-Driven Divergence and Convergence Indicate Adaptive Evolution of the Intracellular Human-Restricted Pathogen, Bartonella bacilliformis. PLoS Neglected Tropical Diseases, 2016, 10, e0004712. | 1.3 | 19 |
| 833 | Molecular and Genomic Characterization of Vibrio mimicus Isolated from a Frozen Shrimp Processing Facility in Mexico. PLoS ONE, 2016, 11, e0144885. | 1.1 | 13 |
| 834 | The Formulation of Bacteriophage in a Semi Solid Preparation for Control of Propionibacterium acnes Growth. PLoS ONE, 2016, 11, e0151184. | 1.1 | 49 |
| 835 | De Novo Assembly of Human Herpes Virus Type 1 (HHV-1) Genome, Mining of Non-Canonical Structures and Detection of Novel Drug-Resistance Mutations Using Short- and Long-Read Next Generation Sequencing Technologies. PLoS ONE, 2016, 11, e0157600. | 1.1 | 43 |
| 836 | A Cytolethal Distending Toxin Variant from Aggregatibacter actinomycetemcomitans with an Aberrant CdtB That Lacks the Conserved Catalytic Histidine 160. PLoS ONE, 2016, 11, e0159231. | 1.1 | 5 |
| 837 | The Complete Chloroplast Genome Sequence of a Relict Conifer Glyptostrobus pensilis: Comparative Analysis and Insights into Dynamics of Chloroplast Genome Rearrangement in Cupressophytes and Pinaceae. PLoS ONE, 2016, 11, e0161809. | 1.1 | 26 |
| 838 | Comparative Genomic and Phenotypic Characterization of Pathogenic and Non-Pathogenic Strains of Xanthomonas arboricola Reveals Insights into the Infection Process of Bacterial Spot Disease of Stone Fruits. PLoS ONE, 2016, 11, e0161977. | 1.1 | 31 |
| 839 | In-silico prediction and deep-DNA sequencing validation indicate phase variation in 115 Neisseria meningitidis genes. BMC Genomics, 2016, 17, 843. | 1.2 | 22 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 840 | RNA-seq of Ranunculus sceleratus and Identification of Orthologous Genes among Four Ranunculus Species. Frontiers in Plant Science, 2016, 7, 732. | 1.7 | 5 |
| 841 | Chloroplast Genome Sequence of Pigeonpea (Cajanus cajan (L.) Millspaugh) and Cajanus scarabaeoides (L.) Thouars: Genome Organization and Comparison with Other Legumes. Frontiers in Plant Science, 2016, 7, 1847. | 1.7 | 34 |
| 842 | Comparative structural analysis of Bru1 region homeologs in Saccharum spontaneum and S. officinarum. BMC Genomics, 2016, 17, 446. | 1.2 | 8 |
| 843 | Population genomics of the symbiotic plasmids of sympatric nitrogenâ€fixing <i>Rhizobium</i> species associated with <i>Phaseolus vulgaris</i>. Environmental Microbiology, 2016, 18, 2660-2676. | 1.8 | 72 |
| 844 | <i>mcr-1.2</i> , a New <i>mcr</i> Variant Carried on a Transferable Plasmid from a Colistin-Resistant KPC Carbapenemase-Producing Klebsiella pneumoniae Strain of Sequence Type 512. Antimicrobial Agents and Chemotherapy, 2016, 60, 5612-5615. | 1.4 | 165 |
| 845 | Yersinia enterocolitica-Specific Infection by Bacteriophages TG1 and Ï•R1-RT Is Dependent on Temperature-Regulated Expression of the Phage Host Receptor OmpF. Applied and Environmental Microbiology, 2016, 82, 5340-5353. | 1.4 | 44 |
| 846 | Identification of Polymorphisms Associated with Drought Adaptation QTL in <i>Brassica napus</i> by Resequencing. G3: Genes, Genomes, Genetics, 2016, 6, 793-803. | 0.8 | 39 |
| 847 | Complete Genome Sequence of Corynebacterium pseudotuberculosis Strain PA01, Isolated from Sheep in ParÃ¡, Brazil. Genome Announcements, 2016, 4, . | 0.8 | 4 |
| 848 | Temperate phages promote colicinâ€dependent fitness of <scp><i>S</i></scp><i>almonella enterica</i> serovar <scp>T</scp>yphimurium. Environmental Microbiology, 2016, 18, 1591-1603. | 1.8 | 35 |
| 849 | Inflated organelle genomes and a circular-mapping mtDNA probably existed at the origin of coloniality in volvocine green algae. European Journal of Phycology, 2016, 51, 369-377. | 0.9 | 20 |
| 850 | <i>Saccharomyces eubayanus</i> and <i>Saccharomyces arboricola</i> reside in North Island native New Zealand forests. Environmental Microbiology, 2016, 18, 1137-1147. | 1.8 | 64 |
| 851 | Characterization of a novel Achromobacter xylosoxidans specific siphoviruse: phiAxp-1. Scientific Reports, 2016, 6, 21943. | 1.6 | 19 |
| 852 | Whole Genome Comparison of <i>Thermus</i> sp. NMX2.A1 Reveals Principal Carbon Metabolism Differences with Closest Relation <i>Thermus scotoductus</i> SA-01. G3: Genes, Genomes, Genetics, 2016, 6, 2791-2797. | 0.8 | 5 |
| 853 | Draft Genome Sequence of Biocontrol Agent Bacillus cereus UW85. Genome Announcements, 2016, 4, . | 0.8 | 19 |
| 854 | Chlamydia trachomatis from Australian Aboriginal people with trachoma are polyphyletic composed of multiple distinctive lineages. Nature Communications, 2016, 7, 10688. | 5.8 | 42 |
| 855 | Whole-Genome Sequencing Applied to the Molecular Epidemiology of Shiga Toxin-Producing Escherichia coli O157:H7 in Argentina. Genome Announcements, 2016, 4, . | 0.8 | 5 |
| 856 | Homologous Recombination within Large Chromosomal Regions Facilitates Acquisition of Î²-Lactam and Vancomycin Resistance in Enterococcus faecium. Antimicrobial Agents and Chemotherapy, 2016, 60, 5777-5786. | 1.4 | 31 |
| 857 | Salmonella Degrades the Host Glycocalyx Leading to Altered Infection and Glycan Remodeling. Scientific Reports, 2016, 6, 29525. | 1.6 | 66 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 858 | Changes in pathogenicity and immunogenicity of Mycoplasma mycoides subsp. mycoides strains revealed by comparative genomics analysis. Scientific Reports, 2016, 6, 19081. | 1.6 | 5 |
| 859 | An account of Genomic Islands of zoonotic origin Staphylococcus aureus genomes â€" In silico approach. , 2016, , . | | 0 |
| 860 | Genomic analysis of nontypeable pneumococci causing invasive pneumococcal disease in South Africa, 2003â€"2013. BMC Genomics, 2016, 17, 470. | 1.2 | 15 |
| 861 | Genome-wide analysis of chromosomal import patterns after natural transformation of Helicobacter pylori. Nature Communications, 2016, 7, 11995. | 5.8 | 59 |
| 862 | Delta-proteobacterial SAR324 group in hydrothermal plumes on the South Mid-Atlantic Ridge. Scientific Reports, 2016, 6, 22842. | 1.6 | 21 |
| 863 | MTGIpick allows robust identification of genomic islands from a single genome. Briefings in Bioinformatics, 2016, 19, bbw118. | 3.2 | 34 |
| 864 | Comparative genomics of mitochondria in chlorarachniophyte algae: endosymbiotic gene transfer and organellar genome dynamics. Scientific Reports, 2016, 6, 21016. | 1.6 | 23 |
| 865 | Complete Genome Sequence of a <i>Bohle iridovirus</i> Isolate from Ornate Burrowing Frogs () Tj ETQq1 1 0.784314 rgBT /Overlock | 0.8 | 12 |
| 866 | (Meta)genomic insights into the pathogenome of Cellulosimicrobium cellulans. Scientific Reports, 2016, 6, 25527. | 1.6 | 20 |
| 867 | Use of single molecule sequencing for comparative genomics of an environmental and a clinical isolate of Clostridium difficile ribotype 078. BMC Genomics, 2016, 17, 1020. | 1.2 | 11 |
| 868 | Genomic diversity of bacteriophages infecting the fish pathogen<i>Flavobacterium psychrophilum</i>. FEMS Microbiology Letters, 2016, 363, fnw272. | 0.7 | 29 |
| 869 | Comparative genomics reveals Lysinibacillus sphaericus group comprises a novel species. BMC Genomics, 2016, 17, 709. | 1.2 | 18 |
| 870 | Draft Genome Sequences of Five Clinical Strains of Brucella melitensis Isolated from Patients Residing in Kuwait. Genome Announcements, 2016, 4, . | 0.8 | 7 |
| 871 | Structural and functional organization of the plasmid regulons of Rhizobium leguminosarum symbiotic genes. Microbiology, 2016, 85, 708-716. | 0.5 | 2 |
| 872 | Complete Genome Sequence of a New Megavirus Family Member Isolated from an Inland Water Lake for the First Time in India. Genome Announcements, 2016, 4, . | 0.8 | 9 |
| 873 | Draft genome sequence of Psychrobacter sp. ENNN9_III, a strain isolated from water in a polluted temperate estuarine system ( Ria de Aveiro , Portugal). Genomics Data, 2016, 8, 21-24. | 1.3 | 0 |
| 874 | High-quality genome sequence and description of Chryseobacterium senegalense sp. nov.. New Microbes and New Infections, 2016, 10, 93-100. | 0.8 | 4 |
| 875 | Noncontiguous finished genome sequence and description of Planococcus massiliensis sp. nov., a moderately halophilic bacterium isolated from the human gut. New Microbes and New Infections, 2016, 10, 36-46. | 0.8 | 14 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 876 | Complete genome sequence of â€˜Halanaeroarchaeum sulfurireducensâ€™ M27-SA2, a sulfur-reducing and acetate-oxidizing haloarchaeon from the deep-sea hypersaline anoxic lake Medee. Standards in Genomic Sciences, 2016, 11, 35. | 1.5 | 15 |
| 877 | The genome and genetics of a high oxidative stress tolerant Serratia sp. LCN16 isolated from the plant parasitic nematode Bursaphelenchus xylophilus. BMC Genomics, 2016, 17, 301. | 1.2 | 18 |
| 878 | Geographic isolates of Lymantria dispar multiple nucleopolyhedrovirus: Genome sequence analysis and pathogenicity against European and Asian gypsy moth strains. Journal of Invertebrate Pathology, 2016, 137, 10-22. | 1.5 | 19 |
| 879 | <i>In Vivo</i> Application of Bacteriophage as a Potential Therapeutic Agent To Control OXA-66-Like Carbapenemase-Producing Acinetobacter baumannii Strains Belonging to Sequence Type 357. Applied and Environmental Microbiology, 2016, 82, 4200-4208. | 1.4 | 49 |
| 880 | Gene and whole genome analyses reveal that the mycobacterial strain JS 623 is not a member of the species M ycobacterium smegmatis. Microbial Biotechnology, 2016, 9, 269-274. | 2.0 | 2 |
| 881 | Characterisation of worldwide <i>Helicobacter pylori</i> strains reveals genetic conservation and essentiality of serine protease HtrA. Molecular Microbiology, 2016, 99, 925-944. | 1.2 | 70 |
| 882 | PacBio SMRT assembly of a complex multi-replicon genome reveals chlorocatechol degradative operon in a region of genome plasticity. Gene, 2016, 586, 239-247. | 1.0 | 22 |
| 883 | Risungbinella massiliensis sp. nov., a new member of Thermoactinomycetaceae isolated from human gut. Antonie Van Leeuwenhoek, 2016, 109, 773-784. | 0.7 | 8 |
| 884 | Complete Genome Sequence of Bacillus subtilis Strain CU1050, Which Is Sensitive to Phage SPÎ². Genome Announcements, 2016, 4, . | 0.8 | 6 |
| 885 | Enhancing the Sweetness of Yoghurt through Metabolic Remodeling of Carbohydrate Metabolism in Streptococcus thermophilus and Lactobacillus delbrueckii subsp. bulgaricus. Applied and Environmental Microbiology, 2016, 82, 3683-3692. | 1.4 | 61 |
| 886 | Mechanisms Involved in Acquisition of <i>bla</i> <sub>NDM</sub> Genes by IncA/C <sub>2</sub> and IncFII <sub>Y</sub> Plasmids. Antimicrobial Agents and Chemotherapy, 2016, 60, 4082-4088. | 1.4 | 49 |
| 887 | Non contiguous-finished genome sequence and description of Microbacterium gorillae sp. nov.. Standards in Genomic Sciences, 2016, 11, 32. | 1.5 | 24 |
| 888 | Improved Complete Genome Sequence of the Extremely Radioresistant Bacterium Deinococcus radiodurans R1 Obtained Using PacBio Single-Molecule Sequencing. Genome Announcements, 2016, 4, . | 0.8 | 26 |
| 889 | Genomic Comparison of Campylobacter spp. and Their Potential for Zoonotic Transmission between Birds, Primates, and Livestock. Applied and Environmental Microbiology, 2016, 82, 7165-7175. | 1.4 | 73 |
| 890 | A systematic study of the whole genome sequence of Amycolatopsis methanolica strain 239 T provides an insight into its physiological and taxonomic properties which correlate with its position in the genus. Synthetic and Systems Biotechnology, 2016, 1, 169-186. | 1.8 | 29 |
| 891 | Software-based analysis of bacteriophage genomes, physical ends, and packaging strategies. BMC Genomics, 2016, 17, 679. | 1.2 | 87 |
| 892 | Genomic diversification of marine cyanophages into stable ecotypes. Environmental Microbiology, 2016, 18, 4240-4253. | 1.8 | 44 |
| 893 | Complete genome sequence of Fictibacillus phosphorivorans G25-29, a strain toxic to nematodes. Journal of Biotechnology, 2016, 239, 20-22. | 1.9 | 8 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 894 | Characterization of <i>Pseudomonas aeruginosa</i> phage K5 genome and identification of its receptor related genes. Journal of Basic Microbiology, 2016, 56, 1344-1353. | 1.8 | 12 |
| 895 | An alphabaculovirus isolated from dead Lymantria dispar larvae shows high genetic similarity to baculovirus previously isolated from Lymantria monacha â€“ An example of adaptation to a new host. Journal of Invertebrate Pathology, 2016, 139, 56-66. | 1.5 | 11 |
| 896 | Comparative genomic evidence for duplication of TLR1 subfamily and miiuy croaker TLR1 perceives LPS stimulation via MyD88 and TIRAP. Fish and Shellfish Immunology, 2016, 56, 336-348. | 1.6 | 39 |
| 897 | Evidence for an Opportunistic and Endophytic Lifestyle of the Bursaphelenchus xylophilus-Associated Bacteria Serratia marcescens PWN146 Isolated from Wilting Pinus pinaster. Microbial Ecology, 2016, 72, 669-681. | 1.4 | 22 |
| 898 | Vibrio natriegens as a fast-growing host for molecular biology. Nature Methods, 2016, 13, 849-851. | 9.0 | 203 |
| 899 | CRISPR Diversity and Microevolution in<i>Clostridium difficile</i>. Genome Biology and Evolution, 2016, 8, 2841-2855. | 1.1 | 60 |
| 900 | Characterisation of a novel integrative and conjugative element ICESsD9 carrying erm(B) and tet(O) resistance determinants in Streptococcus suis, and the distribution of ICESsD9-like elements in clinical isolates. Journal of Global Antimicrobial Resistance, 2016, 7, 13-18. | 0.9 | 17 |
| 901 | Genome-wide analyses of chitin synthases identify horizontal gene transfers towards bacteria and allow a robust and unifying classification into fungi. BMC Evolutionary Biology, 2016, 16, 252. | 3.2 | 43 |
| 902 | Genome Sequence of a Ranavirus Isolated from Pike-Perch <i>Sander lucioperca</i>. Genome Announcements, 2016, 4, . | 0.8 | 11 |
| 903 | Speciation driven by hybridization and chromosomal plasticity in a wild yeast. Nature Microbiology, 2016, 1, 15003. | 5.9 | 161 |
| 904 | Patient-Specific <i>Bacteroides</i> Genome Variants in Pouchitis. MBio, 2016, 7, . | 1.8 | 38 |
| 905 | Comparative genomics of European avian pathogenic E. Coli (APEC). BMC Genomics, 2016, 17, 960. | 1.2 | 84 |
| 906 | Ancestral Gene Flow and Parallel Organellar Genome Capture Result in Extreme Phylogenomic Discord in a Lineage of Angiosperms. Systematic Biology, 2017, 66, syw083. | 2.7 | 132 |
| 907 | MSAViewer: interactive JavaScript visualization of multiple sequence alignments. Bioinformatics, 2016, 32, 3501-3503. | 1.8 | 156 |
| 908 | Isolation and complete genome sequencing of Mimivirus bombay , a Giant Virus in sewage of Mumbai, India. Genomics Data, 2016, 9, 1-3. | 1.3 | 16 |
| 909 | Genome-sequence analysis of Acinetobacter johnsonii MB44 reveals potential nematode-virulent factors. SpringerPlus, 2016, 5, 986. | 1.2 | 15 |
| 910 | Comparison of a Modern and FossilPithovirusReveals Its Genetic Conservation and Evolution. Genome Biology and Evolution, 2016, 8, 2333-2339. | 1.1 | 53 |
| 911 | Tessaracoccus massiliensis sp. nov., a new bacterial species isolated from the human gut. New Microbes and New Infections, 2016, 13, 3-12. | 0.8 | 8 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 912 | Complete Genome Sequence of <i>Moraxella osloensis</i> Strain KMC41, a Producer of 4-Methyl-3-Hexenoic Acid, a Major Malodor Compound in Laundry. Genome Announcements, 2016, 4, . | 0.8 | 8 |
| 913 | A genomic view of food-related and probiotic Enterococcus strains. DNA Research, 2017, 24, dsw043. | 1.5 | 38 |
| 914 | Genomic Sequence of a Ranavirus Isolated from Short-Finned Eel ( <i>Anguilla australis</i> ). Genome Announcements, 2016, 4, . | 0.8 | 10 |
| 915 | Whole genome sequencing revealed host adaptation-focused genomic plasticity of pathogenic Leptospira. Scientific Reports, 2016, 6, 20020. | 1.6 | 86 |
| 916 | Phenotypic differentiation of Streptococcus pyogenes populations is induced by recombination-driven gene-specific sweeps. Scientific Reports, 2016, 6, 36644. | 1.6 | 24 |
| 917 | Parallel evolution of highly conserved plastid genome architecture in red seaweeds and seed plants. BMC Biology, 2016, 14, 75. | 1.7 | 72 |
| 918 | An assemblage of Frankia Cluster II strains from California contains the canonical nod genes and also the sulfotransferase gene nodH. BMC Genomics, 2016, 17, 796. | 1.2 | 97 |
| 919 | Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089. | 3.2 | 207 |
| 920 | Complete Genome Sequence of the Endophytic Biocontrol Strain Bacillus velezensis CC09. Genome Announcements, 2016, 4, . | 0.8 | 19 |
| 921 | Organization and characteristics of the major histocompatibility complex class II region in the Yangtze finless porpoise (Neophocaena asiaeorientalis asiaeorientalis). Scientific Reports, 2016, 6, 22471. | 1.6 | 35 |
| 922 | Quantum changes in<i>Helicobacter pylori</i>gene expression accompany host-adaptation. DNA Research, 2017, 24, dsw046. | 1.5 | 8 |
| 923 | Evidence for the sexual origin of heterokaryosis in arbuscular mycorrhizal fungi. Nature Microbiology, 2016, 1, 16033. | 5.9 | 137 |
| 924 | CRISPR System Acquisition and Evolution of an Obligate Intracellular<i>Chlamydia</i>-Related Bacterium. Genome Biology and Evolution, 2016, 8, 2376-2386. | 1.1 | 23 |
| 925 | European derived<i>Saccharomyces cerevisiae</i>colonisation of New Zealand vineyards aided by humans. FEMS Yeast Research, 2016, 16, fow091. | 1.1 | 29 |
| 926 | Identification and molecular characterization of bacteriophage phiAxp-2 of Achromobacter xylosoxidans. Scientific Reports, 2016, 6, 34300. | 1.6 | 14 |
| 927 | Genomic Evolution of Two Acinetobacter baumannii Clinical Strains from ST-2 Clones Isolated in 2000 and 2010 (ST-2_clon_2000 and ST-2_clon_2010). Genome Announcements, 2016, 4, . | 0.8 | 6 |
| 928 | Separate F-Type Plasmids Have Shaped the Evolution of the <i>H</i> 30 Subclone of Escherichia coli Sequence Type 131. MSphere, 2016, 1, . | 1.3 | 98 |
| 929 | Comparing three complete mitochondrial genomes of the moss genus Orthotrichum Hedw.. Mitochondrial DNA Part B: Resources, 2016, 1, 168-170. | 0.2 | 8 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 930 | Genomic Sequencing of Ranaviruses Isolated from Turbot (Scophthalmus maximus) and Atlantic Cod () Tj ETQq0 0 0 rgBT /Overlock 10 T | 0.8 | 6 |
| 931 | Reclassification of the taxonomic status of SEMIA3007 isolated in Mexico B-11A Mex as Rhizobium leguminosarum bv. viceae by bioinformatic tools. BMC Microbiology, 2016, 16, 260. | 1.3 | 5 |
| 932 | Draft Genome Sequence of 11399, a Transformable Citrus-Pathogenic Strain of Xylella fastidiosa. Genome Announcements, 2016, 4, . | 0.8 | 12 |
| 933 | SIMBA: a web tool for managing bacterial genome assembly generated by Ion PGM sequencing technology. BMC Bioinformatics, 2016, 17, 456. | 1.2 | 8 |
| 934 | Genomic insights from whole genome sequencing of four clonal outbreak Campylobacter jejuni assessed within the global C. jejuni population. BMC Genomics, 2016, 17, 990. | 1.2 | 28 |
| 935 | Comparative genomics analyses revealed two virulent Listeria monocytogenes strains isolated from ready-to-eat food. Gut Pathogens, 2016, 8, 65. | 1.6 | 15 |
| 936 | Whole-genome sequencing and comparative genomic analysis of Escherichia coli O91 strains isolated from symptomatic and asymptomatic human carriers. Gut Pathogens, 2016, 8, 57. | 1.6 | 2 |
| 937 | Genome sequence of a commensal bacterium, Enterococcus faecalis CBA7120, isolated from a Korean fecal sample. Gut Pathogens, 2016, 8, 62. | 1.6 | 9 |
| 938 | Complete genome sequence of Methanoculleus bourgensis strain MAB1, the syntrophic partner of mesophilic acetate-oxidising bacteria (SAOB). Standards in Genomic Sciences, 2016, 11, 80. | 1.5 | 44 |
| 939 | Mitogenome of the extinct helmeted musk ox, Bootherium bombifrons. Mitochondrial DNA Part B: Resources, 2016, 1, 862-863. | 0.2 | 3 |
| 940 | The complete chloroplast genome of <i>Gracilariopsis lemaneiformis</i> (Rhodophyta) gives new insight into the evolution of family Gracilariaceae. Journal of Phycology, 2016, 52, 441-450. | 1.0 | 43 |
| 941 | Draft Genome of Shewanella frigidimarina Ag06-30, a Marine Bacterium Isolated from Potter Peninsula, King George Island, Antarctica. Genome Announcements, 2016, 4, . | 0.8 | 1 |
| 942 | Draft Genome Sequence of White Spot Syndrome Virus Isolated from Cultured <i>Litopenaeus vannamei</i> in Mexico. Genome Announcements, 2016, 4, . | 0.8 | 20 |
| 943 | Influence of Host Ecology and Behavior on Campylobacter jejuni Prevalence and Environmental Contamination Risk in a Synanthropic Wild Bird Species. Applied and Environmental Microbiology, 2016, 82, 4811-4820. | 1.4 | 33 |
| 944 | The plasmid-mediated evolution of the mycobacterial ESX (Type VII) secretion systems. BMC Evolutionary Biology, 2016, 16, 62. | 3.2 | 61 |
| 945 | High-quality draft genome sequence and description of Haemophilus massiliensis sp. nov.. Standards in Genomic Sciences, 2016, 11, 31. | 1.5 | 47 |
| 946 | Complete genome sequence and genomic characterization of Microcystis panniformis FACHB 1757 by third-generation sequencing. Standards in Genomic Sciences, 2016, 11, 11. | 1.5 | 19 |
| 947 | Synteny Portal: a web-based application portal for synteny block analysis. Nucleic Acids Research, 2016, 44, W35-W40. | 6.5 | 42 |

| # | Article | IF | Citations |
|---|---|---|---|
| 948 | Resilience of microbial communities in a simulated drinking water distribution system subjected to disturbances: role of conditionally rare taxa and potential implications for antibiotic-resistant bacteria. Environmental Science: Water Research and Technology, 2016, 2, 645-657. | 1.2 | 48 |
| 949 | Genomic and Phenotypic Analyses Reveal the Emergence of an Atypical Salmonella enterica Serovar Senftenberg Variant in China. Journal of Clinical Microbiology, 2016, 54, 2014-2022. | 1.8 | 14 |
| 950 | Circulation of clonal populations of fluoroquinolone-resistant CTX-M-15-producing Escherichia coli ST410 in humans and animals in Germany. International Journal of Antimicrobial Agents, 2016, 47, 457-465. | 1.1 | 107 |
| 951 | High-quality genome sequence and description of Paenibacillus dakarensis sp. nov.. New Microbes and New Infections, 2016, 10, 132-141. | 0.8 | 10 |
| 952 | The gene cortex controls mimicry and crypsis in butterflies and moths. Nature, 2016, 534, 106-110. | 13.7 | 212 |
| 953 | Noncontiguous finished genome sequence and description of Gabonia massiliensis gen. nov., sp. nov.. New Microbes and New Infections, 2016, 9, 35-44. | 0.8 | 11 |
| 954 | Genome sequence and description of Anaerosalibacter massiliensis sp. nov.. New Microbes and New Infections, 2016, 10, 66-76. | 0.8 | 125 |
| 955 | Noncontiguous finished genome sequence and description of Nocardioides massiliensis sp. nov. GD13T. New Microbes and New Infections, 2016, 10, 47-57. | 0.8 | 6 |
| 956 | Computational methods for predicting genomic islands in microbial genomes. Computational and Structural Biotechnology Journal, 2016, 14, 200-206. | 1.9 | 54 |
| 957 | The complete chloroplast genome sequence of Abies nephrolepis (Pinaceae: Abietoideae). Journal of Asia-Pacific Biodiversity, 2016, 9, 245-249. | 0.2 | 16 |
| 958 | A predicted T4 secretion system and conserved DNA-repeats identified in a subset of related Arthrobacter plasmids. Microbiological Research, 2016, 191, 32-37. | 2.5 | 18 |
| 959 | Noncontiguous finished genome sequence and description of Kallipyga gabonensis sp. nov.. New Microbes and New Infections, 2016, 9, 15-23. | 0.8 | 7 |
| 960 | Non-contiguous finished genome sequence and description of Streptococcus varani sp. nov.. New Microbes and New Infections, 2016, 11, 93-102. | 0.8 | 1 |
| 961 | A novel strain of cynomolgus macaque cytomegalovirus: implications for host-virus co-evolution. BMC Genomics, 2016, 17, 277. | 1.2 | 11 |
| 962 | Whole-genome optical mapping reveals a mis-assembly between two rRNA operons of Corynebacterium pseudotuberculosis strain 1002. BMC Genomics, 2016, 17, 315. | 1.2 | 17 |
| 963 | Draft genome sequence of non-shiga toxin-producing Escherichia coli O157 NCCP15738. Gut Pathogens, 2016, 8, 13. | 1.6 | 4 |
| 964 | Draft genome sequence for virulent and avirulent strains of Xanthomonas arboricola isolated from Prunus spp. in Spain. Standards in Genomic Sciences, 2016, 11, 12. | 1.5 | 16 |
| 965 | Birth of Four Chimeric Plastid Gene Clusters in Japanese Umbrella Pine. Genome Biology and Evolution, 2016, 8, 1776-1784. | 1.1 | 46 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 966 | The chloroplast genome of <i>Phacus orbicularis</i> (Euglenophyceae): an initial datum point for the phacaceae. Journal of Phycology, 2016, 52, 404-411. | 1.0 | 12 |
| 967 | Draft Genome Sequence of Vancomycin-Susceptible, Ampicillin-Intermediate Enterococcus faecium Strain D344RRF. Genome Announcements, 2016, 4, . | 0.8 | 2 |
| 968 | Evolution of Nine Microsatellite Loci in the Fungus Fusarium oxysporum. Journal of Molecular Evolution, 2016, 82, 27-37. | 0.8 | 3 |
| 969 | Identifying Potential Mechanisms Enabling Acidophily in the Ammonia-Oxidizing Archaeon â€œCandidatus Nitrosotalea devanaterraâ€. Applied and Environmental Microbiology, 2016, 82, 2608-2619. | 1.4 | 117 |
| 970 | Genome analysis of Listeria ivanovii strain G770 that caused a deadly aortic prosthesis infection. New Microbes and New Infections, 2016, 10, 87-92. | 0.8 | 20 |
| 971 | Comparative Genomic Analyses of the<i>Moraxella catarrhalis</i>Serosensitive and Seroresistant Lineages Demonstrate Their Independent Evolution. Genome Biology and Evolution, 2016, 8, 955-974. | 1.1 | 20 |
| 972 | Complete chloroplast genome sequences of Eucommia ulmoides: genome structure and evolution. Tree Genetics and Genomes, 2016, 12, 1. | 0.6 | 53 |
| 973 | Genomic characterization of Pasteurella multocida HB01, a serotype A bovine isolate from China. Gene, 2016, 581, 85-93. | 1.0 | 36 |
| 974 | Comparative genome analyses of novel Mangrovimonas-like strains isolated from estuarine mangrove sediments reveal xylan and arabinan utilization genes. Marine Genomics, 2016, 25, 115-121. | 0.4 | 12 |
| 975 | Complete Genome Sequence of Nonhemolytic Streptococcus agalactiae Serotype V Strain 1, Isolated from the Buccal Cavity of a Canine. Genome Announcements, 2016, 4, . | 0.8 | 1 |
| 976 | The genome of an Encephalitozoon cuniculi type III strain reveals insights into the genetic diversity and mode of reproduction of a ubiquitous vertebrate pathogen. Heredity, 2016, 116, 458-465. | 1.2 | 16 |
| 977 | Analysis of the role of the LH92_11085 gene of a biofilm hyper-producing<i>Acinetobacter baumannii</i>strain on biofilm formation and attachment to eukaryotic cells. Virulence, 2016, 7, 443-455. | 1.8 | 52 |
| 978 | A novel chimeric prophage vB_LdeS-phiJB from commercial <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i>. Journal of Industrial Microbiology and Biotechnology, 2016, 43, 681-689. | 1.4 | 11 |
| 979 | Characterization of the temperate phage vB_RleM_PPF1 and its site-specific integration into the Rhizobium leguminosarum F1 genome. Molecular Genetics and Genomics, 2016, 291, 349-362. | 1.0 | 7 |
| 980 | A Combinatorial Kin Discrimination System in Bacillus subtilis. Current Biology, 2016, 26, 733-742. | 1.8 | 103 |
| 981 | Rapid Emergence and Evolution of Staphylococcus aureus Clones Harboring <i>fusC</i> -Containing Staphylococcal Cassette Chromosome Elements. Antimicrobial Agents and Chemotherapy, 2016, 60, 2359-2365. | 1.4 | 41 |
| 982 | Draft Genome Sequence of <i>Acinetobacter bereziniae</i> HPC229, a Carbapenem-Resistant Clinical Strain from Argentina Harboring <i>bla</i> <sub>NDM-1</sub>. Genome Announcements, 2016, 4, . | 0.8 | 9 |
| 983 | On Identifying Minimal Absent and Unique Words: An Efficient Scheme. Cognitive Computation, 2016, 8, 603-613. | 3.6 | 2 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 984 | The<i>Mycobacterium phlei</i>genome: expectations and surprises. Genome Biology and Evolution, 2016, 8, evw049. | 1.1 | 11 |
| 985 | High-quality genome sequencing and description of Dermabacter indicis sp. nov.. New Microbes and New Infections, 2016, 11, 59-67. | 0.8 | 6 |
| 986 | Intraspecies Transfer of the Chromosomal Acinetobacter baumannii <i>bla</i> <sub>NDM-1</sub> Carbapenemase Gene. Antimicrobial Agents and Chemotherapy, 2016, 60, 3032-3040. | 1.4 | 65 |
| 987 | Comparative genomic study of three species within the genus Ornithinibacillus, reflecting the adaption to different habitats. Gene, 2016, 578, 25-31. | 1.0 | 6 |
| 988 | Infraspecific variation within and across complete organellar genomes and nuclear ribosomal repeats in a moss. Molecular Phylogenetics and Evolution, 2016, 96, 195-199. | 1.2 | 13 |
| 989 | Evidence for the critical role of a secondary site<i>rpoB</i>mutation in the compensatory evolution and successful transmission of an MDR tuberculosis outbreak strain. Journal of Antimicrobial Chemotherapy, 2016, 71, 324-332. | 1.3 | 33 |
| 990 | Degradation of Benzene by Pseudomonas veronii 1YdBTEX2 and 1YB2 Is Catalyzed by Enzymes Encoded in Distinct Catabolism Gene Clusters. Applied and Environmental Microbiology, 2016, 82, 167-173. | 1.4 | 18 |
| 991 | Comparative mitochondrial genome analysis of Pythium insidiosum and related oomycete species provides new insights into genetic variation and phylogenetic relationships. Gene, 2016, 575, 34-41. | 1.0 | 11 |
| 992 | Microbial bioinformatics for food safety and production. Briefings in Bioinformatics, 2016, 17, 283-292. | 3.2 | 53 |
| 993 | The chloroplast genome of the marine green macroalga <i>Ulva fasciata</i> Delile (Ulvophyceae,) Tj ETQq1 1 0.784314 rgBT /Overloc | 0.7 | 9 |
| 994 | The Chloroplast Genome of <i>Euglena mutabilis</i>â€"Cluster Arrangement, Intron Analysis, and Intrageneric Trends. Journal of Eukaryotic Microbiology, 2017, 64, 31-44. | 0.8 | 13 |
| 995 | Population genomic insights into variation and evolution of Xanthomonas oryzae pv. oryzae. Scientific Reports, 2017, 7, 40694. | 1.6 | 45 |
| 996 | Adaptation of genetically monomorphic bacteria: evolution of copper resistance through multiple horizontal gene transfers of complex and versatile mobile genetic elements. Molecular Ecology, 2017, 26, 2131-2149. | 2.0 | 53 |
| 997 | Comparative genomic analysis of three white spot syndrome virus isolates of different virulence. Virus Genes, 2017, 53, 249-258. | 0.7 | 28 |
| 998 | Genomic and metabolic traits endow Bacillus velezensis CC09 with a potential biocontrol agent in control of wheat powdery mildew disease. Microbiological Research, 2017, 196, 89-94. | 2.5 | 80 |
| 999 | Rubeoparvulum massiliense gen. nov., sp. nov., a new bacterial genus isolated from the human gut of a Senegalese infant with severe acute malnutrition. New Microbes and New Infections, 2017, 15, 49-60. | 0.8 | 8 |
| 1000 | Genome sequencing and analysis of Kloeckera apiculata strain 34-9, a biocontrol agent against postharvest pathogens in citrus. Genes and Genomics, 2017, 39, 87-99. | 0.5 | 6 |
| 1001 | Paenibacillus phocaensis sp. nov., isolated from the gut microbiota of a healthy infant. New Microbes and New Infections, 2017, 16, 13-24. | 0.8 | 4 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1002 | A Clostridium difficile Lineage Endemic to Costa Rican Hospitals Is Multidrug Resistant by Acquisition of Chromosomal Mutations and Novel Mobile Genetic Elements. Antimicrobial Agents and Chemotherapy, 2017, 61, . | 1.4 | 32 |
| 1003 | Genomic analysis of a Streptococcus pyogenes strain causing endocarditis in a child. New Microbes and New Infections, 2017, 17, 1-6. | 0.8 | 2 |
| 1004 | Whole-Genome Sequences of Mycobacterium tuberculosis TB282 and TB284, a Widespread and a Unique Strain, Respectively, Identified in a Previous Study of Tuberculosis Transmission in Central Los Angeles, California, USA. Genome Announcements, 2017, 5, . | 0.8 | 0 |
| 1005 | Genome Sequencing of the Behavior Manipulating Virus LbFV Reveals a Possible New Virus Family. Genome Biology and Evolution, 2016, 8, 3718-3739. | 1.1 | 21 |
| 1006 | Complete-genome sequencing elucidates outbreak dynamics of CA-MRSA USA300 (ST8-spa t008) in an academic hospital of Paramaribo, Republic of Suriname. Scientific Reports, 2017, 7, 41050. | 1.6 | 33 |
| 1007 | Interaction of Cutibacterium (â€‰formerly Propionibacterium) acnes with bone cells: a step toward understanding bone and joint infection development. Scientific Reports, 2017, 7, 42918. | 1.6 | 42 |
| 1008 | A Natural Chimeric<i>Pseudomonas</i>Bacteriocin with Novel Pore-Forming Activity Parasitizes the Ferrichrome Transporter. MBio, 2017, 8, . | 1.8 | 24 |
| 1009 | Comparative genomics of Crohn's disease-associated adherent-invasive<i>Escherichia coli</i>. Gut, 2017, 66, 1382-1389. | 6.1 | 114 |
| 1010 | Genomic characterization of Ensifer aridi, a proposed new species of nitrogen-fixing rhizobium recovered from Asian, African and American deserts. BMC Genomics, 2017, 18, 85. | 1.2 | 34 |
| 1011 | Genome sequence of Methanobacterium congolense strain Buetzberg, a hydrogenotrophic, methanogenic archaeon, isolated from a mesophilic industrial-scale biogas plant utilizing bio-waste. Journal of Biotechnology, 2017, 247, 1-5. | 1.9 | 48 |
| 1012 | Complete Genome Sequence of Mycoplasma pneumoniae Type 2 Reference Strain FH Using Single-Molecule Real-Time Sequencing Technology. Genome Announcements, 2017, 5, . | 0.8 | 3 |
| 1013 | The Plastid Genome of <i>Polytoma uvella</i> Is the Largest Known among Colorless Algae and Plants and Reflects Contrasting Evolutionary Paths to Nonphotosynthetic Lifestyles. Plant Physiology, 2017, 173, 932-943. | 2.3 | 33 |
| 1014 | Shrimp AHPND-causing plasmids encoding the PirAB toxins as mediated by pirAB-Tn903 are prevalent in various Vibrio species. Scientific Reports, 2017, 7, 42177. | 1.6 | 106 |
| 1015 | Draft Genome Sequence of an Erythromycin-Resistant Propionibacterium acnes Isolate Recovered from Folliculitis of the Scalp. Genome Announcements, 2017, 5, . | 0.8 | 3 |
| 1016 | Escherichia coli sequence type 73 as a cause of community acquired urinary tract infection in men and women in Rio de Janeiro, Brazil. Diagnostic Microbiology and Infectious Disease, 2017, 88, 69-74. | 0.8 | 13 |
| 1017 | Draft Genome Sequence of the Tumor-Targeting Salmonella enterica Serovar Typhimurium Strain SL7207. Genome Announcements, 2017, 5, . | 0.8 | 8 |
| 1018 | Ecological and Evolutionary Insights into Xanthomonas citri Pathovar Diversity. Applied and Environmental Microbiology, 2017, 83, . | 1.4 | 41 |
| 1019 | Curious bivalves: Systematic utility and unusual properties of anomalodesmatan mitochondrial genomes. Molecular Phylogenetics and Evolution, 2017, 110, 60-72. | 1.2 | 24 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1020 | Sputum DNA sequencing in cystic fibrosis: non-invasive access to the lung microbiome and to pathogen details. Microbiome, 2017, 5, 20. | 4.9 | 100 |
| 1021 | Inediibacterium massiliense gen. nov., sp. nov., a new bacterial species isolated from the gut microbiota of a severely malnourished infant. Antonie Van Leeuwenhoek, 2017, 110, 737-750. | 0.7 | 12 |
| 1022 | Phylogenomic relationship of feijoa (Acca sellowiana (O.Berg) Burret) with other Myrtaceae based on complete chloroplast genome sequences. Genetica, 2017, 145, 163-174. | 0.5 | 27 |
| 1023 | Phylogenomics of Trypanosoma cruzi : Few evidence of TcI/TcII mosaicism in TcIII challenges the hypothesis of an ancient TcI/TcII hybridization. Infection, Genetics and Evolution, 2017, 50, 25-27. | 1.0 | 2 |
| 1024 | Comparative genome analysis reveals important genetic differences among serotype O1 and serotype O2 strains of <i>Y.Âruckeri</i> and provides insights into host adaptation and virulence. MicrobiologyOpen, 2017, 6, e00460. | 1.2 | 18 |
| 1025 | Draft Genome Sequence of Corynebacterium pseudotuberculosis Strain PA06 Isolated from a Subauricular Abscess in an Ovine Host. Genome Announcements, 2017, 5, . | 0.8 | 1 |
| 1026 | Structural and functional genomics analysis of methyltransferase genes and networks associate to understand antibiotic resistance inside the pangenome of Pseudomonas aeruginosa. IFMBE Proceedings, 2017, , 702-705. | 0.2 | 1 |
| 1027 | A Locus Encoding Variable Defense Systems against Invading DNA Identified in Streptococcus suis. Genome Biology and Evolution, 2017, 9, 1000-1012. | 1.1 | 17 |
| 1028 | A comparison of the adaptations of strains of Lymantria dispar multiple nucleopolyhedrovirus to hosts from spatially isolated populations. Journal of Invertebrate Pathology, 2017, 146, 41-46. | 1.5 | 12 |
| 1029 | Genome-Wide Abolishment of Mobile Genetic Elements Using Genome Shuffling and CRISPR/Cas-Assisted MAGE Allows the Efficient Stabilization of a Bacterial Chassis. ACS Synthetic Biology, 2017, 6, 1471-1483. | 1.9 | 55 |
| 1030 | Primates, Lice and Bacteria: Speciation and Genome Evolution in the Symbionts of Hominid Lice. Molecular Biology and Evolution, 2017, 34, 1743-1757. | 3.5 | 51 |
| 1031 | Horizontal transfer of chromosomal markers mediated by the large conjugative plasmid pXO16 from Bacillus thuringiensis serovar israelensis. Plasmid, 2017, 91, 76-81. | 0.4 | 12 |
| 1032 | Draft Genome Sequences of 18 Psychrotolerant and 2 Thermotolerant Strains Representative of Particular Ecotypes in the Bacillus cereus Group. Genome Announcements, 2017, 5, . | 0.8 | 4 |
| 1033 | Draft Genome Sequence of Mycobacterium ulcerans S4018 Isolated from a Patient with an Active Buruli Ulcer in Benin, Africa. Genome Announcements, 2017, 5, . | 0.8 | 4 |
| 1034 | Comparative Genome Analyses of <i>Vibrio anguillarum</i> Strains Reveal a Link with Pathogenicity Traits. MSystems, 2017, 2, . | 1.7 | 58 |
| 1035 | Comparative Genomics of the Ectomycorrhizal Sister Species <i>Rhizopogon vinicolor</i> and <i>Rhizopogon vesiculosus</i> (Basidiomycota: Boletales) Reveals a Divergence of the Mating Type <i>B</i> Locus. G3: Genes, Genomes, Genetics, 2017, 7, 1775-1789. | 0.8 | 17 |
| 1036 | Pelagic and benthic communities of the Antarctic ecosystem of Potter Cove: Genomics and ecological implications. Marine Genomics, 2017, 33, 1-11. | 0.4 | 23 |
| 1037 | Mitochondrial Recombination and Introgression during Speciation by Hybridization. Molecular Biology and Evolution, 2017, 34, 1947-1959. | 3.5 | 57 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1038 | Whole genome sequencing and functional features of UMX-103: a new Bacillus strain with biosurfactant producing capability. Genes and Genomics, 2017, 39, 877-886. | 0.5 | 2 |
| 1039 | Inactivation of Transcriptional Regulators during Within-Household Evolution of Escherichia coli. Journal of Bacteriology, 2017, 199, . | 1.0 | 10 |
| 1040 | Pacmanvirus, a New Giant Icosahedral Virus at the Crossroads between Asfarviridae and Faustoviruses. Journal of Virology, 2017, 91, . | 1.5 | 99 |
| 1041 | <i>Pseudomonas aeruginosa</i>adaptation and diversification in the non-cystic fibrosis bronchiectasis lung. European Respiratory Journal, 2017, 49, 1602108. | 3.1 | 75 |
| 1042 | The genome sequence of Agrotis segetum granulovirus, isolate AgseGV-DA, reveals a new Betabaculovirus species of a slow killing granulovirus. Journal of Invertebrate Pathology, 2017, 146, 58-68. | 1.5 | 6 |
| 1043 | Noncontiguous finished genome sequence and description of Streptococcus timonensis sp. nov. isolated from the human stomach. New Microbes and New Infections, 2017, 15, 77-88. | 0.8 | 7 |
| 1044 | Large-Scale Sequence Comparison. Methods in Molecular Biology, 2017, 1525, 191-224. | 0.4 | 3 |
| 1045 | Nanopore sequencing data analysis: state of the art, applications and challenges. Briefings in Bioinformatics, 2018, 19, 1256-1272. | 3.2 | 91 |
| 1046 | <i>Cedratvirus lausannensis</i> â€“ digging into <i>Pithoviridae</i> diversity. Environmental Microbiology, 2017, 19, 4022-4034. | 1.8 | 36 |
| 1047 | Loss of the <i>ssrA</i> genome island led to partial debromination in the PBDE respiring <i>Dehalococcoides mccartyi</i> strain GY50. Environmental Microbiology, 2017, 19, 2906-2915. | 1.8 | 27 |
| 1048 | Whole-Genome Sequence and Variant Analysis of W303, a Widely-Used Strain of <i>Saccharomyces cerevisiae</i>. G3: Genes, Genomes, Genetics, 2017, 7, 2219-2226. | 0.8 | 49 |
| 1049 | Comparative and functional genomics of the Lactococcus lactis taxon; insights into evolution and niche adaptation. BMC Genomics, 2017, 18, 267. | 1.2 | 117 |
| 1050 | Distinct Biological Potential of Streptococcus gordonii and Streptococcus sanguinis Revealed by Comparative Genome Analysis. Scientific Reports, 2017, 7, 2949. | 1.6 | 28 |
| 1051 | Single-virus genomics reveals hidden cosmopolitan and abundant viruses. Nature Communications, 2017, 8, 15892. | 5.8 | 165 |
| 1052 | Persistent Listeria monocytogenes strains isolated from mussel production facilities form more biofilm but are not linked to specific genetic markers. International Journal of Food Microbiology, 2017, 256, 45-53. | 2.1 | 50 |
| 1053 | Dataset of the transcribed 45S ribosomal RNA sequence of the tree crop â€œyerba mateâ€ Data in Brief, 2017, 12, 649-651. | 0.5 | 0 |
| 1054 | Whole-Genome Sequence of Corynebacterium pseudotuberculosis PA04, Isolated from the Lymph Node of a Sheep in the Amazon, Brazil. Genome Announcements, 2017, 5, . | 0.8 | 1 |
| 1055 | Complete Genome Sequence of an Aquaculture-Associated Phage, FL-1, Infecting Flavobacterium spp. Genome Announcements, 2017, 5, . | 0.8 | 1 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1056 | Draft Genome Sequence of Pseudomonas chlororaphis ATCC 9446, a Nonpathogenic Bacterium with Bioremediation and Industrial Potential. Genome Announcements, 2017, 5, . | 0.8 | 6 |
| 1057 | Comparative analyses of whole genome sequences of Leishmania infantum isolates from humans and dogs in northeastern Brazil. International Journal for Parasitology, 2017, 47, 655-665. | 1.3 | 32 |
| 1058 | A New Natural Product Analog of Blasticidin S Reveals Cellular Uptake Facilitated by the NorA Multidrug Transporter. Antimicrobial Agents and Chemotherapy, 2017, 61, . | 1.4 | 10 |
| 1059 | Emergence of a plasmid-borne multidrug resistance gene cfr(C) in foodborne pathogen Campylobacter. Journal of Antimicrobial Chemotherapy, 2017, 72, 1581-1588. | 1.3 | 80 |
| 1060 | Giant viruses with an expanded complement of translation system components. Science, 2017, 356, 82-85. | 6.0 | 234 |
| 1061 | Evolutionary Origin of the Staphylococcal Cassette Chromosome <i>mec</i> (SCC <i>mec</i> ). Antimicrobial Agents and Chemotherapy, 2017, 61, . | 1.4 | 64 |
| 1062 | Deep genomic analysis of the Chlorella sorokiniana SAG 211-8k chloroplast. European Journal of Phycology, 2017, 52, 320-329. | 0.9 | 3 |
| 1063 | Genome-wide analysis of a avirulent and reveal the strain induces pro-tective immunity against challenge with virulent Streptococcus suis Serotype 2. BMC Microbiology, 2017, 17, 67. | 1.3 | 7 |
| 1064 | Networking in microbes: conjugative elements and plasmids in the genus Alteromonas. BMC Genomics, 2017, 18, 36. | 1.2 | 39 |
| 1065 | Draft Genome Sequence of Bacillus licheniformis Strain YNP1-TSU Isolated from Whiterock Springs in Yellowstone National Park. Genome Announcements, 2017, 5, . | 0.8 | 5 |
| 1066 | Identification of Strain-Specific Sequences That Distinguish a Mycoplasma gallisepticum Vaccine Strain from Field Isolates. Journal of Clinical Microbiology, 2017, 55, 244-252. | 1.8 | 14 |
| 1067 | Insight into the Genome of Brochothrix thermosphacta, a Problematic Meat Spoilage Bacterium. Applied and Environmental Microbiology, 2017, 83, . | 1.4 | 61 |
| 1068 | Comparative analysis of chloroplast DNA sequences of Codonopsis lanceolata and Platycodon grandiflorus and application in development of molecular markers. Applied Biological Chemistry, 2017, 60, 23-31. | 0.7 | 2 |
| 1069 | Comparative genome analysis of multiple vancomycin-resistant Enterococcus faecium isolated from two fatal cases. Infection, Genetics and Evolution, 2017, 49, 55-65. | 1.0 | 3 |
| 1070 | Comparative genome analyses of Mycobacterium avium reveal genomic features of its subspecies and strains that cause progression of pulmonary disease. Scientific Reports, 2017, 7, 39750. | 1.6 | 62 |
| 1071 | Expansion of inverted repeat does not decrease substitution rates in <i>Pelargonium</i> plastid genomes. New Phytologist, 2017, 214, 842-851. | 3.5 | 99 |
| 1072 | Experimental pathogenicity and complete genome characterization of a pig origin Pasteurella multocida serogroup F isolate HN07. Veterinary Microbiology, 2017, 198, 23-33. | 0.8 | 30 |
| 1073 | Noncontiguous finished genome sequence and description of Fusobacterium massiliense sp. nov. isolated from human duodenum. New Microbes and New Infections, 2017, 16, 3-12. | 0.8 | 2 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1074 | Transition from heterothallism to homothallism is hypothesised to have facilitated speciation among emerging Botryosphaeriaceae wheat-pathogens. Fungal Genetics and Biology, 2017, 109, 36-45. | 0.9 | 8 |
| 1075 | Plasticity of the <i>MFS1</i> Promoter Leads to Multidrug Resistance in the Wheat Pathogen <i>Zymoseptoria tritici</i>. MSphere, 2017, 2, . | 1.3 | 75 |
| 1076 | Expression of a Peptidoglycan Hydrolase from Lytic Bacteriophages Atu_ph02 and Atu_ph03 Triggers Lysis of Agrobacterium tumefaciens. Applied and Environmental Microbiology, 2017, 83, . | 1.4 | 25 |
| 1077 | Comparative Phenotypic and Genotypic Analysis of Edwardsiella Isolates from Different Hosts and Geographic Origins, with Emphasis on Isolates Formerly Classified as E. tarda, and Evaluation of Diagnostic Methods. Journal of Clinical Microbiology, 2017, 55, 3466-3491. | 1.8 | 70 |
| 1078 | Comparative genomics of Lactobacillus kefiranofaciens ZW3 and related members of Lactobacillus. spp reveal adaptations to dairy and gut environments. Scientific Reports, 2017, 7, 12827. | 1.6 | 33 |
| 1079 | Genomic divergence within non-photosynthetic cyanobacterial endosymbionts in rhopalodiacean diatoms. Scientific Reports, 2017, 7, 13075. | 1.6 | 17 |
| 1080 | Genomic Sequencing of Ranaviruses Isolated from Edible Frogs ( Pelophylax esculentus ). Genome Announcements, 2017, 5, . | 0.8 | 4 |
| 1081 | Evolutionary Comparisons of the Chloroplast Genome in Lauraceae and Insights into Loss Events in the Magnoliids. Genome Biology and Evolution, 2017, 9, 2354-2364. | 1.1 | 70 |
| 1082 | Draft Genome Sequences of Seven Streptococcus agalactiae Strains Isolated from Camelus dromedarius at the Horn of Africa. Genome Announcements, 2017, 5, . | 0.8 | 8 |
| 1083 | Complete Genome Sequences of Three Xanthomonas citri Strains from Texas. Genome Announcements, 2017, 5, . | 0.8 | 7 |
| 1084 | Typing and comparative genome analysis of Brucella melitensis isolated from Lebanon. FEMS Microbiology Letters, 2017, 364, . | 0.7 | 11 |
| 1085 | Microbial taxonomy in the era of OMICS: application of DNA sequences, computational tools and techniques. Antonie Van Leeuwenhoek, 2017, 110, 1357-1371. | 0.7 | 54 |
| 1086 | Structure, proteome and genome of Sinorhizobium meliloti phage Î¦M5: A virus with LUZ24-like morphology and a highly mosaic genome. Journal of Structural Biology, 2017, 200, 343-359. | 1.3 | 17 |
| 1087 | Complete genome analysis of Lactobacillus fermentum SK152 from kimchi reveals genes associated with its antimicrobial activity. FEMS Microbiology Letters, 2017, 364, . | 0.7 | 20 |
| 1088 | Molecular epidemiology of Epizootic haematopoietic necrosis virus (EHNV). Virology, 2017, 511, 320-329. | 1.1 | 2 |
| 1089 | Environmental vibrios represent a source of antagonistic compounds that inhibit pathogenic <i>Vibrio cholerae</i> and <i>Vibrio parahaemolyticus</i> strains. MicrobiologyOpen, 2017, 6, e00504. | 1.2 | 9 |
| 1090 | A Serendipitous Mutation Reveals the Severe Virulence Defect of a Klebsiella pneumoniae <i>fepB</i> Mutant. MSphere, 2017, 2, . | 1.3 | 29 |
| 1091 | Comparative whole genome analysis of three consecutive Salmonella diarizonae isolates. International Journal of Medical Microbiology, 2017, 307, 542-551. | 1.5 | 10 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1092 | Colonic Spirochetes: What Has Genomics Taught Us?. Current Topics in Microbiology and Immunology, 2017, 415, 273-294. | 0.7 | 5 |
| 1093 | Ancestral acquisitions, gene flow and multiple evolutionary trajectories of the type three secretion system and effectors in <i>Xanthomonas</i> plant pathogens. Molecular Ecology, 2017, 26, 5939-5952. | 2.0 | 56 |
| 1094 | Comparative Genomic and Regulatory Analyses of Natamycin Production of Streptomyces lydicus A02. Scientific Reports, 2017, 7, 9114. | 1.6 | 20 |
| 1095 | Evolutionary Dynamics of Cryptophyte Plastid Genomes. Genome Biology and Evolution, 2017, 9, 1859-1872. | 1.1 | 51 |
| 1096 | Identification of the <i>hcb</i> Gene Operon Involved in Catalyzing Aerobic Hexachlorobenzene Dechlorination in Nocardioides sp. Strain PD653. Applied and Environmental Microbiology, 2017, 83, . | 1.4 | 16 |
| 1097 | Noncontiguous finished genome sequences and description of Bacillus massiliglaciei, Bacillus mediterraneensis, Bacillus massilinigeriensis, Bacillus phocaeensis and Bacillus tuaregi, five new species identified by culturomics. New Microbes and New Infections, 2017, 19, 45-59. | 0.8 | 4 |
| 1098 | soxRS induces colistin hetero-resistance in Enterobacter asburiae and Enterobacter cloacae by regulating the acrAB-tolC efflux pump. Journal of Antimicrobial Chemotherapy, 2017, 72, 2715-2721. | 1.3 | 56 |
| 1099 | A comparative genome analysis of Cercospora sojina with other members of the pathogen genus Mycosphaerella on different plant hosts. Genomics Data, 2017, 13, 54-63. | 1.3 | 15 |
| 1100 | Dakarella massiliensis gen. nov., sp. nov., strain ND3T: a new bacterial genus isolated from the female genital tract. New Microbes and New Infections, 2017, 18, 38-46. | 0.8 | 5 |
| 1101 | Noncontiguous finished genome sequences and descriptions of â€˜Paenibacillus bouchesdurhonensis,â€™ â€˜Paenibacillus rubinfantis,â€™ â€˜Paenibacillus senegalimassiliensisâ€™ and â€˜Paenibacillus tuaregiâ€™ identified by culturomics. New Microbes and New Infections, 2017, 20, 1-13. | 0.8 | 1 |
| 1102 | Mitochondrial genomes of the green macroalga <i>Ulva pertusa</i> (Ulvophyceae, Chlorophyta): novel insights into the evolution of mitogenomes in the Ulvophyceae. Journal of Phycology, 2017, 53, 1010-1019. | 1.0 | 23 |
| 1103 | Genome Sequencing of Steroid Producing Bacteria Using Ion Torrent Technology and a Reference Genome. Methods in Molecular Biology, 2017, 1645, 45-58. | 0.4 | 0 |
| 1104 | Population genomics reveals a candidate gene involved in bumble bee pigmentation. Ecology and Evolution, 2017, 7, 3406-3413. | 0.8 | 13 |
| 1105 | Origin and evolutionary history of freshwater Rhodophyta: further insights based on phylogenomic evidence. Scientific Reports, 2017, 7, 2934. | 1.6 | 25 |
| 1106 | Genomic insights into the virulence and salt tolerance of Staphylococcus equorum. Scientific Reports, 2017, 7, 5383. | 1.6 | 34 |
| 1107 | On the brink: the highly reduced plastomes of nonphotosynthetic Ericaceae. New Phytologist, 2017, 216, 254-266. | 3.5 | 46 |
| 1108 | Development of a new real-time quantitative PCR assay for the detection of Staphylococcus aureus genotype B in cow milk, targeting the new gene adlb. Journal of Dairy Science, 2017, 100, 7834-7845. | 1.4 | 20 |
| 1109 | Genetic analysis of a PER-2-producing Shewanella sp. strain harbouring a variety of mobile genetic elements and antibiotic resistance determinants. Journal of Global Antimicrobial Resistance, 2017, 11, 81-86. | 0.9 | 10 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1110 | A novel viral lineage distantly related to herpesviruses discovered within fish genome sequence data. Virus Evolution, 2017, 3, vex016. | 2.2 | 20 |
| 1111 | Ranavirus phylogenomics: Signatures of recombination and inversions among bullfrog ranaculture isolates. Virology, 2017, 511, 330-343. | 1.1 | 50 |
| 1112 | Whole genome comparative analysis of four Georgian grape cultivars. Molecular Genetics and Genomics, 2017, 292, 1377-1389. | 1.0 | 9 |
| 1113 | Complete mitochondrial genome of the freshwater red alga Lympha mucosa (Rhodophyta). Mitochondrial DNA Part B: Resources, 2017, 2, 707-708. | 0.2 | 2 |
| 1114 | Complete Genome Sequences of 12 Isolates of Listeria monocytogenes Belonging to Serotypes 1/2a, 1/2b, and 4b Obtained from Food Products and Food-Processing Environments in Canada. Genome Announcements, 2017, 5, . | 0.8 | 0 |
| 1115 | The natural product carolacton inhibits folate-dependent C1 metabolism by targeting FolD/MTHFD. Nature Communications, 2017, 8, 1529. | 5.8 | 66 |
| 1116 | Whole-Genome Shotgun Sequences of Three Multidrug-Resistant Mycobacterium tuberculosis Strains Isolated from Morocco. Genome Announcements, 2017, 5, . | 0.8 | 1 |
| 1117 | Plastid Genome of Dictyopteris divaricata (Dictyotales, Phaeophyceae): Understanding the Evolution of Plastid Genomes in Brown Algae. Marine Biotechnology, 2017, 19, 627-637. | 1.1 | 22 |
| 1118 | The food-borne pathogen Campylobacter jejuni responds to the bile salt deoxycholate with countermeasures to reactive oxygen species. Scientific Reports, 2017, 7, 15455. | 1.6 | 27 |
| 1119 | Ammoniaâ€oxidising archaea living at low pH: Insights from comparative genomics. Environmental Microbiology, 2017, 19, 4939-4952. | 1.8 | 107 |
| 1120 | Genome sequence and analysis of Escherichia coli production strain LS5218. Metabolic Engineering Communications, 2017, 5, 78-83. | 1.9 | 9 |
| 1121 | Genome-wide detection of genetic loci associated with soybean aphid resistance in soybean germplasm PI 603712. Euphytica, 2017, 213, 1. | 0.6 | 10 |
| 1122 | Whole genome sequence analysis; an improved technology that identifies underlying genotypic differences between closely related Listeria monocytogenes strains. Innovative Food Science and Emerging Technologies, 2017, 44, 89-96. | 2.7 | 8 |
| 1123 | The complete chloroplast genome sequence of tung tree (Vernicia fordii): Organization and phylogenetic relationships with other angiosperms. Scientific Reports, 2017, 7, 1869. | 1.6 | 38 |
| 1124 | Parallel Evolution of Two Clades of an Atlantic-Endemic Pathogenic Lineage of Vibrio parahaemolyticus by Independent Acquisition of Related Pathogenicity Islands. Applied and Environmental Microbiology, 2017, 83, . | 1.4 | 27 |
| 1125 | Comparative Genomics of Two Sequential <i>Candida glabrata</i> Clinical Isolates. G3: Genes, Genomes, Genetics, 2017, 7, 2413-2426. | 0.8 | 62 |
| 1126 | Draft Genome Sequence of Pseudomonas koreensis CI12, a Bacillus cereus â€œHitchhikerâ€• from the Soybean Rhizosphere. Genome Announcements, 2017, 5, . | 0.8 | 10 |
| 1127 | Molecular Mechanism and Genetic Determinants of Buprofezin Degradation. Applied and Environmental Microbiology, 2017, 83, . | 1.4 | 14 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1128 | Cleaning and Disinfection of Biofilms Composed of Listeria monocytogenes and Background Microbiota from Meat Processing Surfaces. Applied and Environmental Microbiology, 2017, 83, . | 1.4 | 111 |
| 1129 | The Proline Variant of the W[F/L/M][T/S]R Cyclic Di-GMP Binding Motif Suppresses Dependence on Signal Association for Regulator Function. Journal of Bacteriology, 2017, 199, . | 1.0 | 12 |
| 1130 | Complete chloroplast genome of Gracilaria firma (Gracilariaceae, Rhodophyta), with discussion on the use of chloroplast phylogenomics in the subclass Rhodymeniophycidae. BMC Genomics, 2017, 18, 40. | 1.2 | 29 |
| 1131 | Transcriptomic buffering of cryptic genetic variation contributes to meningococcal virulence. BMC Genomics, 2017, 18, 282. | 1.2 | 14 |
| 1132 | sRNAs as possible regulators of retrotransposon activity in Cryptococcus gattii VGII. BMC Genomics, 2017, 18, 294. | 1.2 | 1 |
| 1133 | Complete sequence and comparative genomic analysis of eight native Pseudomonas syringae plasmids belonging to the pPT23A family. BMC Genomics, 2017, 18, 365. | 1.2 | 23 |
| 1134 | Hierarchical genomic analysis of carried and invasive serogroup A Neisseria meningitidis during the 2011 epidemic in Chad. BMC Genomics, 2017, 18, 398. | 1.2 | 15 |
| 1135 | Lost in plasmids: next generation sequencing and the complex genome of the tick-borne pathogen Borrelia burgdorferi. BMC Genomics, 2017, 18, 422. | 1.2 | 83 |
| 1136 | Comparative genomic analysis of Shiga toxin-producing and non-Shiga toxin-producing Escherichia coli O157 isolated from outbreaks in Korea. Gut Pathogens, 2017, 9, 7. | 1.6 | 3 |
| 1137 | Complete genome sequence of Clostridium perfringens CBA7123 isolated from a faecal sample from Korea. Gut Pathogens, 2017, 9, 32. | 1.6 | 4 |
| 1138 | Mitogenomic analyses support the recent division of the genus Orthotrichum (Orthotrichaceae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3 | 1.6 | 31 |
| 1139 | Detection of the cryptic prophage-like molecule pBtic235 in Bacillus thuringiensis subsp. israelensis. Research in Microbiology, 2017, 168, 319-330. | 1.0 | 19 |
| 1140 | Comparative Genomics Reveals the Diversity of Restriction-Modification Systems and DNA Methylation Sites in Listeria monocytogenes. Applied and Environmental Microbiology, 2017, 83, . | 1.4 | 31 |
| 1141 | The FhaB/FhaC two-partner secretion system is involved in adhesion of<i>Acinetobacter baumannii</i>AbH12O-A2 strain. Virulence, 2017, 8, 959-974. | 1.8 | 72 |
| 1142 | Comparative genomics of extrachromosomal elements in Bacillus thuringiensis subsp. israelensis. Research in Microbiology, 2017, 168, 331-344. | 1.0 | 28 |
| 1143 | Genome comparison and physiological characterization of eight Streptococcus thermophilus strains isolated from Italian dairy products. Food Microbiology, 2017, 63, 47-57. | 2.1 | 34 |
| 1144 | Improved production of propionic acid using genome shuffling. Biotechnology Journal, 2017, 12, 1600120. | 1.8 | 23 |
| 1145 | Comparative genome analysis of two Streptococcus phocae subspecies provides novel insights into pathogenicity. Marine Genomics, 2017, 31, 53-61. | 0.4 | 6 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1146 | Synteny Explorer: An Interactive Visualization Application for Teaching Genome Evolution. IEEE Transactions on Visualization and Computer Graphics, 2017, 23, 711-720. | 2.9 | 7 |
| 1147 | The complete chloroplast genome sequence of Glycyrrhiza lepidota (Nutt.) Pursh - An American wild licorice. Journal of Crop Science and Biotechnology, 2017, 20, 295-303. | 0.7 | 10 |
| 1149 | Structured Populations of Sulfolobus acidocaldarius with Susceptibility to Mobile Genetic Elements. Genome Biology and Evolution, 2017, 9, 1699-1710. | 1.1 | 17 |
| 1150 | Integrated Genomic and Proteomic Analyses of High-level Chloramphenicol Resistance in Campylobacter jejuni. Scientific Reports, 2017, 7, 16973. | 1.6 | 12 |
| 1151 | EpichloÃ« hybrida, sp. nov., an emerging model system for investigating fungal allopolyploidy. Mycologia, 2017, 109, 1-15. | 0.8 | 43 |
| 1152 | Revealing the genomic differences between two subgroups in &lt;i&gt;Lactobacillus gasseri&lt;/i&gt;. Bioscience of Microbiota, Food and Health, 2017, 36, 155-159. | 0.8 | 8 |
| 1153 | The complete genome sequence of Ensifer meliloti strain CCMM B554 (FSM-MA), a highly effective nitrogen-fixing microsymbiont of Medicago truncatula Gaertn. Standards in Genomic Sciences, 2017, 12, 75. | 1.5 | 3 |
| 1154 | Genetic Drift and Indel Mutation in the Evolution of Yeast Mitochondrial Genome Size. Genome Biology and Evolution, 2017, 9, 3088-3099. | 1.1 | 31 |
| 1155 | Draft Genome Sequence of <i>Myroides</i> sp. N17-2, a Multidrug-Resistant Bacterium Isolated from Radiation-Polluted Soils. Genome Announcements, 2017, 5, . | 0.8 | 2 |
| 1156 | Determination of Nucleopolyhedrovirusâ€™ Taxonomic Position. , 2017, , . |  | 1 |
| 1157 | Genome analysis of E. coli isolated from Crohnâ€™s disease patients. BMC Genomics, 2017, 18, 544. | 1.2 | 37 |
| 1158 | Genomic Analysis of Bacillus licheniformis CBA7126 Isolated from a Human Fecal Sample. Frontiers in Pharmacology, 2017, 8, 724. | 1.6 | 10 |
| 1159 | Genomic Analysis of a Pathogenic Bacterium, Paeniclostridium sordellii CBA7122 Containing the Highest Number of rRNA Operons, Isolated from a Human Stool Sample. Frontiers in Pharmacology, 2017, 8, 840. | 1.6 | 27 |
| 1160 | The Chloroplast Genome of Passiflora edulis (Passifloraceae) Assembled from Long Sequence Reads: Structural Organization and Phylogenomic Studies in Malpighiales. Frontiers in Plant Science, 2017, 8, 334. | 1.7 | 79 |
| 1161 | Comparative Analysis of Ralstonia solanacearum Methylomes. Frontiers in Plant Science, 2017, 8, 504. | 1.7 | 13 |
| 1162 | A Dynamic Tandem Repeat in Monocotyledons Inferred from a Comparative Analysis of Chloroplast Genomes in Melanthiaceae. Frontiers in Plant Science, 2017, 8, 693. | 1.7 | 13 |
| 1163 | Comparative Genomics of Ralstonia solanacearum Identifies Candidate Genes Associated with Cool Virulence. Frontiers in Plant Science, 2017, 8, 1565. | 1.7 | 25 |
| 1164 | XCAVATOR: accurate detection and genotyping of copy number variants from second and third generation whole-genome sequencing experiments. BMC Genomics, 2017, 18, 747. | 1.2 | 29 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1165 | Complete Genome Sequences of Two Strains of the Meat Spoilage Bacterium Brochothrix thermosphacta Isolated from Ground Chicken. Genome Announcements, 2017, 5, . | 0.8 | 3 |
| 1166 | Chloroplast Genome Sequence of Clusterbean (Cyamopsis tetragonoloba L.): Genome Structure and Comparative Analysis. Genes, 2017, 8, 212. | 1.0 | 46 |
| 1167 | Complete Chloroplast Genome of Pinus massoniana (Pinaceae): Gene Rearrangements, Loss of ndh Genes, and Short Inverted Repeats Contraction, Expansion. Molecules, 2017, 22, 1528. | 1.7 | 33 |
| 1168 | Variation in the Genetic Repertoire of Viruses Infecting Micromonas pusilla Reflects Horizontal Gene Transfer and Links to Their Environmental Distribution. Viruses, 2017, 9, 116. | 1.5 | 15 |
| 1169 | Stumbling across the Same Phage: Comparative Genomics of Widespread Temperate Phages Infecting the Fish Pathogen Vibrio anguillarum. Viruses, 2017, 9, 122. | 1.5 | 43 |
| 1170 | Deciphering Single Nucleotide Polymorphisms and Evolutionary Trends in Isolates of the Cydia pomonella granulovirus. Viruses, 2017, 9, 227. | 1.5 | 16 |
| 1171 | Generation of Small Colony Variants in Biofilms by &lt;i&gt;Escherichia coli&lt;/i&gt; Harboring a Conjugative F Plasmid. Microbes and Environments, 2017, 32, 40-46. | 0.7 | 21 |
| 1172 | Comparative Analysis of the Complete Chloroplast Genome of Four Endangered Herbals of Notopterygium. Genes, 2017, 8, 124. | 1.0 | 54 |
| 1173 | Comparative Genomics of Mycoplasma bovis Strains Reveals That Decreased Virulence with Increasing Passages Might Correlate with Potential Virulence-Related Factors. Frontiers in Cellular and Infection Microbiology, 2017, 7, 177. | 1.8 | 39 |
| 1174 | Bacillus thuringiensis and Bacillus weihenstephanensis Inhibit the Growth of Phytopathogenic Verticillium Species. Frontiers in Microbiology, 2016, 7, 2171. | 1.5 | 74 |
| 1175 | Genomic Analysis of a New Serovar of Leptospira weilii Serogroup Manhao. Frontiers in Microbiology, 2017, 8, 149. | 1.5 | 18 |
| 1176 | Effect of Temperature on the Prevalence of Saccharomyces Non cerevisiae Species against a S. cerevisiae Wine Strain in Wine Fermentation: Competition, Physiological Fitness, and Influence in Final Wine Composition. Frontiers in Microbiology, 2017, 8, 150. | 1.5 | 90 |
| 1177 | Characterization of Potential Polysaccharide Utilization Systems in the Marine Bacteroidetes Gramella Flava JLT2011 Using a Multi-Omics Approach. Frontiers in Microbiology, 2017, 8, 220. | 1.5 | 57 |
| 1178 | An In vitro Study of Bio-Control and Plant Growth Promotion Potential of Salicaceae Endophytes. Frontiers in Microbiology, 2017, 8, 386. | 1.5 | 126 |
| 1179 | Evidence for Contemporary Switching of the O-Antigen Gene Cluster between Shiga Toxin-Producing Escherichia coli Strains Colonizing Cattle. Frontiers in Microbiology, 2017, 8, 424. | 1.5 | 13 |
| 1180 | Pan-Genomic Analysis Permits Differentiation of Virulent and Non-virulent Strains of Xanthomonas arboricola That Cohabit Prunus spp. and Elucidate Bacterial Virulence Factors. Frontiers in Microbiology, 2017, 8, 573. | 1.5 | 38 |
| 1181 | Comparative Genomics and Transcriptional Analysis of Flavobacterium columnare Strain ATCC 49512. Frontiers in Microbiology, 2017, 8, 588. | 1.5 | 46 |
| 1182 | Genomics Reveals a Unique Clone of Burkholderia cenocepacia Harboring an Actively Excising Novel Genomic Island. Frontiers in Microbiology, 2017, 8, 590. | 1.5 | 24 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1183 | A Genotypic Analysis of Five P. aeruginosa Strains after Biofilm Infection by Phages Targeting Different Cell Surface Receptors. Frontiers in Microbiology, 2017, 8, 1229. | 1.5 | 41 |
| 1184 | Complete Mitochondrial Genome of Phytophthora nicotianae and Identification of Molecular Markers for the Oomycetes. Frontiers in Microbiology, 2017, 8, 1484. | 1.5 | 22 |
| 1185 | Genome Plasticity and Polymorphisms in Critical Genes Correlate with Increased Virulence of Dutch Outbreak-Related Coxiella burnetii Strains. Frontiers in Microbiology, 2017, 8, 1526. | 1.5 | 26 |
| 1186 | New Insights into the Diversity of the Genus Faecalibacterium. Frontiers in Microbiology, 2017, 8, 1790. | 1.5 | 71 |
| 1187 | pirABvp-Bearing Vibrio parahaemolyticus and Vibrio campbellii Pathogens Isolated from the Same AHPND-Affected Pond Possess Highly Similar Pathogenic Plasmids. Frontiers in Microbiology, 2017, 8, 1859. | 1.5 | 66 |
| 1188 | Complete Genome Sequence of Vibrio campbellii LMB 29 Isolated from Red Drum with Four Native Megaplasmids. Frontiers in Microbiology, 2017, 8, 2035. | 1.5 | 38 |
| 1189 | Double-Face Meets the Bacterial World: The Opportunistic Pathogen Stenotrophomonas maltophilia. Frontiers in Microbiology, 2017, 8, 2190. | 1.5 | 66 |
| 1190 | Comparative Genomics of a Bovine Mycobacterium tuberculosis Isolate and Other Strains Reveals Its Potential Mechanism of Bovine Adaptation. Frontiers in Microbiology, 2017, 8, 2500. | 1.5 | 11 |
| 1191 | Severe infections emerge from commensal bacteria by adaptive evolution. ELife, 2017, 6, . | 2.8 | 93 |
| 1192 | Exception to the Rule: Genomic Characterization of Naturally Occurring Unusual Vibrio cholerae Strains with a Single Chromosome. International Journal of Genomics, 2017, 2017, 1-14. | 0.8 | 18 |
| 1193 | Comparative analyses of plastid genomes from fourteen Cornales species: inferences for phylogenetic relationships and genome evolution. BMC Genomics, 2017, 18, 956. | 1.2 | 40 |
| 1194 | Genomic divergence and cohesion in a species of pelagic freshwater bacteria. BMC Genomics, 2017, 18, 794. | 1.2 | 14 |
| 1195 | Bacteriophages are the major drivers of Shigella flexneri serotype 1c genome plasticity: a complete genome analysis. BMC Genomics, 2017, 18, 722. | 1.2 | 10 |
| 1196 | Legionnairesâ€™ Disease Outbreak Caused by Endemic Strain of <i>Legionella pneumophila</i>, New York, New York, USA, 2015. Emerging Infectious Diseases, 2017, 23, 1784-1791. | 2.0 | 33 |
| 1197 | The First Chloroplast Genome Sequence of Boswellia sacra, a Resin-Producing Plant in Oman. PLoS ONE, 2017, 12, e0169794. | 1.1 | 19 |
| 1198 | Comparative Genome Sequencing Reveals Within-Host Genetic Changes in Neisseria meningitidis during Invasive Disease. PLoS ONE, 2017, 12, e0169892. | 1.1 | 26 |
| 1199 | Genomic confirmation of vancomycin-resistant Enterococcus transmission from deceased donor to liver transplant recipient. PLoS ONE, 2017, 12, e0170449. | 1.1 | 16 |
| 1200 | Comprehensive bioinformatics analysis of Mycoplasma pneumoniae genomes to investigate underlying population structure and type-specific determinants. PLoS ONE, 2017, 12, e0174701. | 1.1 | 27 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1201 | Comparative genomics of two super-shedder isolates of Escherichia coli O157:H7. PLoS ONE, 2017, 12, e0182940. | 1.1 | 19 |
| 1202 | The complete chloroplast genome sequences of three Adenophora species and comparative analysis with Campanuloid species (Campanulaceae). PLoS ONE, 2017, 12, e0183652. | 1.1 | 19 |
| 1203 | The mitochondrial genome of the plant-pathogenic fungus Stemphylium lycopersici uncovers a dynamic structure due to repetitive and mobile elements. PLoS ONE, 2017, 12, e0185545. | 1.1 | 52 |
| 1204 | Prevalence of binary toxin positive Clostridium difficile in diarrhoeal humans in the absence of epidemic ribotype 027. PLoS ONE, 2017, 12, e0187658. | 1.1 | 11 |
| 1205 | Isolation and characterization of a N4-like lytic bacteriophage infecting Vibrio splendidus, a pathogen of fish and bivalves. PLoS ONE, 2017, 12, e0190083. | 1.1 | 33 |
| 1206 | Promiscuous signaling by a regulatory system unique to the pandemic PMEN1 pneumococcal lineage. PLoS Pathogens, 2017, 13, e1006339. | 2.1 | 38 |
| 1207 | The Use of Next-Generation Sequencing in the Identification of a Fastidious Pathogen: A Lesson From a Clinical Setup. Evolutionary Bioinformatics, 2017, 13, 117693431668607. | 0.6 | 17 |
| 1208 | Comparative genomics of the tardigrades Hypsibius dujardini and Ramazzottius varieornatus. PLoS Biology, 2017, 15, e2002266. | 2.6 | 170 |
| 1209 | Anaerobically Grown Escherichia coli Has an Enhanced Mutation Rate and Distinct Mutational Spectra. PLoS Genetics, 2017, 13, e1006570. | 1.5 | 60 |
| 1210 | First insights in the variability of Borrelia recurrentis genomes. PLoS Neglected Tropical Diseases, 2017, 11, e0005865. | 1.3 | 14 |
| 1211 | Expression and evolutionary patterns of mycobacteriophage D29 and its temperate close relatives. BMC Microbiology, 2017, 17, 225. | 1.3 | 24 |
| 1212 | Alignment-free sequence comparison: benefits, applications, and tools. Genome Biology, 2017, 18, 186. | 3.8 | 371 |
| 1213 | Genome characterization of a novel binary toxin-positive strain of Clostridium difficile and comparison with the epidemic 027 and 078 strains. Gut Pathogens, 2017, 9, 42. | 1.6 | 15 |
| 1214 | A VP24-truncated isolate of white spot syndrome virus is inefficient in per os infection. Veterinary Research, 2017, 48, 87. | 1.1 | 15 |
| 1215 | Genome sequencing and analysis of the first spontaneous Nanosilver resistant bacterium Proteus mirabilis strain SCDR1. Antimicrobial Resistance and Infection Control, 2017, 6, 119. | 1.5 | 16 |
| 1216 | High-quality draft genome sequence of a biofilm forming lignocellulolytic Aspergillus niger strain ATCC 10864. Standards in Genomic Sciences, 2017, 12, 37. | 1.5 | 10 |
| 1217 | Complete genome sequence of Thermotoga sp. strain RQ7. Standards in Genomic Sciences, 2017, 12, 62. | 1.5 | 9 |
| 1218 | Draft genome sequence of Bacillus velezensis 2A-2B strain: a rhizospheric inhabitant of Sporobolus airoides (Torr.) Torr., with antifungal activity against root rot causing phytopathogens. Standards in Genomic Sciences, 2017, 12, 73. | 1.5 | 26 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1219 | Complete genome sequence analysis of Archaeoglobus fulgidus strain 7324 (DSM 8774), a hyperthermophilic archaeal sulfate reducer from a North Sea oil field. Standards in Genomic Sciences, 2017, 12, 79. | 1.5 | 19 |
| 1220 | NucDiff: in-depth characterization and annotation of differences between two sets of DNA sequences. BMC Bioinformatics, 2017, 18, 338. | 1.2 | 43 |
| 1221 | Whole genome sequencing for the molecular characterization of carbapenem-resistant Klebsiella pneumoniae strains isolated at the Italian ASST Fatebenefratelli Sacco Hospital, 2012â€"2014. BMC Infectious Diseases, 2017, 17, 666. | 1.3 | 33 |
| 1222 | The genomic sequence of<i>Exiguobacterium chiriqhucha</i>str. N139 reveals a species that thrives in cold waters and extreme environmental conditions. PeerJ, 2017, 5, e3162. | 0.9 | 27 |
| 1223 | Complete Genome Sequences of Two Geographically Distinct Legionella micdadei Clinical Isolates. Genome Announcements, 2017, 5, . | 0.8 | 0 |
| 1224 | Draft Genome Sequences of Seven 4-Formylaminooxyvinylglycine Producers Belonging to the Pseudomonas fluorescens Species Complex. Genome Announcements, 2017, 5, . | 0.8 | 6 |
| 1225 | Comparative genomic analysis of Acinetobacter strains isolated from murine colonic crypts. BMC Genomics, 2017, 18, 525. | 1.2 | 14 |
| 1226 | Approaches for in silico finishing of microbial genome sequences. Genetics and Molecular Biology, 2017, 40, 553-576. | 0.6 | 17 |
| 1227 | Draft Genome Sequence of Micrococcus luteus (Schroeter) Cohn (ATCC 12698). Genome Announcements, 2017, 5, . | 0.8 | 2 |
| 1228 | Draft Genome Sequences of Two Highly Erythromycin-Resistant Streptococcus gallolyticus subsp. gallolyticus Isolates Containing a Novel Tn 916 -Like Element, Tn 6331. Genome Announcements, 2017, 5, . | 0.8 | 7 |
| 1229 | Draft Genome Sequence of Flavobacterium johnsoniae CI04, an Isolate from the Soybean Rhizosphere. Genome Announcements, 2017, 5, . | 0.8 | 5 |
| 1230 | A GRASP-Based Heuristic for the Sorting by Length-Weighted Inversions Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 352-363. | 1.9 | 3 |
| 1231 | Evaluating the use of whole-genome sequencing for outbreak investigations in the lack of closely related reference genome. Infection, Genetics and Evolution, 2018, 59, 1-6. | 1.0 | 7 |
| 1232 | Coexistence of mcr-1 , bla KPC-2 and two copies of fosA3 in a clinical Escherichia coli strain isolated from urine. Infection, Genetics and Evolution, 2018, 60, 77-79. | 1.0 | 9 |
| 1233 | Complete Sequence of the IncA/C <sub>1</sub> Plasmid pCf587 Carrying <i>bla</i> <sub>PER-2</sub> from Citrobacter freundii. Antimicrobial Agents and Chemotherapy, 2018, 62, . | 1.4 | 9 |
| 1234 | Culture-Facilitated Comparative Genomics of the Facultative Symbiont Hamiltonella defensa. Genome Biology and Evolution, 2018, 10, 786-802. | 1.1 | 37 |
| 1235 | Considerations for Visualizing Comparison. IEEE Transactions on Visualization and Computer Graphics, 2018, 24, 413-423. | 2.9 | 118 |
| 1236 | Emergence, transmission and phylogeny of meticillin-resistant Staphylococcus aureus sequence type 8 (USA300) in Taiwan. Journal of Hospital Infection, 2018, 100, 355-358. | 1.4 | 13 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1237 | Peptoniphilus lacydonensis sp. nov., a new human-associated species isolated from a patient with chronic refractory sinusitis. New Microbes and New Infections, 2018, 23, 61-69. | 0.8 | 14 |
| 1238 | Novel sequencing technologies to support industrial biotechnology. FEMS Microbiology Letters, 2018, 365, . | 0.7 | 15 |
| 1239 | Genomic analysis of oral <i>Campylobacter concisus</i> strains identified a potential bacterial molecular marker associated with active Crohnâ€™s disease. Emerging Microbes and Infections, 2018, 7, 1-14. | 3.0 | 25 |
| 1240 | Safety assessment and functional properties of four enterococci strains isolated from regional Argentinean cheese. International Journal of Food Microbiology, 2018, 277, 1-9. | 2.1 | 16 |
| 1241 | Comparative genome and transcriptome analysis reveal the medicinal basis and environmental adaptation of artificially cultivated Taiwanofungus camphoratus. Mycological Progress, 2018, 17, 871-883. | 0.5 | 9 |
| 1242 | T Cell-Independent Gamma Interferon and B Cells Cooperate To Prevent Mortality Associated with Disseminated Chlamydia muridarum Genital Tract Infection. Infection and Immunity, 2018, 86, . | 1.0 | 18 |
| 1243 | riboSeed: leveraging prokaryotic genomic architecture to assemble across ribosomal regions. Nucleic Acids Research, 2018, 46, e68-e68. | 6.5 | 10 |
| 1244 | Comparison of closely related, uncultivated <i>Coxiella</i> tick endosymbiont population genomes reveals clues about the mechanisms of symbiosis. Environmental Microbiology, 2018, 20, 1751-1764. | 1.8 | 33 |
| 1245 | Evolution of the Plastid Genomes in Diatoms. Advances in Botanical Research, 2018, 85, 129-155. | 0.5 | 51 |
| 1246 | Raising the Stakes: Loss of Efflux Pump Regulation Decreases Meropenem Susceptibility in Burkholderia pseudomallei. Clinical Infectious Diseases, 2018, 67, 243-250. | 2.9 | 34 |
| 1247 | Draft genome sequence of Penicillium chrysogenum strain HKF2, a fungus with potential for production of prebiotic synthesizing enzymes. 3 Biotech, 2018, 8, 106. | 1.1 | 11 |
| 1248 | Potato late blight field resistance from QTL dPI09c is conferred by the NB-LRR gene R8. Journal of Experimental Botany, 2018, 69, 1545-1555. | 2.4 | 56 |
| 1249 | Bacteriophages of the Urinary Microbiome. Journal of Bacteriology, 2018, 200, . | 1.0 | 70 |
| 1250 | Genetic characterization and modification of a bioethanol-producing yeast strain. Applied Microbiology and Biotechnology, 2018, 102, 2213-2223. | 1.7 | 5 |
| 1251 | A Genome Comparison of T7-like Podoviruses That Infect Caulobacter crescentus. Current Microbiology, 2018, 75, 760-765. | 1.0 | 4 |
| 1252 | Intrageneric Variability Between the Chloroplast Genomes of <i>Trachelomonas grandis</i> and <i>Trachelomonas volvocina</i> and Phylogenomic Analysis of Phototrophic Euglenoids. Journal of Eukaryotic Microbiology, 2018, 65, 648-660. | 0.8 | 3 |
| 1253 | The genome sequence of a new strain of Mycobacterium ulcerans ecovar Liflandii, emerging as a sturgeon pathogen. Aquaculture, 2018, 489, 141-147. | 1.7 | 17 |
| 1254 | Comparative Genomics for Prokaryotes. Methods in Molecular Biology, 2018, 1704, 55-78. | 0.4 | 15 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1255 | Genome Rearrangement Analysis: Cut and Join Genome Rearrangements and Gene Cluster Preserving Approaches. Methods in Molecular Biology, 2018, 1704, 261-289. | 0.4 | 5 |
| 1256 | Taxonogenomic description of four new Clostridium species isolated from human gut: â€˜Clostridium amazonitimonenseâ€™ , â€˜Clostridium merdaeâ€™ , â€˜Clostridium massilidielmoenseâ€™ and â€˜Clostridium nigerienseâ€™. New Microbes and New Infections, 2018, 21, 128-139. | 0.8 | 28 |
| 1257 | Patterns of Genomic Variation in the Opportunistic Pathogen Candida glabrata Suggest the Existence of Mating and a Secondary Association with Humans. Current Biology, 2018, 28, 15-27.e7. | 1.8 | 114 |
| 1258 | Successive Emergence of Ceftazidime-Avibactam Resistance through Distinct Genomic Adaptations in <i>bla</i> <sub>KPC-2</sub> -Harboring Klebsiella pneumoniae Sequence Type 307 Isolates. Antimicrobial Agents and Chemotherapy, 2018, 62, . | 1.4 | 162 |
| 1259 | Methylation in Mycobacterium tuberculosis is lineage specific with associated mutations present globally. Scientific Reports, 2018, 8, 160. | 1.6 | 31 |
| 1260 | Clinical and molecular features of MDR livestock-associated MRSA ST9 with staphylococcal cassette chromosome mecXII in humans. Journal of Antimicrobial Chemotherapy, 2018, 73, 33-40. | 1.3 | 47 |
| 1261 | Microbial culturomics to isolate halophilic bacteria from table salt: genome sequence and description of the moderately halophilic bacterium Bacillus salis sp. nov.. New Microbes and New Infections, 2018, 23, 28-38. | 0.8 | 4 |
| 1262 | Transfer of a bla CTX-M-1-carrying plasmid between different Escherichia coli strains within the human gut explored by whole genome sequencing analyses. Scientific Reports, 2018, 8, 280. | 1.6 | 28 |
| 1263 | Weak Epistasis May Drive Adaptation in Recombining Bacteria. Genetics, 2018, 208, 1247-1260. | 1.2 | 51 |
| 1264 | Draft Genome Sequences of <i>Pseudomonas putida</i> UV4 and UV4/95, Toluene Dioxygenase-Expressing Producers of <i>cis</i> -1,2-Dihydrodiols. Genome Announcements, 2018, 6, . | 0.8 | 4 |
| 1265 | Staphylococcus aureus undergoes major transcriptional reorganization during growth with Enterococcus faecalis in milk. Food Microbiology, 2018, 73, 17-28. | 2.1 | 15 |
| 1266 | Genomic diversity and distribution of Bifidobacterium longum subsp. longum across the human lifespan. Scientific Reports, 2018, 8, 85. | 1.6 | 99 |
| 1267 | Complete genome sequence of Tsukamurella sp. MH1: A wide-chain length alkane-degrading actinomycete. Journal of Biotechnology, 2018, 268, 1-5. | 1.9 | 5 |
| 1268 | The putative functions of lysogeny in mediating the survivorship of Escherichia coli in seawater and marine sediment. FEMS Microbiology Ecology, 2018, 94, . | 1.3 | 6 |
| 1269 | Genomic analysis and immune response in a murine mastitis model of vB_EcoM-UFV13, a potential biocontrol agent for use in dairy cows. Scientific Reports, 2018, 8, 6845. | 1.6 | 26 |
| 1270 | Comparative genomic and metabolic analysis of three Lactobacillus paracasei cheese isolates reveals considerable genomic differences in strains from the same niche. BMC Genomics, 2018, 19, 205. | 1.2 | 29 |
| 1271 | Comparative genomics of the wheat fungal pathogen Pyrenophora tritici-repentis reveals chromosomal variations and genome plasticity. BMC Genomics, 2018, 19, 279. | 1.2 | 56 |
| 1272 | Development of race-specific molecular marker for<i>Xanthomonas campestris</i>pv.<i>campestris</i>race 3, the causal agent of black rot of crucifers. Canadian Journal of Plant Science, 2018, 98, 1119-1125. | 0.3 | 12 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1273 | Draft genome sequence of Fermentimonas caenicola strain SIT8, isolated from the human gut. Standards in Genomic Sciences, 2018, 13, 8. | 1.5 | 7 |
| 1274 | Draft Genome Sequences of Four Parasaccharibacter apium Strains Isolated from Honey Bees. Genome Announcements, 2018, 6, . | 0.8 | 9 |
| 1275 | Ancient DNA study reveals HLA susceptibility locus for leprosy in medieval Europeans. Nature Communications, 2018, 9, 1569. | 5.8 | 67 |
| 1276 | Male-killing toxin in a bacterial symbiont of Drosophila. Nature, 2018, 557, 252-255. | 13.7 | 111 |
| 1277 | A new strategy to infer circularity applied to four new complete frog mitogenomes. Ecology and Evolution, 2018, 8, 4011-4018. | 0.8 | 15 |
| 1278 | Draft Genome Sequences of 12 Clinical and Environmental Methicillin-Resistant Staphylococcus pseudintermedius Strains Isolated from a Veterinary Teaching Hospital in Washington State. Genome Announcements, 2018, 6, . | 0.8 | 0 |
| 1279 | Genomic characterization of Nitrospirillum amazonense strain CBAmC, a nitrogen-fixing bacterium isolated from surface-sterilized sugarcane stems. Molecular Genetics and Genomics, 2018, 293, 997-1016. | 1.0 | 17 |
| 1280 | Morphologic and Genomic Analyses of New Isolates Reveal a Second Lineage of Cedratviruses. Journal of Virology, 2018, 92, . | 1.5 | 21 |
| 1281 | Complete genome sequence of Bacillus velezensis QST713: A biocontrol agent that protects Agaricus bisporus crops against the green mould disease. Journal of Biotechnology, 2018, 278, 10-19. | 1.9 | 67 |
| 1282 | Molecular basis for the structural diversity in serogroup O2-antigen polysaccharides in Klebsiella pneumoniae. Journal of Biological Chemistry, 2018, 293, 4666-4679. | 1.6 | 42 |
| 1283 | Molecular Characterization of OXA-198 Carbapenemase-Producing Pseudomonas aeruginosa Clinical Isolates. Antimicrobial Agents and Chemotherapy, 2018, 62, . | 1.4 | 23 |
| 1284 | <i>In Vitro</i> Culture of the Insect Endosymbiont <i>Spiroplasma poulsonii</i> Highlights Bacterial Genes Involved in Host-Symbiont Interaction. MBio, 2018, 9, . | 1.8 | 51 |
| 1285 | Isolation and identification of Salmonella pullorum bacteriophage YSP2 and its use as a therapy for chicken diarrhea. Virus Genes, 2018, 54, 446-456. | 0.7 | 25 |
| 1286 | Genome variation in nine co-occurring toxic Cylindrospermopsis raciborskii strains. Harmful Algae, 2018, 73, 157-166. | 2.2 | 35 |
| 1287 | A Novel Glaesserella sp. Isolated from Pigs with Severe Respiratory Infections Has a Mosaic Genome with Virulence Factors Putatively Acquired by Horizontal Transfer. Applied and Environmental Microbiology, 2018, 84, . | 1.4 | 17 |
| 1288 | Draft Genome Sequences of 11 <i>Salmonella enterica</i> Serovar Typhimurium Strains Isolated from Human Systemic and Nonsystemic Sites in Brazil. Genome Announcements, 2018, 6, . | 0.8 | 2 |
| 1289 | Large Diversity of Nonstandard Genes and Dynamic Evolution of Chloroplast Genomes in Siphonous Green Algae (Bryopsidales, Chlorophyta). Genome Biology and Evolution, 2018, 10, 1048-1061. | 1.1 | 27 |
| 1290 | Microbial Culturomics Application for Global Health: Noncontiguous Finished Genome Sequence and Description of <i>Pseudomonas massiliensis</i> Strain CB-1<sup>T</sup> sp. nov. in Brazil. OMICS A Journal of Integrative Biology, 2018, 22, 164-175. | 1.0 | 6 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1291 | <i>Bacillus kwashiorkori</i> sp. nov., a new bacterial species isolated from a malnourished child using culturomics. MicrobiologyOpen, 2018, 7, e00535. | 1.2 | 6 |
| 1292 | The Linum usitatissimum L. plastome reveals atypical structural evolution, new editing sites, and the phylogenetic position of Linaceae within Malpighiales. Plant Cell Reports, 2018, 37, 307-328. | 2.8 | 43 |
| 1293 | Planctomycetes attached to algal surfaces: Insight into their genomes. Genomics, 2018, 110, 231-238. | 1.3 | 39 |
| 1294 | Comparative Genomic Analyses of <i>Clavibacter michiganensis</i> subsp. <i>insidiosus</i> and Pathogenicity on <i>Medicago truncatula</i>. Phytopathology, 2018, 108, 172-185. | 1.1 | 15 |
| 1295 | Characterisation of Lactococcus lactis isolates from herbs, fruits and vegetables for use as biopreservatives against Listeria monocytogenes in cheese. Food Control, 2018, 85, 472-483. | 2.8 | 41 |
| 1296 | The first complete organellar genomes of an Antarctic red alga, Pyropia endiviifolia: insights into its genome architecture and phylogenetic position within genus Pyropia (Bangiales, Rhodophyta). Journal of Oceanology and Limnology, 2018, 36, 1315-1328. | 0.6 | 12 |
| 1297 | The complete chloroplast genome sequence of Dodonaea viscosa: comparative and phylogenetic analyses. Genetica, 2018, 146, 101-113. | 0.5 | 54 |
| 1298 | Complete plastid genome sequences of three tropical <i>Alseodaphne</i> trees in the family Lauraceae. Holzforschung, 2018, 72, 337-345. | 0.9 | 23 |
| 1299 | Challenges of Francisella classification exemplified by an atypical clinical isolate. Diagnostic Microbiology and Infectious Disease, 2018, 90, 241-247. | 0.8 | 3 |
| 1300 | Genome-Wide Identification of Fitness Factors in Mastitis-Associated Escherichia coli. Applied and Environmental Microbiology, 2018, 84, . | 1.4 | 21 |
| 1301 | The genetic basis underlying variation in production of the flavour compound diacetyl by Lactobacillus rhamnosus strains in milk. International Journal of Food Microbiology, 2018, 265, 30-39. | 2.1 | 23 |
| 1302 | HomBlocks: A multiple-alignment construction pipeline for organelle phylogenomics based on locally collinear block searching. Genomics, 2018, 110, 18-22. | 1.3 | 183 |
| 1303 | From plants to nematodes: Serratia grimesii BXF1 genome reveals an adaptation to the modulation of multi-species interactions. Microbial Genomics, 2018, 4, . | 1.0 | 19 |
| 1304 | Genomic Alterations of Staphylococcus aureus ATCC 25923 after Prolonged Passage in the Laboratory. Microbiology Resource Announcements, 2018, 7, . | 0.3 | 1 |
| 1305 | Using Core Genome Alignments To Assign Bacterial Species. MSystems, 2018, 3, . | 1.7 | 54 |
| 1306 | Draft Genome Sequence of <i>Rhizobium</i> sp. Strain T2.30D-1.1, Isolated from 538.5 Meters Deep on the Subsurface of the Iberian Pyrite Belt. Microbiology Resource Announcements, 2018, 7, . | 0.3 | 5 |
| 1307 | Identification and characterization of novel conserved RNA structures in Drosophila. BMC Genomics, 2018, 19, 899. | 1.2 | 6 |
| 1308 | Closed Genome Sequence of Salmonella enterica Serovar Richmond Strain CFSAN000191, Obtained with Nanopore Sequencing. Microbiology Resource Announcements, 2018, 7, . | 0.3 | 4 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1309 | Complete Genome Sequence of Marinobacter flavimaris LMG 23834 <sup>T</sup> , Which Is Potentially Useful in Bioremediation. Genome Announcements, 2018, 6, . | 0.8 | 3 |
| 1310 | Closed Genome Sequences of Two Clostridium botulinum Strains Obtained by Nanopore Sequencing. Microbiology Resource Announcements, 2018, 7, . | 0.3 | 13 |
| 1311 | Evolution of six novel ORFs in the plastome of Mankyua chejuense and phylogeny of eusporangiate ferns. Scientific Reports, 2018, 8, 16466. | 1.6 | 10 |
| 1312 | Comparative genomics of Botryosphaeria dothidea and B. kuwatsukai, causal agents of apple ring rot, reveals both species expansion of pathogenicity-related genes and variations in virulence gene content during speciation. IMA Fungus, 2018, 9, 243-257. | 1.7 | 37 |
| 1313 | A Nonribosomal Peptide Synthase Gene Driving Virulence in Mycobacterium tuberculosis. MSphere, 2018, 3, . | 1.3 | 20 |
| 1314 | Impacts of horizontal gene transfer on the compact genome of the clavulanic acid-producing Streptomyces strain F613-1. 3 Biotech, 2018, 8, 472. | 1.1 | 3 |
| 1315 | Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelersâ€™ diarrhea. Microbiome, 2018, 6, 201. | 4.9 | 20 |
| 1316 | Combinatorial Loss of the Enzymatic Activities of Viral Uracil-DNA Glycosylase and Viral dUTPase Impairs Murine Gammaherpesvirus Pathogenesis and Leads to Increased Recombination-Based Deletion in the Viral Genome. MBio, 2018, 9, . | 1.8 | 11 |
| 1317 | Position and Content Paradigms in Genome Rearrangements: The Wild and Crazy World of Permutations in Genomics. Bulletin of Mathematical Biology, 2018, 80, 3227-3246. | 0.9 | 13 |
| 1318 | Nonmutational mechanism of inheritance in the Archaeon Sulfolobus solfataricus. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12271-12276. | 3.3 | 8 |
| 1319 | Gene inversion potentiates bacterial evolvability and virulence. Nature Communications, 2018, 9, 4662. | 5.8 | 61 |
| 1320 | Presence of anAgrobacterium-Type Tumor-Inducing Plasmid inNeorhizobiumsp. NCHU2750 and the Link to Phytopathogenicity. Genome Biology and Evolution, 2018, 10, 3188-3195. | 1.1 | 13 |
| 1321 | Genetic Loci Associated With Fluoride Resistance in Streptococcus mutans. Frontiers in Microbiology, 2018, 9, 3093. | 1.5 | 16 |
| 1322 | Genome Sequences and Comparative Analysis of Two Extended-Spectrum Extensively-Drug Resistant Mycobacterium tuberculosis Strains. Frontiers in Pharmacology, 2018, 9, 1492. | 1.6 | 2 |
| 1323 | High-Quality Draft Genome Sequence of Xanthomonas sp. Strain CPBF 424, a Walnut-Pathogenic Strain with Atypical Features. Microbiology Resource Announcements, 2018, 7, . | 0.3 | 7 |
| 1324 | High-Quality Draft Genome Sequence of Xanthomonas arboricola pv. juglandis CPBF 1521, Isolated from Leaves of a Symptomatic Walnut Tree in Portugal without a Past of Phytosanitary Treatment. Microbiology Resource Announcements, 2018, 7, . | 0.3 | 5 |
| 1325 | Comparative analysis of Faecalibacterium prausnitzii genomes shows a high level of genome plasticity and warrants separation into new species-level taxa. BMC Genomics, 2018, 19, 931. | 1.2 | 78 |
| 1326 | Loss of Bacitracin Resistance Due to a Large Genomic Deletion among <i>Bacillus anthracis</i> Strains. MSystems, 2018, 3, . | 1.7 | 9 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1327 | Clinical, immunological and bacteriological characteristics of H7N9 patients nosocomially co-infected by Acinetobacter Baumannii: a case control study. BMC Infectious Diseases, 2018, 18, 664. | 1.3 | 8 |
| 1328 | Sequencing of organellar genomes of Gymnomitrion concinnatum (Jungermanniales) revealed the first exception in the structure and gene order of evolutionary stable liverworts mitogenomes. BMC Plant Biology, 2018, 18, 321. | 1.6 | 21 |
| 1329 | Emergence of a dalbavancin induced glycopeptide/lipoglycopeptide non-susceptible <i>Staphylococcus aureus</i> during treatment of a cardiac device-related endocarditis. Emerging Microbes and Infections, 2018, 7, 1-10. | 3.0 | 50 |
| 1330 | A Strain of an Emerging Indian Xanthomonas oryzae pv. oryzae Pathotype Defeats the Rice Bacterial Blight Resistance Gene xa13 Without Inducing a Clade III SWEET Gene and Is Nearly Identical to a Recent Thai Isolate. Frontiers in Microbiology, 2018, 9, 2703. | 1.5 | 17 |
| 1331 | High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. Nature Communications, 2018, 9, 5114. | 5.8 | 2,816 |
| 1332 | The afc antifungal activity cluster, which is under tight regulatory control of ShvR, is essential for transition from intracellular persistence of Burkholderia cenocepacia to acute pro-inflammatory infection. PLoS Pathogens, 2018, 14, e1007473. | 2.1 | 13 |
| 1333 | Intergeneric Relationships within the Early-Diverging Angiosperm Family Nymphaeaceae Based on Chloroplast Phylogenomics. International Journal of Molecular Sciences, 2018, 19, 3780. | 1.8 | 11 |
| 1334 | SWPhylo â€“ A Novel Tool for Phylogenomic Inferences by Comparison of Oligonucleotide Patterns and Integration of Genome-Based and Gene-Based Phylogenetic Trees. Evolutionary Bioinformatics, 2018, 14, 117693431875929. | 0.6 | 2 |
| 1335 | Species Identification of Conyza bonariensis Assisted by Chloroplast Genome Sequencing. Frontiers in Genetics, 2018, 9, 374. | 1.1 | 24 |
| 1336 | Punctuated plastome reduction and hostâ€"parasite horizontal gene transfer in the holoparasitic plant genus <i>Aphyllon</i>. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20181535. | 1.2 | 25 |
| 1337 | Comparing Two <i>Mycobacterium tuberculosis</i> Genomes from Chinese Immigrants with Native Genomes Using Mauve Alignments. Tuberculosis and Respiratory Diseases, 2018, 81, 216. | 0.7 | 4 |
| 1338 | Implications of stx loss for clinical diagnostics of Shiga toxin-producing Escherichia coli. European Journal of Clinical Microbiology and Infectious Diseases, 2018, 37, 2361-2370. | 1.3 | 17 |
| 1339 | Complete genome sequence of Kocuria rhizophila BT304, isolated from the small intestine of castrated beef cattle. Gut Pathogens, 2018, 10, 42. | 1.6 | 5 |
| 1340 | A Cotransformation Method To Identify a Restriction-Modification Enzyme That Reduces Conjugation Efficiency in Campylobacter jejuni. Applied and Environmental Microbiology, 2018, 84, . | 1.4 | 2 |
| 1341 | Comparison of Highly and Weakly Virulent Dickeya solani Strains, With a View on the Pangenome and Panregulon of This Species. Frontiers in Microbiology, 2018, 9, 1940. | 1.5 | 50 |
| 1342 | S-plot2: Rapid Visual and Statistical Analysis of Genomic Sequences. Evolutionary Bioinformatics, 2018, 14, 117693431879735. | 0.6 | 8 |
| 1343 | Plastid genome analysis of three Nemaliophycidae red algal species suggests environmental adaptation for iron limited habitats. PLoS ONE, 2018, 13, e0196995. | 1.1 | 9 |
| 1344 | Comparative genomics of cocci-shaped Sporosarcina strains with diverse spatial isolation. BMC Genomics, 2018, 19, 310. | 1.2 | 9 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1345 | Complete Chloroplast Genome Sequence of Broomcorn Millet (Panicum miliaceum L.) and Comparative Analysis with Other Panicoideae Species. Agronomy, 2018, 8, 159. | 1.3 | 14 |
| 1346 | Function of BriC peptide in the pneumococcal competence and virulence portfolio. PLoS Pathogens, 2018, 14, e1007328. | 2.1 | 44 |
| 1347 | Characterization of a Salmonella Enteritidis bacteriophage showing broad lytic activity against Gram-negative enteric bacteria. Journal of Microbiology, 2018, 56, 917-925. | 1.3 | 22 |
| 1348 | Prophage-driven genomic structural changes promote Bartonella vertical evolution. Genome Biology and Evolution, 2018, 10, 3089-3103. | 1.1 | 13 |
| 1349 | Genome sequencing and functional analysis of an environmental isolate Escherichia coli Cont-1 revealed its genetic basis of arsenic-transformation and niche adaptation. Ecological Genetics and Genomics, 2018, 9, 34-42. | 0.3 | 1 |
| 1350 | Capsular Switching and ICE Transformation Occurred in Human Streptococcus agalactiae ST19 With High Pathogenicity to Fish. Frontiers in Veterinary Science, 2018, 5, 281. | 0.9 | 3 |
| 1351 | Complete genome of streamlined marine actinobacterium Pontimonas salivibrio strain CL-TW6T adapted to coastal planktonic lifestyle. BMC Genomics, 2018, 19, 625. | 1.2 | 10 |
| 1352 | Complete genome sequence reveals evolutionary dynamics of an emerging and variant pathovar of Xanthomonas euvesicatoria. Genome Biology and Evolution, 2018, 10, 3104-3109. | 1.1 | 8 |
| 1353 | Desiccation tolerance in Acinetobacter baumannii is mediated by the two-component response regulator BfmR. PLoS ONE, 2018, 13, e0205638. | 1.1 | 67 |
| 1354 | Whole-Genome Sequence of the Novel Antarctobacter heliothermus Strain SMS3, Found in Association with the Marine Diatom Skeletonema marinoi. Journal of Genomics, 2018, 6, 113-116. | 0.6 | 4 |
| 1355 | Genome Analysis of the Yeast M14, an Industrial Brewing Yeast Strain Widely Used in China. Journal of the American Society of Brewing Chemists, 2018, 76, 223-235. | 0.8 | 1 |
| 1356 | High genomic variability in the plant pathogenic bacterium Pectobacterium parmentieri deciphered from de novo assembled complete genomes. BMC Genomics, 2018, 19, 751. | 1.2 | 28 |
| 1357 | Mitochondrial and Plastid Genomes from Coralline Red Algae Provide Insights into the Incongruent Evolutionary Histories of Organelles. Genome Biology and Evolution, 2018, 10, 2961-2972. | 1.1 | 29 |
| 1358 | Tracking key virulence loci encoding aerobactin and salmochelin siderophore synthesis in Klebsiella pneumoniae. Genome Medicine, 2018, 10, 77. | 3.6 | 153 |
| 1359 | In vivo evolution of drug-resistant Mycobacterium tuberculosis in patients during long-term treatment. BMC Genomics, 2018, 19, 640. | 1.2 | 18 |
| 1360 | The Energy-Coupling Factor Transporter Module EcfAAâ€™T, a Novel Candidate for the Genetic Basis of Fatty Acid-Auxotrophic Small-Colony Variants of Staphylococcus aureus. Frontiers in Microbiology, 2018, 9, 1863. | 1.5 | 12 |
| 1361 | A New Freshwater Cyanosiphovirus Harboring Integrase. Frontiers in Microbiology, 2018, 9, 2204. | 1.5 | 26 |
| 1362 | Novel diagnostic marker genes differentiate<i>Saccharomyces</i>with respect to their potential application. Journal of the Institute of Brewing, 2018, 124, 416-424. | 0.8 | 2 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1363 | High and Variable Rates of Repeat-Mediated Mitochondrial Genome Rearrangement in a Genus of Plants. Molecular Biology and Evolution, 2018, 35, 2773-2785. | 3.5 | 60 |
| 1364 | Characterizing Mobilized Virulence Factors and Multidrug Resistance Genes in Carbapenemase-Producing Klebsiella pneumoniae in a Sri Lankan Hospital. Frontiers in Microbiology, 2018, 9, 2044. | 1.5 | 13 |
| 1365 | Nanopore sequencing and full genome de novo assembly of human cytomegalovirus TB40/E reveals clonal diversity and structural variations. BMC Genomics, 2018, 19, 577. | 1.2 | 17 |
| 1366 | Genome sequences and description of novel exopolysaccharides producing species Komagataeibacter pomaceti sp. nov. and reclassification of Komagataeibacter kombuchae (Dutta and Gachhui 2007) Yamada et al., 2013 as a later heterotypic synonym of Komagataeibacter hansenii (GosselÃ© et al. 1983) Yamada et al., 2013. Systematic and Applied Microbiology, 2018, 41, 581-592. | 1.2 | 46 |
| 1367 | | | |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1381 | Characterization of the mitochondrial genomes of three species in the ectomycorrhizal genus Cantharellus and phylogeny of Agaricomycetes. International Journal of Biological Macromolecules, 2018, 118, 756-769. | 3.6 | 43 |
| 1382 | A clone of the emergent Streptococcus pyogenes emm89 clade responsible for a large outbreak in a post-surgery oncology unit in France. Medical Microbiology and Immunology, 2018, 207, 287-296. | 2.6 | 10 |
| 1383 | Genomic analysis of a Raoultella ornithinolytica strain causing prosthetic joint infection in an immunocompetent patient. Scientific Reports, 2018, 8, 9462. | 1.6 | 10 |
| 1384 | Intrageneric chloroplast genome comparison in the genus Euglena (Phylum: Euglenophyta) with annotated chloroplast genomes of Euglena hiemalis and Euglena clara. Journal of Applied Phycology, 2018, 30, 3167-3177. | 1.5 | 2 |
| 1385 | The origin and remolding of genomic islands of differentiation in the European sea bass. Nature Communications, 2018, 9, 2518. | 5.8 | 86 |
| 1386 | Whole genome comparison of two Starmerella bacillaris strains with other wine yeasts uncovers genes involved in modulating important winemaking traits. FEMS Yeast Research, 2018, 18, . | 1.1 | 15 |
| 1387 | Rapid Detection of Candida auris Based on Loop-Mediated Isothermal Amplification (LAMP). Journal of Clinical Microbiology, 2018, 56, . | 1.8 | 46 |
| 1388 | Draft Genome Sequence of a White Spot Syndrome Virus Isolate Obtained in Ecuador. Genome Announcements, 2018, 6, . | 0.8 | 16 |
| 1389 | Utilization of Hybrid Assembly Approach to Determine the Genome of an Opportunistic Pathogenic Fungus, Candida albicans TIMM 1768. Genome Biology and Evolution, 2018, 10, 2017-2022. | 1.1 | 30 |
| 1390 | Characterization and comparative mitogenomic analysis of six newly sequenced mitochondrial genomes from ectomycorrhizal fungi (Russula) and phylogenetic analysis of the Agaricomycetes. International Journal of Biological Macromolecules, 2018, 119, 792-802. | 3.6 | 67 |
| 1391 | Distinctive characters of Nostoc genomes in cyanolichens. BMC Genomics, 2018, 19, 434. | 1.2 | 30 |
| 1392 | Otitis in a cat associated with Corynebacterium provencense. BMC Veterinary Research, 2018, 14, 200. | 0.7 | 5 |
| 1393 | Growth of Carnobacterium spp. isolated from chilled vacuum-packaged meat under relevant acidic conditions. International Journal of Food Microbiology, 2018, 286, 120-127. | 2.1 | 20 |
| 1394 | Mesophilic Sporeformers Identified in Whey Powder by Using Shotgun Metagenomic Sequencing. Applied and Environmental Microbiology, 2018, 84, . | 1.4 | 15 |
| 1395 | Emergence of a vanG-carrying and multidrug resistant ICE in zoonotic pathogen Streptococccus suis. Veterinary Microbiology, 2018, 222, 109-113. | 0.8 | 14 |
| 1396 | Whole genome sequencing and identification of Bacillus endophyticus and B. anthracis isolated from anthrax outbreaks in South Africa. BMC Microbiology, 2018, 18, 67. | 1.3 | 11 |
| 1397 | Comparative Chloroplast Genomics of Dipsacales Species: Insights Into Sequence Variation, Adaptive Evolution, and Phylogenetic Relationships. Frontiers in Plant Science, 2018, 9, 689. | 1.7 | 110 |
| 1398 | Horse Y chromosome assembly displays unique evolutionary features and putative stallion fertility genes. Nature Communications, 2018, 9, 2945. | 5.8 | 56 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1399 | SNP hot-spots in the clam parasite QPX. BMC Genomics, 2018, 19, 486. | 1.2 | 2 |
| 1400 | Genetic Separation of Listeria monocytogenes Causing Central Nervous System Infections in Animals. Frontiers in Cellular and Infection Microbiology, 2018, 8, 20. | 1.8 | 22 |
| 1401 | Phylogeny of Vibrio vulnificus from the Analysis of the Core-Genome: Implications for Intra-Species Taxonomy. Frontiers in Microbiology, 2017, 8, 2613. | 1.5 | 50 |
| 1402 | Orpheovirus IHUMI-LCC2: A New Virus among the Giant Viruses. Frontiers in Microbiology, 2017, 8, 2643. | 1.5 | 70 |
| 1403 | Phase Variable Expression of a Single Phage Receptor in Campylobacter jejuni NCTC12662 Influences Sensitivity Toward Several Diverse CPS-Dependent Phages. Frontiers in Microbiology, 2018, 9, 82. | 1.5 | 31 |
| 1404 | Exploring the Genomic Traits of Non-toxigenic Vibrio parahaemolyticus Strains Isolated in Southern Chile. Frontiers in Microbiology, 2018, 9, 161. | 1.5 | 37 |
| 1405 | Pantoea ananatis Genetic Diversity Analysis Reveals Limited Genomic Diversity as Well as Accessory Genes Correlated with Onion Pathogenicity. Frontiers in Microbiology, 2018, 9, 184. | 1.5 | 48 |
| 1406 | Comparative Genomics of Environmental and Clinical Burkholderia cenocepacia Strains Closely Related to the Highly Transmissible Epidemic ET12 Lineage. Frontiers in Microbiology, 2018, 9, 383. | 1.5 | 16 |
| 1407 | Genomic Structural Variations Affecting Virulence During Clonal Expansion of Pseudomonas syringae pv. actinidiae Biovar 3 in Europe. Frontiers in Microbiology, 2018, 9, 656. | 1.5 | 18 |
| 1408 | A Novel mcr-1 Variant Carried by an IncI2-Type Plasmid Identified From a Multidrug Resistant Enterotoxigenic Escherichia coli. Frontiers in Microbiology, 2018, 9, 815. | 1.5 | 12 |
| 1409 | The PL6-Family Plasmids of Haloquadratum Are Virus-Related. Frontiers in Microbiology, 2018, 9, 1070. | 1.5 | 3 |
| 1410 | Comparative Genomics Reveals Evidence of Genome Reduction and High Extracellular Protein Degradation Potential in Kangiella. Frontiers in Microbiology, 2018, 9, 1224. | 1.5 | 11 |
| 1411 | Clinical Staphylococcus argenteus Develops to Small Colony Variants to Promote Persistent Infection. Frontiers in Microbiology, 2018, 9, 1347. | 1.5 | 20 |
| 1412 | â€˜Candidatus Aquirickettsiella gammariâ€™ (Gammaproteobacteria: Legionellales: Coxiellaceae): A bacterial pathogen of the freshwater crustacean Gammarus fossarum (Malacostraca: Amphipoda). Journal of Invertebrate Pathology, 2018, 156, 41-53. | 1.5 | 23 |
| 1413 | Bacillus safensis FO-36b and Bacillus pumilus SAFR-032: a whole genome comparison of two spacecraft assembly facility isolates. BMC Microbiology, 2018, 18, 57. | 1.3 | 16 |
| 1414 | Physiological and Comparative Genomic Analysis of Arthrobacter sp. SRS-W-1-2016 Provides Insights on Niche Adaptation for Survival in Uraniferous Soils. Genes, 2018, 9, 31. | 1.0 | 42 |
| 1415 | The Unexplored Diversity of Pleolipoviruses: The Surprising Case of Two Viruses with Identical Major Structural Modules. Genes, 2018, 9, 131. | 1.0 | 8 |
| 1416 | Understanding plastome evolution in Hemiparasitic Santalales: Complete chloroplast genomes of three species, Dendrotrophe varians, Helixanthera parasitica, and Macrosolen cochinchinensis. PLoS ONE, 2018, 13, e0200293. | 1.1 | 32 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1417 | <i>Fusobacterium</i> Genomics Using MinION and Illumina Sequencing Enables Genome Completion and Correction. MSphere, 2018, 3, . | 1.3 | 23 |
| 1418 | Whole-Genome Comparison Reveals Heterogeneous Divergence and Mutation Hotspots in Chloroplast Genome of Eucommia ulmoides Oliver. International Journal of Molecular Sciences, 2018, 19, 1037. | 1.8 | 30 |
| 1419 | Comparative Plastid Genomes of Primula Species: Sequence Divergence and Phylogenetic Relationships. International Journal of Molecular Sciences, 2018, 19, 1050. | 1.8 | 43 |
| 1420 | Pseudomonas PB1-Like Phages: Whole Genomes from Metagenomes Offer Insight into an Abundant Group of Bacteriophages. Viruses, 2018, 10, 331. | 1.5 | 23 |
| 1421 | An integrative, multi-omics approach towards the prioritization of Klebsiella pneumoniae drug targets. Scientific Reports, 2018, 8, 10755. | 1.6 | 50 |
| 1422 | Cell-Derived Viral Genes Evolve under Stronger Purifying Selection in Rhadinoviruses. Journal of Virology, 2018, 92, . | 1.5 | 3 |
| 1423 | Anaerococcus jeddahensis sp. nov., a New Bacterial Species Isolated From Healthy Nomadic Bedouin Woman From Saudi Arabia. Current Microbiology, 2018, 75, 1419-1428. | 1.0 | 6 |
| 1424 | Genome comparison of different Zymomonas mobilis strains provides insights on conservation of the evolution. PLoS ONE, 2018, 13, e0195994. | 1.1 | 6 |
| 1425 | Novel multidomain, multifunctional glycoside hydrolases from highly lignocellulolytic <i>Caldicellulosiruptor</i> species. AICHE Journal, 2018, 64, 4218-4228. | 1.8 | 19 |
| 1426 | Population genomics of hypervirulent Klebsiella pneumoniae clonal-group 23 reveals early emergence and rapid global dissemination. Nature Communications, 2018, 9, 2703. | 5.8 | 205 |
| 1427 | The first plastid genome of a filamentous taxon â€˜Bangiaâ€™ sp. OUCPT-01 in the Bangiales. Scientific Reports, 2018, 8, 10688. | 1.6 | 6 |
| 1428 | Analysis of Phylogenetic Variation of Stenotrophomonas maltophilia Reveals Human-Specific Branches. Frontiers in Microbiology, 2018, 9, 806. | 1.5 | 39 |
| 1429 | Complete Genome Sequence of Clostridium kluyveri JZZ Applied in Chinese Strong-Flavor Liquor Production. Current Microbiology, 2018, 75, 1429-1433. | 1.0 | 11 |
| 1430 | SssP1, a Streptococcus suis Fimbria-Like Protein Transported by the SecY2/A2 System, Contributes to Bacterial Virulence. Applied and Environmental Microbiology, 2018, 84, . | 1.4 | 16 |
| 1431 | Comparative mitochondrial genomics of cryptophyte algae: gene shuffling and dynamic mobile genetic elements. BMC Genomics, 2018, 19, 275. | 1.2 | 23 |
| 1432 | The genome sequence of a SNP type 3K strain of <i>Mycobacterium leprae</i> isolated from a seventhâ€century Hungarian case of lepromatous leprosy. International Journal of Osteoarchaeology, 2018, 28, 439-447. | 0.6 | 13 |
| 1433 | Gene loss and genome rearrangement in the plastids of five Hemiparasites in the family Orobanchaceae. BMC Plant Biology, 2018, 18, 30. | 1.6 | 72 |
| 1434 | The reporting of a Bacillus anthracis B-clade strain in South Africa after more than 20Âyears. BMC Research Notes, 2018, 11, 264. | 0.6 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1435 | Chloroplast genome analyses and genomic resource development for epilithic sister genera Oresitrophe and Mukdenia (Saxifragaceae), using genome skimming data. BMC Genomics, 2018, 19, 235. | 1.2 | 106 |
| 1436 | Comparative genomics and systematics of Betaphycus, Eucheuma, and Kappaphycus (Solieriaceae:) Tj ETQq1 1 0.784314 rgBT /Overl | 1.5 | 11 |
| 1437 | Genome sequencing and functional characterization of the non-pathogenic Klebsiella pneumoniae KpGe bacteria. Microbes and Infection, 2018, 20, 293-301. | 1.0 | 28 |
| 1438 | xenoGI: reconstructing the history of genomic island insertions in clades of closely related bacteria. BMC Bioinformatics, 2018, 19, 32. | 1.2 | 12 |
| 1439 | Elucidation of the anti-hyperammonemic mechanism of Lactobacillus amylovorus JBD401 by comparative genomic analysis. BMC Genomics, 2018, 19, 292. | 1.2 | 12 |
| 1440 | Larger Than Life: Isolation and Genomic Characterization of a Jumbo Phage That Infects the Bacterial Plant Pathogen, Agrobacterium tumefaciens. Frontiers in Microbiology, 2018, 9, 1861. | 1.5 | 23 |
| 1441 | Characterization of the Complete Chloroplast Genomes of Buddleja colvilei and B. sessilifolia: Implications for the Taxonomy of Buddleja L.. Molecules, 2018, 23, 1248. | 1.7 | 17 |
| 1442 | The genome of a prasinoviruses-related freshwater virus reveals unusual diversity of phycodnaviruses. BMC Genomics, 2018, 19, 49. | 1.2 | 10 |
| 1443 | Genomic mapping of ST85 blaNDM-1 and blaOXA-94 producing Acinetobacter baumannii isolates from Syrian Civil War Victims. International Journal of Infectious Diseases, 2018, 74, 100-108. | 1.5 | 23 |
| 1444 | Three Distinct Contact-Dependent Growth Inhibition Systems Mediate Interbacterial Competition by the Cystic Fibrosis Pathogen Burkholderia dolosa. Journal of Bacteriology, 2018, 200, . | 1.0 | 19 |
| 1445 | Comparative Genome Analysis of 2 <i>Mycobacterium Tuberculosis</i> Strains from Pakistan: Insights Globally Into Drug Resistance, Virulence, and Niche Adaptation. Evolutionary Bioinformatics, 2018, 14, 117693431879025. | 0.6 | 3 |
| 1446 | Tracking microevolution events among ST11 carbapenemase-producing hypervirulent <i>Klebsiella pneumoniae</i> outbreak strains. Emerging Microbes and Infections, 2018, 7, 1-8. | 3.0 | 65 |
| 1447 | The complete methylome of an entomopathogenic bacterium reveals the existence of loci with unmethylated Adenines. Scientific Reports, 2018, 8, 12091. | 1.6 | 27 |
| 1448 | Linking genotype and phenotype in an economically viable propionic acid biosynthesis process. Biotechnology for Biofuels, 2018, 11, 224. | 6.2 | 10 |
| 1449 | Comparative genomic analysis of multidrug-resistant <em>Streptococcus pneumoniae</em> isolates. Infection and Drug Resistance, 2018, Volume 11, 659-670. | 1.1 | 7 |
| 1450 | What's the Difference?. , 2018, , . |  | 14 |
| 1451 | Cooperative Metabolic Adaptations in the Host Can Favor Asymptomatic Infection and Select for Attenuated Virulence in an Enteric Pathogen. Cell, 2018, 175, 146-158.e15. | 13.5 | 127 |
| 1452 | Comparison between complete genomes of an isolate of Pseudomonas syringae pv. actinidiae from Japan and a New Zealand isolate of the pandemic lineage. Scientific Reports, 2018, 8, 10915. | 1.6 | 23 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1453 | Near-Complete Genome Sequence of Pseudomonas palleroniana MAB3, a Beneficial 1-Aminocyclopropane-1-Carboxylate Deaminase-Producing Bacterium Able To Promote the Growth of Mushrooms and Plants. Genome Announcements, 2018, 6, . | 0.8 | 3 |
| 1454 | Positions 299 and 302 of the GerAA subunit are important for function of the GerA spore germination receptor in Bacillus subtilis. PLoS ONE, 2018, 13, e0198561. | 1.1 | 7 |
| 1455 | Nextâ€generation lineage discovery: A case study of tuberous Claytonia L.. American Journal of Botany, 2018, 105, 536-548. | 0.8 | 15 |
| 1456 | Genomic comparisons of Rhizobium species using in silico AFLP-PCR, endonuclease restriction, and AMPylating enzymes. Electronic Journal of Biotechnology, 2018, 34, 67-75. | 1.2 | 0 |
| 1457 | Comparison of genomes and proteomes of four whole genome-sequenced Campylobacter jejuni from different phylogenetic backgrounds. PLoS ONE, 2018, 13, e0190836. | 1.1 | 7 |
| 1458 | Genomic differences between nasal Staphylococcus aureus from hog slaughterhouse workers and their communities. PLoS ONE, 2018, 13, e0193820. | 1.1 | 11 |
| 1459 | Diversity of CTX-M-1-producing E. coli from German food samples and genetic diversity of the bla CTX-M-1 region on IncI1 ST3 plasmids. Veterinary Microbiology, 2018, 221, 98-104. | 0.8 | 54 |
| 1460 | Genome Rearrangement Shapes Prochlorococcus Ecological Adaptation. Applied and Environmental Microbiology, 2018, 84, . | 1.4 | 17 |
| 1461 | Microbial genomic island discovery, visualization and analysis. Briefings in Bioinformatics, 2019, 20, 1685-1698. | 3.2 | 86 |
| 1462 | Complete Genome Sequence of Actinosynnema pretiosum X47, An Industrial Strain that Produces the Antibiotic Ansamitocin AP-3. Current Microbiology, 2019, 76, 954-958. | 1.0 | 6 |
| 1463 | <i>Passiflora</i> plastome sequencing reveals widespread genomic rearrangements. Journal of Systematics and Evolution, 2019, 57, 1-14. | 1.6 | 61 |
| 1464 | Noncontiguous finished genome sequence and description of <i>Intestinimonas massilien</i>sis sp. nov strain <scp>GD</scp>2<sup>T</sup>, the second <i>Intestinimonas</i> species cultured from the human gut. MicrobiologyOpen, 2019, 8, e00621. | 1.2 | 19 |
| 1465 | Genome Alignment. , 2019, , 268-283. |  | 0 |
| 1466 | Genome Sequence and Antifungal Activity of Two Niche-Sharing Pseudomonas protegens Related Strains Isolated from Hydroponics. Microbial Ecology, 2019, 77, 1025-1035. | 1.4 | 2 |
| 1467 | Accurate multiple alignment of distantly related genome sequences using filtered spaced word matches as anchor points. Bioinformatics, 2019, 35, 211-218. | 1.8 | 11 |
| 1468 | Plastid Genomes of Five Species of Riverweeds (Podostemaceae): Structural Organization and Comparative Analysis in Malpighiales. Frontiers in Plant Science, 2019, 10, 1035. | 1.7 | 43 |
| 1469 | Morphologic and genomic characterization of a broad host range Salmonella enterica serovar Pullorum lytic phage vB_SPuM_SP116. Microbial Pathogenesis, 2019, 136, 103659. | 1.3 | 24 |
| 1470 | Genomic and Ecogenomic Characterization of Proteus mirabilis Bacteriophages. Frontiers in Microbiology, 2019, 10, 1783. | 1.5 | 13 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1471 | Phylogenetic, genomic, and biogeographic characterization of a novel and ubiquitous marine invertebrate-associated Rickettsiales parasite, <i>Candidatus</i> Aquarickettsia rohweri, gen. nov., sp. nov. ISME Journal, 2019, 13, 2938-2953. | 4.4 | 82 |
| 1472 | Thirteen New Plastid Genomes from Mixotrophic and Autotrophic Species Provide Insights into Heterotrophy Evolution in Neottieae Orchids. Genome Biology and Evolution, 2019, 11, 2457-2467. | 1.1 | 26 |
| 1473 | Elucidating Viral Communities During a Phytoplankton Bloom on the West Antarctic Peninsula. Frontiers in Microbiology, 2019, 10, 1014. | 1.5 | 28 |
| 1474 | Genomic Polymorphism Associated with the Emergence of Virulent Isolates of Mycobacterium bovis in the Nile Delta. Scientific Reports, 2019, 9, 11657. | 1.6 | 17 |
| 1475 | Shared Pathogenomic Patterns Characterize a New Phylotype, Revealing Transition toward Host-Adaptation Long before Speciation of Mycobacterium tuberculosis. Genome Biology and Evolution, 2019, 11, 2420-2438. | 1.1 | 29 |
| 1476 | Development of gene-based molecular markers tagging low alkaloid pauper locus in white lupin (Lupinus albus L.). Journal of Applied Genetics, 2019, 60, 269-281. | 1.0 | 17 |
| 1477 | Engineered Interspecies Amino Acid Cross-Feeding Increases Population Evenness in a Synthetic Bacterial Consortium. MSystems, 2019, 4, . | 1.7 | 39 |
| 1478 | Comparison of single-nucleotide variants identified by Illumina and Oxford Nanopore technologies in the context of a potential outbreak of Shiga toxinâ€"producing Escherichia coli. GigaScience, 2019, 8, . | 3.3 | 42 |
| 1479 | Frog Virus 3 Genomes Reveal Prevalent Recombination between Ranavirus Lineages and Their Origins in Canada. Journal of Virology, 2019, 93, . | 1.5 | 20 |
| 1480 | Complete genome and plasmid sequence of a novel Bacillus sp. BD59S, a parasporal protein synthesizing bacterium. 3 Biotech, 2019, 9, 318. | 1.1 | 1 |
| 1481 | Dual Role of <i>gnaA</i> in Antibiotic Resistance and Virulence in Acinetobacter baumannii. Antimicrobial Agents and Chemotherapy, 2019, 63, . | 1.4 | 23 |
| 1482 | Defining the human gut hostâ€"phage network through single-cell viral tagging. Nature Microbiology, 2019, 4, 2192-2203. | 5.9 | 95 |
| 1483 | The complete mitochondrial genomes of five important medicinal Ganoderma species: Features, evolution, and phylogeny. International Journal of Biological Macromolecules, 2019, 139, 397-408. | 3.6 | 62 |
| 1484 | Genomeâ€wide nucleotide variation distinguishes<i>Aspergillus flavus</i>from<i>Aspergillus oryzae</i>and helps to reveal origins of atoxigenic<i>A. flavus</i>biocontrol strains. Journal of Applied Microbiology, 2019, 127, 1511-1520. | 1.4 | 15 |
| 1485 | The importance of genome sequence quality to microbial comparative genomics. BMC Genomics, 2019, 20, 662. | 1.2 | 35 |
| 1486 | Whole-Genome Alignment. Methods in Molecular Biology, 2019, 1910, 121-147. | 0.4 | 5 |
| 1487 | Efficient merging of genome profile alignments. Bioinformatics, 2019, 35, i71-i80. | 1.8 | 1 |
| 1488 | Closed Genome Sequences of Three Salmonella enterica Strains Belonging to Serovars Saintpaul, Weltevreden, and Thompson, Isolated from Mexico. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 4 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1489 | Extensive chloroplast genome rearrangement amongst three closely related Halamphora spp. (Bacillariophyceae), and evidence for rapid evolution as compared to land plants. PLoS ONE, 2019, 14, e0217824. | 1.1 | 16 |
| 1490 | Chloroplast and mitochondrial genetic variation of larches at the Siberian tundra-taiga ecotone revealed by de novo assembly. PLoS ONE, 2019, 14, e0216966. | 1.1 | 13 |
| 1491 | Functional genome annotation depicts probiotic properties of Bacillus velezensis FTC01. Gene, 2019, 713, 143971. | 1.0 | 22 |
| 1492 | Chromosome-Level Alpaca Reference Genome VicPac3.1 Improves Genomic Insight Into the Biology of New World Camelids. Frontiers in Genetics, 2019, 10, 586. | 1.1 | 19 |
| 1493 | Quorum Quenching Enzyme APTM01, an Acylhomoserine-Lactone Acylase from Marine Bacterium of Pseudoalteromonas tetraodonis Strain MQS005. Current Microbiology, 2019, 76, 1387-1397. | 1.0 | 10 |
| 1494 | Resistome and a Novel <i>bla</i><sub>NDM-1</sub>-Harboring Plasmid of an <i>Acinetobacter haemolyticus</i> Strain from a Children's Hospital in Puebla, Mexico. Microbial Drug Resistance, 2019, 25, 1023-1031. | 0.9 | 27 |
| 1495 | Insights From the Genome Sequence of Mycobacterium paragordonae, a Potential Novel Live Vaccine for Preventing Mycobacterial Infections: The Putative Role of Type VII Secretion Systems for an Intracellular Lifestyle Within Free-Living Environmental Predators. Frontiers in Microbiology, 2019, 10, 1524. | 1.5 | 8 |
| 1496 | High colonization rate of a novel carbapenem-resistant Klebsiella lineage among migratory birds at Qinghai Lake, China. Journal of Antimicrobial Chemotherapy, 2019, 74, 2895-2903. | 1.3 | 21 |
| 1497 | Mycoheterotrophic Epirixanthes (Polygalaceae) has a typical angiosperm mitogenome but unorthodox plastid genomes. Annals of Botany, 2019, 124, 791-807. | 1.4 | 14 |
| 1498 | Differentiations in Gene Content and Expression Response to Virulence Induction Between Two Agrobacterium Strains. Frontiers in Microbiology, 2019, 10, 1554. | 1.5 | 25 |
| 1499 | geneCo: a visualized comparative genomic method to analyze multiple genome structures. Bioinformatics, 2019, 35, 5303-5305. | 1.8 | 19 |
| 1500 | Nanopore sequencing for fast determination of plasmids, phages, virulence markers, and antimicrobial resistance genes in Shiga toxin-producing Escherichia coli. PLoS ONE, 2019, 14, e0220494. | 1.1 | 86 |
| 1501 | Retrospective Analysis of Archived Pyrazinamide Resistant Mycobacterium tuberculosis Complex Isolates from Ugandaâ€"Evidence of Interspecies Transmission. Microorganisms, 2019, 7, 221. | 1.6 | 6 |
| 1502 | Comparative genomics of Mycobacterium mucogenicum and Mycobacterium neoaurum clade members emphasizing tRNA and non-coding RNA. BMC Evolutionary Biology, 2019, 19, 124. | 3.2 | 10 |
| 1503 | Plastid genome evolution in tribe Desmodieae (Fabaceae: Papilionoideae). PLoS ONE, 2019, 14, e0218743. | 1.1 | 23 |
| 1504 | Terpene Synthase Genes Originated from Bacteria through Horizontal Gene Transfer Contribute to Terpenoid Diversity in Fungi. Scientific Reports, 2019, 9, 9223. | 1.6 | 31 |
| 1505 | Comparative genomic analyses of<i>Mycoplasma synoviae</i>vaccine strain MS-H and its wild-type parent strain 86079/7NS: implications for the identification of virulence factors and applications in diagnosis of<i>M. synoviae</i>. Avian Pathology, 2019, 48, 537-548. | 0.8 | 14 |
| 1506 | Comparative Genome Analysis of Uropathogenic Morganella morganii Strains. Frontiers in Cellular and Infection Microbiology, 2019, 9, 167. | 1.8 | 30 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1507 | Biological properties and genomics analysis of vB_KpnS_GH-K3, a Klebsiella phage with a putative depolymerase-like protein. Virus Genes, 2019, 55, 696-706. | 0.7 | 26 |
| 1508 | Penicillin-Binding Protein Typing, Antibiotic Resistance Gene Identification, and Molecular Phylogenetic Analysis of Meropenem-Resistant Streptococcus pneumoniae Serotype 19A-CC3111 Strains in Japan. Antimicrobial Agents and Chemotherapy, 2019, 63, . | 1.4 | 13 |
| 1509 | Whole genome analysis of Aspergillus sojae SMF 134 supports its merits as a starter for soybean fermentation. Journal of Microbiology, 2019, 57, 874-883. | 1.3 | 16 |
| 1510 | Deletion of the major Escherichia coli multidrug transporter AcrB reveals transporter plasticity and redundancy in bacterial cells. PLoS ONE, 2019, 14, e0218828. | 1.1 | 15 |
| 1511 | The complete chloroplast genome of pearl millet (<i>Pennisetum glaucum</i> (L.) R. Br.) and comparative analysis within the family poaceae. Cereal Research Communications, 2019, 47, 1-10. | 0.8 | 3 |
| 1512 | Differential efficiency of wild type rhizogenic strains for rol gene transformation of plants. Applied Microbiology and Biotechnology, 2019, 103, 6657-6672. | 1.7 | 20 |
| 1513 | Genomic analysis of the four ecologically distinct cactus host populations of Drosophila mojavensis. BMC Genomics, 2019, 20, 732. | 1.2 | 17 |
| 1514 | A new PacBio genome sequence of an Australian Pyrenophora tritici-repentis race 1 isolate. BMC Research Notes, 2019, 12, 642. | 0.6 | 12 |
| 1515 | Can Insertion Sequences Proliferation Influence Genomic Plasticity? Comparative Analysis of Acinetobacter baumannii Sequence Type 78, a Persistent Clone in Italian Hospitals. Frontiers in Microbiology, 2019, 10, 2080. | 1.5 | 23 |
| 1516 | Adaptive Evolution of Sphingobium hydrophobicum C1T in Electronic Waste Contaminated River Sediment. Frontiers in Microbiology, 2019, 10, 2263. | 1.5 | 7 |
| 1517 | De Novo Assembly Discovered Novel Structures in Genome of Plastids and Revealed Divergent Inverted Repeats in Mammillaria (Cactaceae, Caryophyllales). Plants, 2019, 8, 392. | 1.6 | 28 |
| 1518 | Amphibian skin-associated Pigmentiphaga: Genome sequence and occurrence across geography and hosts. PLoS ONE, 2019, 14, e0223747. | 1.1 | 8 |
| 1519 | The complete mitochondrial genome sequence of the medicinal fungus Inonotus obliquus (Hymenochaetaceae, Basidiomycota). Mitochondrial DNA Part B: Resources, 2019, 4, 3504-3506. | 0.2 | 5 |
| 1520 | Phenotypic characteristics contributing to the enhanced growth ofEscherichia colibloom strains. Environmental Microbiology Reports, 2019, 11, 817-824. | 1.0 | 1 |
| 1521 | Comparative Mitochondrial Genome Analysis of Two Ectomycorrhizal Fungi (Rhizopogon) Reveals Dynamic Changes of Intron and Phylogenetic Relationships of the Subphylum Agaricomycotina. International Journal of Molecular Sciences, 2019, 20, 5167. | 1.8 | 65 |
| 1522 | <i>lptG</i> contributes to changes in membrane permeability and the emergence of multidrug hypersusceptibility in a cystic fibrosis isolate of <i>Pseudomonas aeruginosa</i>. MicrobiologyOpen, 2019, 8, e844. | 1.2 | 6 |
| 1523 | The architecture of the Plasmodiophora brassicae nuclear and mitochondrial genomes. Scientific Reports, 2019, 9, 15753. | 1.6 | 17 |
| 1524 | The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. Nucleic Acids Research, 2020, 48, D606-D612. | 6.5 | 552 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1525 | Bioinformatics for Marine Products: An Overview of Resources, Bottlenecks, and Perspectives. Marine Drugs, 2019, 17, 576. | 2.2 | 26 |
| 1526 | Evolutionary Dynamics of Transferred Sequences Between Organellar Genomes in Cucurbita. Journal of Molecular Evolution, 2019, 87, 327-342. | 0.8 | 4 |
| 1527 | Gene Composition as a Potential Barrier to Large Recombinations in the Bacterial Pathogen Klebsiella pneumoniae. Genome Biology and Evolution, 2019, 11, 3240-3251. | 1.1 | 18 |
| 1528 | Himalayan Saccharomyces eubayanus Genome Sequences Reveal Genetic Markers Explaining Heterotic Maltotriose Consumption by Saccharomyces pastorianus Hybrids. Applied and Environmental Microbiology, 2019, 85, . | 1.4 | 21 |
| 1529 | Draft genome sequence of Bacillus paralicheniformis TRQ65, a biological control agent and plant growth-promoting bacterium isolated from wheat (Triticum turgidum subsp. durum) rhizosphere in the Yaqui Valley, Mexico. 3 Biotech, 2019, 9, 436. | 1.1 | 32 |
| 1530 | Molecular tools for the characterization of seizure susceptibility in genetic rodent models of epilepsy. Epilepsy and Behavior, 2021, 121, 106594. | 0.9 | 6 |
| 1531 | Comparative Study on A Novel Pathogen of European Seabass. Diversity of Aeromonas veronii in the Aegean Sea. Microorganisms, 2019, 7, 504. | 1.6 | 13 |
| 1532 | Characterization of a Novel Thermobifida fusca Bacteriophage P318. Viruses, 2019, 11, 1042. | 1.5 | 0 |
| 1533 | Multiplex PCR for genotyping <i>Flavobacterium columnare</i>. Journal of Fish Diseases, 2019, 42, 1531-1542. | 0.9 | 17 |
| 1534 | Large Phenotypic and Genetic Diversity of Prophages Induced from the Fish Pathogen Vibrio anguillarum. Viruses, 2019, 11, 983. | 1.5 | 19 |
| 1535 | gapFinisher: A reliable gap filling pipeline for SSPACE-LongRead scaffolder output. PLoS ONE, 2019, 14, e0216885. | 1.1 | 14 |
| 1536 | Plastid Genomes of Carnivorous Plants Drosera rotundifolia and Nepenthes Ã— ventrata Reveal Evolutionary Patterns Resembling Those Observed in Parasitic Plants. International Journal of Molecular Sciences, 2019, 20, 4107. | 1.8 | 13 |
| 1537 | Production of WW males lacking the masculine Z chromosome and mining the Macrobrachium rosenbergii genome for sex-chromosomes. Scientific Reports, 2019, 9, 12408. | 1.6 | 25 |
| 1538 | Identification of Novel Bacteriophages with Therapeutic Potential That Target <i>Enterococcus faecalis</i>. Infection and Immunity, 2019, 87, . | 1.0 | 50 |
| 1539 | Comparative genomics of 11 complete chloroplast genomes of Senecioneae (Asteraceae) species: DNA barcodes and phylogenetics. , 2019, 60, 17. |  | 29 |
| 1540 | Draft Assembly of<i>Phytophthora capsici</i>from Long-Read Sequencing Uncovers Complexity. Molecular Plant-Microbe Interactions, 2019, 32, 1559-1563. | 1.4 | 33 |
| 1541 | Comparative genomics of Aeromonas veronii: Identification of a pathotype impacting aquaculture globally. PLoS ONE, 2019, 14, e0221018. | 1.1 | 50 |
| 1542 | Investigation into limiting dilution and tick transmissibility phenotypes associated with attenuation of the S24 vaccine strain. Parasites and Vectors, 2019, 12, 419. | 1.0 | 4 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1543 | A novel salt-tolerant genotype illuminates the sucrose gene evolution in freshwater bloom-forming cyanobacterium <i>Microcystis aeruginosa</i>. FEMS Microbiology Letters, 2019, 366, . | 0.7 | 5 |
| 1544 | Phylogenomic and epidemiological insights into two clinical Mycobacterium bovis BCG strains circulating in South Africa. International Journal of Infectious Diseases, 2019, 87, 32-38. | 1.5 | 2 |
| 1545 | Characteristics and Complete Genome Analysis of Bacillus asahii OM18, a Bacterium in Relation to Soil Fertility in Alkaline Soils Under Long-Term Organic Manure Amendment. Current Microbiology, 2019, 76, 1512-1519. | 1.0 | 4 |
| 1546 | A hybrid sub-lineage of Listeria monocytogenes comprising hypervirulent isolates. Nature Communications, 2019, 10, 4283. | 5.8 | 76 |
| 1547 | Comparative Genomics and Phylogenomic Analysis of the Genus Salinivibrio. Frontiers in Microbiology, 2019, 10, 2104. | 1.5 | 23 |
| 1548 | Genome Mining and Comparative Pathogenomic Analysis of An Endemic Methicillin-Resistant Staphylococcus Aureus (MRSA) Clone, ST612-CC8-t1257-SCCmec_IVd(2B), Isolated in South Africa. Pathogens, 2019, 8, 166. | 1.2 | 9 |
| 1549 | Assembly and comparative analyses of the mitochondrial genome of Castanospermum australe (Papilionoideae, Leguminosae). Australian Systematic Botany, 2019, 32, 484-494. | 0.3 | 4 |
| 1550 | An African Salmonella Typhimurium ST313 sublineage with extensive drug-resistance and signatures of host adaptation. Nature Communications, 2019, 10, 4280. | 5.8 | 80 |
| 1551 | Whole genome sequencing of a ST2594 MRSA strain causing non-mucosal preoperative colonization and low-grade postoperative infection. Antonie Van Leeuwenhoek, 2019, 112, 961-964. | 0.7 | 1 |
| 1552 | The Genome Sequence of M228, a Chinese Isolate of Pseudomonas syringae pv. actinidiae, Illustrates Insertion Sequence Element Mobility. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 7 |
| 1553 | Whole-genome sequencing data-based modeling for the investigation of an outbreak of community-associated methicillin-resistant Staphylococcus aureus in a neonatal intensive care unit in Hong Kong. European Journal of Clinical Microbiology and Infectious Diseases, 2019, 38, 563-573. | 1.3 | 23 |
| 1554 | Megaphages infect Prevotella and variants are widespread in gut microbiomes. Nature Microbiology, 2019, 4, 693-700. | 5.9 | 141 |
| 1555 | The complete mitochondrial genome sequence of the edible mushroom Stropharia rugosoannulata (Strophariaceae, Basidiomycota). Mitochondrial DNA Part B: Resources, 2019, 4, 570-572. | 0.2 | 3 |
| 1556 | Plastid Genomes from Diverse Glaucophyte Genera Reveal a Largely Conserved Gene Content and Limited Architectural Diversity. Genome Biology and Evolution, 2019, 11, 174-188. | 1.1 | 16 |
| 1557 | Transcriptional Reprogramming of Rice Cells by Xanthomonas oryzae TALEs. Frontiers in Plant Science, 2019, 10, 162. | 1.7 | 38 |
| 1558 | Rational construction of genome-reduced and high-efficient industrial Streptomyces chassis based on multiple comparative genomic approaches. Microbial Cell Factories, 2019, 18, 16. | 1.9 | 55 |
| 1559 | Comparative analysis reveals the Genomic Islands in Pasteurella multocida population genetics: on Symbiosis and adaptability. BMC Genomics, 2019, 20, 63. | 1.2 | 9 |
| 1560 | Design and Preclinical Development of a Phage Product for the Treatment of Antibiotic-Resistant Staphylococcus aureus Infections. Viruses, 2019, 11, 88. | 1.5 | 109 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1561 | Virulence Characteristics and an Action Mode of Antibiotic Resistance in Multidrug-Resistant Pseudomonas aeruginosa. Scientific Reports, 2019, 9, 487. | 1.6 | 59 |
| 1562 | Dissecting the Evolutionary Development of the Species <i>Bifidobacterium animalis</i> through Comparative Genomics Analyses. Applied and Environmental Microbiology, 2019, 85, . | 1.4 | 11 |
| 1563 | Genome analysis of Salmonella enterica subsp. diarizonae isolates from invasive human infections reveals enrichment of virulence-related functions in lineage ST1256. BMC Genomics, 2019, 20, 99. | 1.2 | 24 |
| 1564 | Detecting useful genetic markers and reconstructing the phylogeny of an important medicinal resource plant, Artemisia selengensis, based on chloroplast genomics. PLoS ONE, 2019, 14, e0211340. | 1.1 | 43 |
| 1565 | Preventive effect of the phage VB-SavM-JYL01 on rabbit necrotizing pneumonia caused by Staphylococcus aureus. Veterinary Microbiology, 2019, 229, 72-80. | 0.8 | 31 |
| 1566 | Comparative genomic analysis of subspecies of Pantoea stewartii reveals distinct variations. Journal of Plant Pathology, 2019, 101, 997-1004. | 0.6 | 1 |
| 1567 | The complete organelle genomes of Physochlaina orientalis: Insights into short sequence repeats across seed plant mitochondrial genomes. Molecular Phylogenetics and Evolution, 2019, 137, 274-284. | 1.2 | 19 |
| 1568 | The implication of plastid transcriptome analysis in petaloid monocotyledons: A case study of Lilium lancifolium (Liliaceae, Liliales). Scientific Reports, 2019, 9, 6662. | 1.6 | 3 |
| 1569 | Draft Genome Sequence of <i>Rhodoplanes</i> sp. Strain T2.26MG-98, Isolated from 492.6 Meters Deep on the Subsurface of the Iberian Pyrite Belt. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 8 |
| 1570 | Global Biogeographic Distribution Patterns of Thermoacidophilic Verrucomicrobia Methanotrophs Suggest Allopatric Evolution. Frontiers in Microbiology, 2019, 10, 1129. | 1.5 | 31 |
| 1571 | Successful treatment and digestive decolonisation of a patient with osteitis caused by a carbapenemase-producing Klebsiella pneumoniae isolate harbouring both NDM-1 and OXA-48 enzymes. Journal of Global Antimicrobial Resistance, 2019, 18, 225-229. | 0.9 | 9 |
| 1572 | Genetic and Phenotypic Features of a Novel Acinetobacter Species, Strain A47, Isolated From the Clinical Setting. Frontiers in Microbiology, 2019, 10, 1375. | 1.5 | 4 |
| 1573 | Isolation and Characterization T4- and T7-Like Phages that Infect the Bacterial Plant Pathogen Agrobacterium tumefaciens. Viruses, 2019, 11, 528. | 1.5 | 9 |
| 1574 | Microbial characterization of heavy metal resistant bacterial strains isolated from an electroplating wastewater treatment plant. Ecotoxicology and Environmental Safety, 2019, 181, 472-480. | 2.9 | 49 |
| 1575 | An <i>In Vitro</i> Enrichment Strategy for Formulating Synergistic Synbiotics. Applied and Environmental Microbiology, 2019, 85, . | 1.4 | 15 |
| 1576 | Comparative genomic analysis of Pectobacterium carotovorum subsp. brasiliense SX309 provides novel insights into its genetic and phenotypic features. BMC Genomics, 2019, 20, 486. | 1.2 | 29 |
| 1577 | Characterization of a bacteriophage with broad host range against strains of Pseudomonas aeruginosa isolated from domestic animals. BMC Microbiology, 2019, 19, 134. | 1.3 | 35 |
| 1578 | Enrichment of G4DNA and a Large Inverted Repeat Coincide in the Mitochondrial Genomes of Termitomyces. Genome Biology and Evolution, 2019, 11, 1857-1869. | 1.1 | 23 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1579 | Genomic analysis and lactose transporter expression in Kluyveromyces marxianus CCT 7735. Fungal Biology, 2019, 123, 687-697. | 1.1 | 4 |
| 1580 | Antimicrobial activity of bioactive starch packaging films against Listeria monocytogenes and reconstituted meat microbiota on ham. International Journal of Food Microbiology, 2019, 305, 108253. | 2.1 | 37 |
| 1581 | Temperate Bacteriophages from Chronic Pseudomonas aeruginosa Lung Infections Show Disease-Specific Changes in Host Range and Modulate Antimicrobial Susceptibility. MSystems, 2019, 4, . | 1.7 | 38 |
| 1582 | A mitochondrial genome phylogeny of Mytilidae (Bivalvia: Mytilida). Molecular Phylogenetics and Evolution, 2019, 139, 106533. | 1.2 | 41 |
| 1583 | Whole-genome sequencing reveals recent and frequent genetic recombination between clonal lineages of Cryphonectria parasitica in western Europe. Fungal Genetics and Biology, 2019, 130, 122-133. | 0.9 | 16 |
| 1584 | Diversification of Vibrio anguillarum Driven by the Bacteriophage CHOED. Frontiers in Microbiology, 2019, 10, 1396. | 1.5 | 11 |
| 1586 | Genomic sequencing of Troides aeacus nucleopolyhedrovirus (TraeNPV) from golden birdwing larvae (Troides aeacus formosanus) to reveal defective Autographa californica NPV genomic features. BMC Genomics, 2019, 20, 419. | 1.2 | 5 |
| 1587 | Extremely diverse structural organization in the complete mitochondrial genome of seedless Phoenix dactylifera L. Vegetos, 2019, 32, 92-97. | 0.8 | 3 |
| 1588 | Comparative Genomics of Thiohalobacter thiocyanaticus HRh1T and Guyparkeria sp. SCN-R1, Halophilic Chemolithoautotrophic Sulfur-Oxidizing Gammaproteobacteria Capable of Using Thiocyanate as Energy Source. Frontiers in Microbiology, 2019, 10, 898. | 1.5 | 20 |
| 1589 | Complete plastid genome of Kappaphycus alvarezii: insights of large-scale rearrangements among Florideophyceae plastid genomes. Journal of Applied Phycology, 2019, 31, 3997-4005. | 1.5 | 9 |
| 1590 | Genetic characterization of susceptible and multi-drug resistant Mannheimia haemolytica isolated from high-risk stocker calves prior to and after antimicrobial metaphylaxis. Veterinary Microbiology, 2019, 235, 110-117. | 0.8 | 11 |
| 1591 | Improving End-User Trust in the Quality of Commercial Probiotic Products. Frontiers in Microbiology, 2019, 10, 739. | 1.5 | 109 |
| 1592 | Pacbio Sequencing Reveals Identical Organelle Genomes between American Cranberry (Vaccinium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 | 1.0 | 12 |
| 1593 | De novo genome sequencing and secretome analysis of Tilletia indica inciting Karnal bunt of wheat provides pathogenesis-related genes. 3 Biotech, 2019, 9, 219. | 1.1 | 19 |
| 1594 | Comparative Analysis of the Two Acinetobacter baumannii Multilocus Sequence Typing (MLST) Schemes. Frontiers in Microbiology, 2019, 10, 930. | 1.5 | 133 |
| 1595 | Omics-based comparative analysis of putative mobile genetic elements in Lactococcus lactis. FEMS Microbiology Letters, 2019, 366, . | 0.7 | 4 |
| 1596 | Genome characterization of an extensively drugâ€resistant <i>Streptococcus pneumoniae</i> serotype 11A strain. Microbiology and Immunology, 2019, 63, 206-212. | 0.7 | 0 |
| 1597 | Antarctic Streptomyces fildesensis So13.3 strain as a promising source for antimicrobials discovery. Scientific Reports, 2019, 9, 7488. | 1.6 | 27 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1598 | Mobile genetic elements explain size variation in the mitochondrial genomes of four closely-related Armillaria species. BMC Genomics, 2019, 20, 351. | 1.2 | 49 |
| 1599 | Breaking Free: The Genomics of Allopolyploidy-Facilitated Niche Expansion in White Clover. Plant Cell, 2019, 31, 1466-1487. | 3.1 | 89 |
| 1600 | The Complete Chloroplast Genome of Euphrasia regelii, Pseudogenization of ndh Genes and the Phylogenetic Relationships Within Orobanchaceae. Frontiers in Genetics, 2019, 10, 444. | 1.1 | 31 |
| 1601 | Guarani Virophage, a New Sputnik-Like Isolate From a Brazilian Lake. Frontiers in Microbiology, 2019, 10, 1003. | 1.5 | 19 |
| 1602 | Comparative Genomic Analysis of<i>Lactobacillus plantarum</i>: An Overview. International Journal of Genomics, 2019, 2019, 1-11. | 0.8 | 45 |
| 1603 | Chromosomal genome assembly of the ethanol production strain CBS 11270 indicates a highly dynamic genome structure in the yeast species Brettanomyces bruxellensis. PLoS ONE, 2019, 14, e0215077. | 1.1 | 8 |
| 1604 | The Cano-eMLST Program: An Approach for the Calculation of Canonical Extended Multi-Locus Sequence Typing, Making Comparison of Genetic Differences Among Bunches of Bacterial Strains. Microorganisms, 2019, 7, 98. | 1.6 | 2 |
| 1605 | Extended insight into the Mycobacterium chelonae-abscessus complex through whole genome sequencing of Mycobacterium salmoniphilum outbreak and Mycobacterium salmoniphilum-like strains. Scientific Reports, 2019, 9, 4603. | 1.6 | 12 |
| 1606 | Strain- and Species-Level Variation in the Microbiome of Diabetic Wounds Is Associated with Clinical Outcomes and Therapeutic Efficacy. Cell Host and Microbe, 2019, 25, 641-655.e5. | 5.1 | 192 |
| 1607 | Comparative Genomic Analysis of the Virulence Plasmid from Salmonella enterica Subspecies enterica Serovar Enteritidis. Russian Journal of Genetics, 2019, 55, 144-153. | 0.2 | 3 |
| 1608 | The complete chloroplast genome sequence of <i>Rubus coreanus</i>, an excellent diseases-resistant resource. Mitochondrial DNA Part B: Resources, 2019, 4, 216-217. | 0.2 | 5 |
| 1609 | Post-transcriptional Regulation of FLOWERING LOCUS T Modulates Heat-Dependent Source-Sink Development in Potato. Current Biology, 2019, 29, 1614-1624.e3. | 1.8 | 58 |
| 1610 | The bacteriocin from the prophylactic candidate Streptococcus suis 90-1330 is widely distributed across S. suis isolates and appears encoded in an integrative and conjugative element. PLoS ONE, 2019, 14, e0216002. | 1.1 | 8 |
| 1611 | Complete genome sequence of fowl adenovirus-8b UPM04217 isolate associated with the inclusion body hepatitis disease in commercial broiler chickens in Malaysia reveals intermediate evolution. VirusDisease, 2019, 30, 426-432. | 1.0 | 6 |
| 1612 | Illumina sequencing of clinical samples for virus detection in a public health laboratory. Scientific Reports, 2019, 9, 5409. | 1.6 | 34 |
| 1613 | Phage-Encoded LuxR-Type Receptors Responsive to Host-Produced Bacterial Quorum-Sensing Autoinducers. MBio, 2019, 10, . | 1.8 | 46 |
| 1614 | Isolation and Bacteriocin-Related Typing of Streptococcus dentisani. Frontiers in Cellular and Infection Microbiology, 2019, 9, 110. | 1.8 | 28 |
| 1615 | Genome sequence and description of Traorella massiliensis gen. nov., sp. nov., a new bacterial genus isolated from human left colon. New Microbes and New Infections, 2019, 29, 100520. | 0.8 | 2 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1616 | Complete chloroplast genome of Anathallis obovata (Orchidaceae: Pleurothallidinae). Revista Brasileira De Botanica, 2019, 42, 345-352. | 0.5 | 3 |
| 1617 | Trapping the Enemy: Vermamoeba vermiformis Circumvents Faustovirus Mariensis Dissemination by Enclosing Viral Progeny inside Cysts. Journal of Virology, 2019, 93, . | 1.5 | 20 |
| 1618 | Genome Features and Secondary Metabolites Biosynthetic Potential of the Class Ktedonobacteria. Frontiers in Microbiology, 2019, 10, 893. | 1.5 | 61 |
| 1619 | Accurate high throughput alignment via line sweep-based seed processing. Nature Communications, 2019, 10, 1939. | 5.8 | 11 |
| 1620 | The complete chloroplast genome sequences of four Viola species (Violaceae) and comparative analyses with its congeneric species. PLoS ONE, 2019, 14, e0214162. | 1.1 | 35 |
| 1621 | Characterizing the Biology of Lytic Bacteriophage vB_EaeM_Ï†Eap-3 Infecting Multidrug-Resistant Enterobacter aerogenes. Frontiers in Microbiology, 2019, 10, 420. | 1.5 | 43 |
| 1622 | Genomic characterization of an atypical enteropathogenic Escherichia coli strain isolated in Fujian province, China. Science China Life Sciences, 2019, 62, 1261-1263. | 2.3 | 0 |
| 1623 | Phylogenetic Studies on the Prodigiosin Biosynthetic Operon. Current Microbiology, 2019, 76, 597-606. | 1.0 | 9 |
| 1624 | Inference of Convergent Gene Acquisition Among Pseudomonas syringae Strains Isolated From Watermelon, Cantaloupe, and Squash. Frontiers in Microbiology, 2019, 10, 270. | 1.5 | 17 |
| 1625 | Comparative analysis of the mitochondrial genomes of Orthonectida: insights into the evolution of an invertebrate parasite species. Molecular Genetics and Genomics, 2019, 294, 715-727. | 1.0 | 18 |
| 1626 | Using WGS to identify antibiotic resistance genes and predict antimicrobial resistance phenotypes in MDR Acinetobacter baumannii in Tanzania. Journal of Antimicrobial Chemotherapy, 2019, 74, 1484-1493. | 1.3 | 46 |
| 1627 | Genome Sequence of <i>Rhizobium jaguaris</i> CCGE525 <sup>T</sup> , a Strain Isolated from <i>Calliandra grandiflora</i> Nodules from a Rain Forest in Mexico. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 3 |
| 1628 | Identification of Streptococcus pneumoniae by a real-time PCR assay targeting SP2020. Scientific Reports, 2019, 9, 3285. | 1.6 | 53 |
| 1629 | Complete genome sequencing of Lactobacillus plantarum CAUH2 reveals a novel plasmid pCAUH203 associated with oxidative stress tolerance. 3 Biotech, 2019, 9, 116. | 1.1 | 8 |
| 1630 | FLOWERING LOCUS T, GIGANTEA, SEPALLATA, and FRIGIDA homologs are candidate genes involved in white lupin (Lupinus albus L.) early flowering. Molecular Breeding, 2019, 39, 1. | 1.0 | 24 |
| 1631 | Insight into the genome and brackish water adaptation strategies of toxic and bloom-forming Baltic Sea Dolichospermum sp. UHCC 0315. Scientific Reports, 2019, 9, 4888. | 1.6 | 14 |
| 1632 | Metabolic analyses reveal common adaptations in two invasive Haemophilus influenzae strains. Pathogens and Disease, 2019, 77, . | 0.8 | 9 |
| 1633 | Conserved and specific features of Streptococcus pyogenes and Streptococcus agalactiae transcriptional landscapes. BMC Genomics, 2019, 20, 236. | 1.2 | 30 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1634 | A Novel Chimeric Mitochondrial Gene Confers Cytoplasmic Effects on Seed Oil Content in Polyploid Rapeseed (Brassica napus). Molecular Plant, 2019, 12, 582-596. | 3.9 | 26 |
| 1635 | Nanopore ultra-long read sequencing technology for antimicrobial resistance detection in Mannheimia haemolytica. Journal of Microbiological Methods, 2019, 159, 138-147. | 0.7 | 22 |
| 1636 | Gen2Epi: an automated whole-genome sequencing pipeline for linking full genomes to antimicrobial susceptibility and molecular epidemiological data in Neisseria gonorrhoeae. BMC Genomics, 2019, 20, 165. | 1.2 | 8 |
| 1637 | Genomic and metagenomic signatures of giant viruses are ubiquitous in water samples from sewage, inland lake, waste water treatment plant, and municipal water supply in Mumbai, India. Scientific Reports, 2019, 9, 3690. | 1.6 | 9 |
| 1638 | The Genome of Drosophila innubila Reveals Lineage-Specific Patterns of Selection in Immune Genes. Molecular Biology and Evolution, 2019, 36, 1405-1417. | 3.5 | 37 |
| 1639 | Complete Genome Sequences of Two Isolates of Fusobacterium necrophorum subsp. funduliforme, Obtained from Blood from Patients with Lemierreâ€™s Syndrome. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 0 |
| 1640 | Characterization of the emerging multidrug-resistant <i>Salmonella enterica</i> serovar Indiana strains in China. Emerging Microbes and Infections, 2019, 8, 29-39. | 3.0 | 23 |
| 1641 | Impact of a bathing tradition on shared gut microbes among Japanese families. Scientific Reports, 2019, 9, 4380. | 1.6 | 16 |
| 1642 | Fine-Tuning of Ïƒ E Activation Suppresses Multiple Assembly-Defective Mutations in Escherichia coli. Journal of Bacteriology, 2019, 201, . | 1.0 | 6 |
| 1643 | Extended Spectrum Beta-Lactamase-Producing Gram-Negative Bacteria Recovered From an Amazonian Lake Near the City of BelÃ©m, Brazil. Frontiers in Microbiology, 2019, 10, 364. | 1.5 | 38 |
| 1644 | Sequencing the Obligate Intracellular Rhabdochlamydia helvetica within Its Tick Host Ixodes ricinus to Investigate Their Symbiotic Relationship. Genome Biology and Evolution, 2019, 11, 1334-1344. | 1.1 | 21 |
| 1645 | Impact of antibiotic treatment and host innate immune pressure on enterococcal adaptation in the human bloodstream. Science Translational Medicine, 2019, 11, . | 5.8 | 32 |
| 1646 | Comparative genomic analysis unravels the transmission pattern and intra-species divergence of acute hepatopancreatic necrosis disease (AHPND)-causing Vibrio parahaemolyticus strains. Molecular Genetics and Genomics, 2019, 294, 1007-1022. | 1.0 | 14 |
| 1647 | Biological and molecular characterization of two Anticarsia gemmatalis multiple nucleopolyhedrovirus clones exhibiting contrasting virulence. Journal of Invertebrate Pathology, 2019, 164, 23-31. | 1.5 | 3 |
| 1648 | Don't overlook the little guy: An evaluation of the frequency of small plasmids co-conjugating with larger carbapenemase gene containing plasmids. Plasmid, 2019, 103, 1-8. | 0.4 | 36 |
| 1649 | Biological characteristics and genome-wide sequence analysis of endophytic nitrogen-fixing bacteria <i>Klebsiella variicola</i> GN02. Biotechnology and Biotechnological Equipment, 2019, 33, 108-117. | 0.5 | 15 |
| 1650 | First clinical isolate of Escherichia coli harboring mcr-1 gene in Mexico. PLoS ONE, 2019, 14, e0214648. | 1.1 | 23 |
| 1651 | Probiotic Potential and Safety Evaluation of Enterococcus faecalis OB14 and OB15, Isolated From Traditional Tunisian Testouri Cheese and Rigouta, Using Physiological and Genomic Analysis. Frontiers in Microbiology, 2019, 10, 881. | 1.5 | 81 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1652 | Genomic analysis of the aggressive tree pathogen Ceratocystis albifundus. Fungal Biology, 2019, 123, 351-363. | 1.1 | 11 |
| 1653 | An efficient genomic signature ranking method for genomic island prediction from a single genome. Journal of Theoretical Biology, 2019, 467, 142-149. | 0.8 | 9 |
| 1654 | Host Resistance, Genomics and Population Dynamics in a Salmonella Enteritidis and Phage System. Viruses, 2019, 11, 188. | 1.5 | 16 |
| 1655 | The chloroplast genome of the marine microalga <i>Tisochrysis lutea</i>. Mitochondrial DNA Part B: Resources, 2019, 4, 253-255. | 0.2 | 11 |
| 1656 | A linear nonribosomal octapeptide from Fusarium graminearum facilitates cell-to-cell invasion of wheat. Nature Communications, 2019, 10, 922. | 5.8 | 74 |
| 1657 | An N-nitrosating metalloenzyme constructs the pharmacophore of streptozotocin. Nature, 2019, 566, 94-99. | 13.7 | 108 |
| 1658 | Genome Analysis ofShigella flexneriSerotype 3b Strain SFL1520 Reveals Significant Horizontal Gene Acquisitions Including a Multidrug Resistance Cassette. Genome Biology and Evolution, 2019, 11, 776-785. | 1.1 | 9 |
| 1659 | CAMISIM: simulating metagenomes and microbial communities. Microbiome, 2019, 7, 17. | 4.9 | 117 |
| 1660 | Resource Concentration Modulates the Fate of Dissimilated Nitrogen in a Dual-Pathway Actinobacterium. Frontiers in Microbiology, 2019, 10, 3. | 1.5 | 20 |
| 1661 | The complete plastome of real yellow wood (Podocarpus latifolius): gene organization and comparison with related species. Holzforschung, 2019, 73, 525-536. | 0.9 | 2 |
| 1662 | Pseudomonas Diversity Within Urban Freshwaters. Frontiers in Microbiology, 2019, 10, 195. | 1.5 | 16 |
| 1663 | Genome Analyses of a New <i>Mycoplasma</i> Species from the Scorpion <i>Centruroides vittatus</i>. G3: Genes, Genomes, Genetics, 2019, 9, 993-997. | 0.8 | 2 |
| 1664 | Sequencing of Capsicum Organellar Genomes. Compendium of Plant Genomes, 2019, , 153-172. | 0.3 | 0 |
| 1665 | Combining Strengths for Multi-genome Visual Analytics Comparison. Bioinformatics and Biology Insights, 2019, 13, 117793221882512. | 1.0 | 1 |
| 1666 | Identification and molecular characterization of Serratia marcescens phages vB_SmaA_2050H1 and vB_SmaM_2050HW. Archives of Virology, 2019, 164, 1085-1094. | 0.9 | 11 |
| 1667 | Phylogenomic characterization of red seabream iridovirus from Florida pompano Trachinotus carolinus maricultured in the Caribbean Sea. Archives of Virology, 2019, 164, 1209-1212. | 0.9 | 9 |
| 1668 | Bacteriophages of the Human Gut: The â€œKnown Unknownâ€• of the Microbiome. Cell Host and Microbe, 2019, 25, 195-209. | 5.1 | 436 |
| 1669 | Genome Sequence of the Plant Growth-Promoting Rhizobacterium Pantoea agglomerans C1. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 12 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1670 | Bacterial phylogeny in the Cayley graph. Discrete Mathematics, Algorithms and Applications, 2019, 11, 1950059. | 0.4 | 4 |
| 1671 | Comparative Genomic Analysis of <i>Rhodococcus equi</i>: An Insight into Genomic Diversity and Genome Evolution. International Journal of Genomics, 2019, 2019, 1-14. | 0.8 | 7 |
| 1672 | Aquatic Hemiptera in Southwest Cameroon: Biodiversity of Potential Reservoirs of Mycobacterium ulcerans and Multiple Wolbachia Sequence Types Revealed by Metagenomics. Diversity, 2019, 11, 225. | 0.7 | 2 |
| 1673 | Draft Genome Sequence of Bacillus lehensis M136, Isolated from the Manleluag Hyperalkaline Spring in Pangasinan, Philippines. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 0 |
| 1674 | Whole-Genome Sequencing of a Salmonella enterica subsp. enterica Serovar Infantis Strain Isolated from Broiler Chicken in Peru. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 25 |
| 1675 | Genome Sequence of an Aspergillus flavus CA14 Strain That Is Widely Used in Gene Function Studies. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 4 |
| 1676 | Whole-Genome Sequence of Rickettsia parkeri Strain Atlantic Rainforest, Isolated from a Colombian Tick. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 9 |
| 1677 | Complete Genome Sequence of Pseudomonas aeruginosa Reference Strain PAK. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 26 |
| 1678 | Draft Genome Sequence of Heavy Metal-Resistant Aeromonas veronii CTe-01, Isolated from a Peruvian Wastewater Treatment Plant. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 3 |
| 1679 | Has gene expression neofunctionalization in the fire ant antennae contributed to queen discrimination behavior?. Ecology and Evolution, 2019, 9, 12754-12766. | 0.8 | 6 |
| 1680 | Twelve complete chloroplast genomes of wild peanuts: great genetic resources and a better understanding of Arachis phylogeny. BMC Plant Biology, 2019, 19, 504. | 1.6 | 16 |
| 1681 | Genomic Analysis of Fluoroquinolone- and Tetracycline-Resistant <i>Campylobacter jejuni</i> Sequence Type 6964 in Humans and Poultry, New Zealand, 2014â€“2016. Emerging Infectious Diseases, 2019, 25, 2226-2234. | 2.0 | 27 |
| 1682 | De novo Assembly of the Brugia malayi Genome Using Long Reads from a Single MinION Flowcell. Scientific Reports, 2019, 9, 19521. | 1.6 | 9 |
| 1683 | Characterization of the mitochondrial genome of the pathogenic fungus Scytalidium auriculariicola (Leotiomycetes) and insights into its phylogenetics. Scientific Reports, 2019, 9, 17447. | 1.6 | 21 |
| 1684 | Genetic Diversity of Composite Enterotoxigenic Staphylococcus epidermidis Pathogenicity Islands. Genome Biology and Evolution, 2019, 11, 3498-3509. | 1.1 | 21 |
| 1685 | Characterization of antibiotic resistance genes in the species of the rumen microbiota. Nature Communications, 2019, 10, 5252. | 5.8 | 68 |
| 1686 | Complete plastid genome of Suriana maritima L. (Surianaceae) and its implications in phylogenetic reconstruction of Fabales. Journal of Genetics, 2019, 98, 1. | 0.4 | 1 |
| 1687 | Comparative genomics of Mycoplasma pneumoniae isolated from children with pneumonia: South Korea, 2010â€“2016. BMC Genomics, 2019, 20, 910. | 1.2 | 7 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1688 | VCGIDB: A Database and Web Resource for the Genomic Islands from Vibrio cholerae. Pathogens, 2019, 8, 261. | 1.2 | 5 |
| 1689 | deltaRpkm: an R package for a rapid detection of differential gene presence between related bacterial genomes. BMC Bioinformatics, 2019, 20, 621. | 1.2 | 3 |
| 1690 | Transduction as a Potential Dissemination Mechanism of a Clonal qnrB19-Carrying Plasmid Isolated From Salmonella of Multiple Serotypes and Isolation Sources. Frontiers in Microbiology, 2019, 10, 2503. | 1.5 | 12 |
| 1691 | Complete genome sequence analysis of a lytic Shigella flexneri vB_SflS-ISF001 bacteriophage. Turkish Journal of Biology, 2019, 43, 99-112. | 2.1 | 15 |
| 1692 | Modification of the genome topology network and its application to the comparison of group B Streptococcus genomes. BMC Genomics, 2019, 20, 886. | 1.2 | 0 |
| 1693 | Search for Ancestral Features in Genomes of Rhizobium leguminosarum bv. viciae Strains Isolated from the Relict Legume Vavilovia formosa. Genes, 2019, 10, 990. | 1.0 | 8 |
| 1694 | Genomic and evolutionary features of two AHPND positive Vibrio parahaemolyticus strains isolated from shrimp (Penaeus monodon) of south-west Bangladesh. BMC Microbiology, 2019, 19, 270. | 1.3 | 15 |
| 1695 | Isolation and Characterization of a Novel Klebsiella pneumoniae N4-like Bacteriophage KP8. Viruses, 2019, 11, 1115. | 1.5 | 13 |
| 1696 | Chromosome-level genome assembly for giant panda provides novel insights into Carnivora chromosome evolution. Genome Biology, 2019, 20, 267. | 3.8 | 31 |
| 1697 | Prophages in Lactobacillus reuteri Are Associated with Fitness Trade-Offs but Can Increase Competitiveness in the Gut Ecosystem. Applied and Environmental Microbiology, 2019, 86, . | 1.4 | 44 |
| 1698 | Gclust: A Parallel Clustering Tool for Microbial Genomic Data. Genomics, Proteomics and Bioinformatics, 2019, 17, 496-502. | 3.0 | 7 |
| 1699 | Interaction of Phthorimaea operculella granulovirus with a Nosema sp. microsporidium in larvae of Phthorimaea operculella. Journal of Invertebrate Pathology, 2019, 160, 76-86. | 1.5 | 3 |
| 1700 | A Cryptic Non-Inducible Prophage Confers Phage-Immunity on the Streptococcus thermophilus M17PTZA496. Viruses, 2019, 11, 7. | 1.5 | 26 |
| 1701 | A novel integrative conjugative element mediates transfer of multi-drug resistance between Streptococcus suis strains of different serotypes. Veterinary Microbiology, 2019, 229, 110-116. | 0.8 | 23 |
| 1702 | Phoenix phylogeny, and analysis of genetic variation in a diverse collection of date palm (Phoenix) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 | 1.8 | 27 |
| 1703 | Understanding the Evolution of Mitochondrial Genomes in Phaeophyceae Inferred from Mitogenomes of Ishige okamurae (Ishigeales) and Dictyopteris divaricata (Dictyotales). Journal of Molecular Evolution, 2019, 87, 16-26. | 0.8 | 10 |
| 1704 | A Remote <i>cis</i>-Regulatory Region Is Required for <i>NIN</i> Expression in the Pericycle to Initiate Nodule Primordium Formation in <i>Medicago truncatula</i>. Plant Cell, 2019, 31, 68-83. | 3.1 | 101 |
| 1705 | Diversity and distribution of Klebsiella capsules in Escherichia coli. Environmental Microbiology Reports, 2019, 11, 107-117. | 1.0 | 15 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1706 | Draft Genome Sequences of Proteus mirabilis K1609 and K670: A Model Strains for Territoriality Examination. Current Microbiology, 2019, 76, 144-152. | 1.0 | 3 |
| 1707 | Discrimination of Mycobacterium leprae and Mycobacterium haemophilum in Clinical Isolates and Specimens by Multiplex PCR Assay and Prediction of Drug Susceptibility. Journal of Clinical Microbiology, 2019, 57, . | 1.8 | 3 |
| 1708 | Evaluating the evolution and function of the dynamic Venom Y protein in ectoparasitoid wasps. Insect Molecular Biology, 2019, 28, 499-508. | 1.0 | 5 |
| 1709 | Common and distinctive adaptive traits expressed in <i>Dickeya dianthicola</i> and <i>Dickeya solani</i> pathogens when exploiting potato plant host. Environmental Microbiology, 2019, 21, 1004-1018. | 1.8 | 42 |
| 1710 | The Complete Plastid Genome of Magnolia zenii and Genetic Comparison to Magnoliaceae species. Molecules, 2019, 24, 261. | 1.7 | 38 |
| 1711 | Characterization and Genome Analysis of Staphylococcus aureus Podovirus CSA13 and Its Anti-Biofilm Capacity. Viruses, 2019, 11, 54. | 1.5 | 28 |
| 1712 | Construction of a Genomic Bacterial Artificial Chromosome (BAC) Library for the Prawn Macrobrachium rosenbergii and Initial Analysis of ZW Chromosome-Derived BAC Inserts. Marine Biotechnology, 2019, 21, 206-216. | 1.1 | 11 |
| 1713 | Genome mining reveals the origin of a bald phenotype and a cryptic nucleocidin gene cluster in Streptomyces asterosporus DSM 41452. Journal of Biotechnology, 2019, 292, 23-31. | 1.9 | 21 |
| 1714 | Phage defense mechanisms and their genomic and phenotypic implications in the fish pathogen<i>Vibrio anguillarum</i>. FEMS Microbiology Ecology, 2019, 95, . | 1.3 | 40 |
| 1715 | Comparative genomics for non-O1/O139 Vibrio cholerae isolates recovered from the Yangtze River Estuary versus V. cholerae representative isolates from serogroup O1. Molecular Genetics and Genomics, 2019, 294, 417-430. | 1.0 | 8 |
| 1716 | Genetic basis for the establishment of endosymbiosis in <i>Paramecium</i>. ISME Journal, 2019, 13, 1360-1369. | 4.4 | 30 |
| 1717 | Characterization and complete genome analysis of the surfactin-producing, plant-protecting bacterium Bacillus velezensis 9D-6. BMC Microbiology, 2019, 19, 5. | 1.3 | 62 |
| 1718 | Comparative mitochondrial genome analysis of the firefly, Inflata indica (Coleoptera: Lampyridae) and the first evidence of heteroplasmy in fireflies. International Journal of Biological Macromolecules, 2019, 121, 671-676. | 3.6 | 13 |
| 1719 | Comparative Genomics of Lactobacillus brevis Reveals a Significant Plasmidome Overlap of Brewery and Insect Isolates. Current Microbiology, 2019, 76, 37-47. | 1.0 | 13 |
| 1720 | Long-range PCR and high-throughput sequencing of Ostreid herpesvirus 1 indicate high genetic diversity and complex evolution process. Virology, 2019, 526, 81-90. | 1.1 | 29 |
| 1721 | In vitro and in vivo evaluation of Lactobacillus strains and comparative genomic analysis of Lactobacillus plantarum CGMCC12436 reveal candidates of colonise-related genes. Food Research International, 2019, 119, 813-821. | 2.9 | 11 |
| 1722 | Whole-Genome Alignment and Comparative Annotation. Annual Review of Animal Biosciences, 2019, 7, 41-64. | 3.6 | 62 |
| 1723 | Characterization and comparison of the mitochondrial genomes from two Lyophyllum fungal species and insights into phylogeny of Agaricomycetes. International Journal of Biological Macromolecules, 2019, 121, 364-372. | 3.6 | 42 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1724 | Molecular phylogenetics supports a clade of red algal parasites retaining native plastids: taxonomy and terminology revised. Journal of Phycology, 2019, 55, 279-288. | 1.0 | 8 |
| 1725 | The complete chloroplast and mitochondrial genomes of the diatom <i>Nitzschia palea</i> (Bacillariophyceae) demonstrate high sequence similarity to the endosymbiont organelles of the dinotom <i>Durinskia baltica</i>. Journal of Phycology, 2019, 55, 352-364. | 1.0 | 20 |
| 1726 | Conservation of mitochondrial genome arrangements in brittle stars (Echinodermata, Ophiuroidea). Molecular Phylogenetics and Evolution, 2019, 130, 115-120. | 1.2 | 18 |
| 1727 | Genetic, evolutionary and phylogenetic aspects of the plastome of annatto (Bixa orellana L.), the Amazonian commercial species of natural dyes. Planta, 2019, 249, 563-582. | 1.6 | 15 |
| 1728 | Characterization and comparative analysis of six complete mitochondrial genomes from ectomycorrhizal fungi of the Lactarius genus and phylogenetic analysis of the Agaricomycetes. International Journal of Biological Macromolecules, 2019, 121, 249-260. | 3.6 | 56 |
| 1729 | â€œTupanvirusâ€, a new genus in the family Mimiviridae. Archives of Virology, 2019, 164, 325-331. | 0.9 | 23 |
| 1730 | Impact of probiotic <i>Lactobacillus</i> sp. on autochthonous lactobacilli in weaned piglets. Journal of Applied Microbiology, 2019, 126, 242-254. | 1.4 | 16 |
| 1731 | Comparative genomic analysis of Lactobacillus mucosae LM1 identifies potential niche-specific genes and pathways for gastrointestinal adaptation. Genomics, 2019, 111, 24-33. | 1.3 | 47 |
| 1732 | Reconstruction and in silico analysis of new Marinobacter adhaerens t76_800 with potential for long-chain hydrocarbon bioremediation associated with marine environmental lipases. Marine Genomics, 2020, 49, 100685. | 0.4 | 5 |
| 1733 | Phylogenetic determinants of toxin gene distribution in genomes of Brevibacillus laterosporus. Genomics, 2020, 112, 1042-1053. | 1.3 | 19 |
| 1734 | Complete plastome sequencing of Allium paradoxum reveals unusual rearrangements and the loss of the ndh genes as compared to Allium ursinum and other onions. Gene, 2020, 726, 144154. | 1.0 | 11 |
| 1735 | A case of â€˜blown packâ€™ spoilage of vacuumâ€packaged pork likely associated with Clostridium estertheticum in Canada. Letters in Applied Microbiology, 2020, 70, 13-20. | 1.0 | 15 |
| 1736 | Construction and comparative analysis of mitochondrial genome in the brown tide forming alga Aureococcus anophagefferens (Pelagophyceae, Ochrophyta). Journal of Applied Phycology, 2020, 32, 441-450. | 1.5 | 13 |
| 1737 | Vampirovibrio chlorellavorus draft genome sequence, annotation, and preliminary characterization of pathogenicity determinants. Phycological Research, 2020, 68, 23-29. | 0.8 | 3 |
| 1738 | Comparative plastid genomics of <i>Pinus</i> species: Insights into sequence variations and phylogenetic relationships. Journal of Systematics and Evolution, 2020, 58, 118-132. | 1.6 | 30 |
| 1739 | Plastid phylogenomics improve phylogenetic resolution in the Lauraceae. Journal of Systematics and Evolution, 2020, 58, 423-439. | 1.6 | 56 |
| 1740 | The complete genome sequence of Rahnella aquatilis ZF7 reveals potential beneficial properties and stress tolerance capabilities. Archives of Microbiology, 2020, 202, 483-499. | 1.0 | 16 |
| 1741 | Informatic tools and platforms for enhancing plant R-gene discovery process. , 2020, , 121-135. |  | 1 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1742 | Comparative genomic analysis reveals a high prevalence of inter-species inÂvivo transfer of carbapenem-resistance plasmids in patients with haematological malignancies. Clinical Microbiology and Infection, 2020, 26, 780.e1-780.e8. | 2.8 | 21 |
| 1743 | Complete genome and bimodal genomic structure of the amoebal symbiont Neochlamydia strain S13 revealed by ultra-long reads obtained from MinION. Journal of Human Genetics, 2020, 65, 41-48. | 1.1 | 1 |
| 1744 | A Comparative Characterization of the Mitochondrial Genomes of Paramoeba aparasomata and Neoparamoeba pemaquidensis (Amoebozoa, Paramoebidae). Journal of Eukaryotic Microbiology, 2020, 67, 167-175. | 0.8 | 2 |
| 1745 | Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. Plant Journal, 2020, 101, 455-472. | 2.8 | 94 |
| 1746 | The complete mitochondrial genomes of two model ectomycorrhizal fungi (Laccaria): features, intron dynamics and phylogenetic implications. International Journal of Biological Macromolecules, 2020, 145, 974-984. | 3.6 | 52 |
| 1747 | An Improved Melon Reference Genome With Single-Molecule Sequencing Uncovers a Recent Burst of Transposable Elements With Potential Impact on Genes. Frontiers in Plant Science, 2019, 10, 1815. | 1.7 | 48 |
| 1748 | Chloroplast genome of an extremely endangered conifer Thuja sutchuenensis Franch.: gene organization, comparative and phylogenetic analysis. Physiology and Molecular Biology of Plants, 2020, 26, 409-418. | 1.4 | 10 |
| 1749 | The complete chloroplast genome sequence of yellow mustard (Sinapis alba L.) and its phylogenetic relationship to other Brassicaceae species. Gene, 2020, 731, 144340. | 1.0 | 43 |
| 1750 | PaSiT: a novel approach based on short-oligonucleotide frequencies for efficient bacterial identification and typing. Bioinformatics, 2020, 36, 2337-2344. | 1.8 | 5 |
| 1751 | Genome sequence of Pseudomonas aeruginosa PAO1161, a PAO1 derivative with the ICEPae1161 integrative and conjugative element. BMC Genomics, 2020, 21, 14. | 1.2 | 17 |
| 1752 | Detection and phylogeny of Staphylococcus aureus sequence type 398 in Taiwan. Journal of Biomedical Science, 2020, 27, 15. | 2.6 | 14 |
| 1753 | Distinct Catalytic Behaviors between Two 1,4-Dioxane-Degrading Monooxygenases: Kinetics, Inhibition, and Substrate Range. Environmental Science &amp; Technology, 2020, 54, 1898-1908. | 4.6 | 29 |
| 1754 | Isolation and subunit compositions of the xylanosome complexes produced by Cellulosimicrobium species. Enzyme and Microbial Technology, 2020, 133, 109445. | 1.6 | 4 |
| 1755 | Genomic sequence data and single nucleotide polymorphism genotyping of Bacillus anthracis strains isolated from animal anthrax outbreaks in Northern Cape Province, South Africa. Data in Brief, 2020, 28, 105040. | 0.5 | 3 |
| 1756 | Characterization of the ferret TRB locus guided by V, D, J, and C gene expression analysis. Immunogenetics, 2020, 72, 101-108. | 1.2 | 14 |
| 1757 | Organellomic data sets confirm a cryptic consensus on (unrooted) landâ€plant relationships and provide new insights into bryophyte molecular evolution. American Journal of Botany, 2020, 107, 91-115. | 0.8 | 38 |
| 1758 | Complete genome sequence and comparative analysis of Streptomyces seoulensis, a pioneer strain of nickel superoxide dismutase. Genes and Genomics, 2020, 42, 273-281. | 0.5 | 4 |
| 1759 | Plant growth-promoting activities and genomic analysis of the stress-resistant Bacillus megaterium STB1, a bacterium of agricultural and biotechnological interest. Biotechnology Reports (Amsterdam,) Tj ETQq1 1 0.784314 rg BT /Overlo | 2.1 | 83 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1760 | The mitochondrial genome of Morchella importuna (272.2Âkb) is the largest among fungi and contains numerous introns, mitochondrial non-conserved open reading frames and repetitive sequences. International Journal of Biological Macromolecules, 2020, 143, 373-381. | 3.6 | 63 |
| 1761 | Evolution of an <i>Eleusine</i>-Specific Subgroup of <i>Pyricularia oryzae</i> Through a Gain of an Avirulence Gene. Molecular Plant-Microbe Interactions, 2020, 33, 153-165. | 1.4 | 16 |
| 1762 | Evolutionary changes of an intestinal <i>Lactobacillus reuteri</i> during probiotic manufacture. MicrobiologyOpen, 2020, 9, e972. | 1.2 | 3 |
| 1764 | An angular dioxygenase gene cluster responsible for the initial phenazine-1-carboxylic acid degradation step in Rhodococcus sp. WH99 can protect sensitive organisms from toxicity. Science of the Total Environment, 2020, 706, 135726. | 3.9 | 7 |
| 1765 | â€œParasite turnover zoneâ€•at secondary contact: A new pattern in hostâ€“parasite population genetics. Molecular Ecology, 2020, 29, 4653-4664. | 2.0 | 7 |
| 1766 | Transposon Insertion in the purL Gene Induces Biofilm Depletion in Escherichia coli ATCC 25922. Pathogens, 2020, 9, 774. | 1.2 | 9 |
| 1767 | Transit From Autotrophism to Heterotrophism: Sequence Variation and Evolution of Chloroplast Genomes in Orobanchaceae Species. Frontiers in Genetics, 2020, 11, 542017. | 1.1 | 6 |
| 1768 | Development of PCR-based markers and whole-genome selection model for anthracnose resistance in white lupin (Lupinus albus L.). Journal of Applied Genetics, 2020, 61, 531-545. | 1.0 | 8 |
| 1769 | The algal selenoproteomes. BMC Genomics, 2020, 21, 699. | 1.2 | 7 |
| 1770 | Characteristics of Organellar Genomes and Nuclear Internal Transcribed Spacers in the Tertiary Relict Genus Dipelta and Their Phylogenomic Implications. Frontiers in Genetics, 2020, 11, 573226. | 1.1 | 3 |
| 1771 | p-Aminophenylalanine Involved in the Biosynthesis of Antitumor Dnacin B1 for Quinone Moiety Formation. Molecules, 2020, 25, 4186. | 1.7 | 2 |
| 1772 | Signs of a phyllospheric lifestyle in the genome of the stress-tolerant strain Azospirillum brasilense Az19. Systematic and Applied Microbiology, 2020, 43, 126130. | 1.2 | 5 |
| 1773 | Translocation of Viable Gut Microbiota to Mesenteric Adipose Drives Formation of Creeping Fat in Humans. Cell, 2020, 183, 666-683.e17. | 13.5 | 211 |
| 1774 | The Genome and Transcriptome Analysis of the Vigna mungo Chloroplast. Plants, 2020, 9, 1247. | 1.6 | 6 |
| 1775 | Concordance of disk diffusion, broth microdilution, and wholeâ€genome sequencing for determination of in vitro antimicrobial susceptibility of Mannheimia haemolytica. Journal of Veterinary Internal Medicine, 2020, 34, 2158-2168. | 0.6 | 4 |
| 1776 | Genome Complexity Browser: Visualization and quantification of genome variability. PLoS Computational Biology, 2020, 16, e1008222. | 1.5 | 1 |
| 1777 | The complete mitochondrial genome of medicinal fungus Taiwanofungus camphoratus reveals gene rearrangements and intron dynamics of Polyporales. Scientific Reports, 2020, 10, 16500. | 1.6 | 18 |
| 1778 | Characterization of Mobile Genetic Elements Using Long-Read Sequencing for Tracking Listeria monocytogenes from Food Processing Environments. Pathogens, 2020, 9, 822. | 1.2 | 11 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1779 | Whitefly genomes contain ribotoxin coding genes acquired from plants. Scientific Reports, 2020, 10, 15503. | 1.6 | 24 |
| 1780 | The complete chloroplast genome of Gleditsia sinensis and Gleditsia japonica: genome organization, comparative analysis, and development of taxon specific DNA mini-barcodes. Scientific Reports, 2020, 10, 16309. | 1.6 | 11 |
| 1781 | Evolution of a Record-Setting AT-Rich Genome: Indel Mutation, Recombination, and Substitution Bias. Genome Biology and Evolution, 2020, 12, 2344-2354. | 1.1 | 16 |
| 1782 | Antimicrobial Resistance in Wildlife in Guadeloupe (French West Indies): Distribution of a Single blaCTXâ€"Mâ€"1/IncI1/ST3 Plasmid Among Humans and Wild Animals. Frontiers in Microbiology, 2020, 11, 1524. | 1.5 | 25 |
| 1783 | Comparative Genomic and Metabolomic Analyses of Two Pseudomonas aeruginosa Strains With Different Antifungal Activities. Frontiers in Microbiology, 2020, 11, 1841. | 1.5 | 15 |
| 1784 | Beyond Cholera: Characterization of zot-Encoding Filamentous Phages in the Marine Fish Pathogen Vibrio anguillarum. Viruses, 2020, 12, 730. | 1.5 | 16 |
| 1785 | Draft-genome sequence data and phylogenomic comparison of two marine-sourced bacterial strains Pseudoalteromonas sp. MIP2626 and Psychrobacter sp. BI730. Data in Brief, 2020, 31, 105898. | 0.5 | 2 |
| 1786 | New insights into the variability of lactic acid production in Lachancea thermotolerans at the phenotypic and genomic level. Microbiological Research, 2020, 238, 126525. | 2.5 | 18 |
| 1787 | Phylogenetic and evolutionary features of the plastome of Tropaeolum pentaphyllum Lam. (Tropaeolaceae). Planta, 2020, 252, 17. | 1.6 | 9 |
| 1788 | Intraspecific variation within Castor bean (Ricinus communis L.) based on chloroplast genomes. Industrial Crops and Products, 2020, 155, 112779. | 2.5 | 29 |
| 1789 | Adaptive divergence across Southern Ocean gradients in the pelagic diatom <i>Fragilariopsis kerguelensis</i>. Molecular Ecology, 2020, 29, 4913-4924. | 2.0 | 15 |
| 1790 | Klenkia terrae resistant to DNA extraction in germ-free mice stools illustrates the extraction pitfall faced by metagenomics. Scientific Reports, 2020, 10, 10228. | 1.6 | 1 |
| 1791 | An xa5 Resistance Gene-Breaking Indian Strain of the Rice Bacterial Blight Pathogen Xanthomonas oryzae pv. oryzae Is Nearly Identical to a Thai Strain. Frontiers in Microbiology, 2020, 11, 579504. | 1.5 | 8 |
| 1792 | Persistence of extendedâ€spectrum Î²â€lactamase plasmids among Enterobacteriaceae in commercial broiler farms. Microbiology and Immunology, 2020, 64, 712-718. | 0.7 | 5 |
| 1793 | The complete chloroplast genome sequences of five pinnate-leaved Primula species and phylogenetic analyses. Scientific Reports, 2020, 10, 20782. | 1.6 | 13 |
| 1794 | Draft genome sequences of concurrent Escherichia coli blood and fecal isolates from a patient with bacteremia and diarrhea belie BioFire-based detection of fecal enteropathogenic E. coli. Pathogens and Disease, 2020, 78, . | 0.8 | 1 |
| 1795 | Whole-Genome Analysis of Clinical Vibrio cholerae O1 in Kolkata, India, and Dhaka, Bangladesh, Reveals Two Lineages of Circulating Strains, Indicating Variation in Genomic Attributes. MBio, 2020, 11, . | 1.8 | 17 |
| 1796 | Repeated gain and loss of a single gene modulates the evolution of vascular plant pathogen lifestyles. Science Advances, 2020, 6, . | 4.7 | 58 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1797 | Bacteriophages vB_Sen-TO17 and vB_Sen-E22, Newly Isolated Viruses from Chicken Feces, Specific for Several Salmonella enterica Strains. International Journal of Molecular Sciences, 2020, 21, 8821. | 1.8 | 13 |
| 1798 | Distribution and Evolution of the Bacteriophage WO and Its Antagonism With Wolbachia. Frontiers in Microbiology, 2020, 11, 595629. | 1.5 | 12 |
| 1799 | Chloroplast genomes elucidate diversity, phylogeny, and taxonomy of Pulsatilla (Ranunculaceae). Scientific Reports, 2020, 10, 19781. | 1.6 | 20 |
| 1800 | Genome-based characterization of two Colombian clinical Providencia rettgeri isolates co-harboring NDM-1, VIM-2, and other Î²-lactamases. BMC Microbiology, 2020, 20, 345. | 1.3 | 12 |
| 1801 | Infection Kinetics and Phylogenetic Analysis of vB_EcoD_SU57, a Virulent T1-Like Drexlerviridae Coliphage. Frontiers in Microbiology, 2020, 11, 565556. | 1.5 | 9 |
| 1802 | The complete chloroplast genome of Isochrysis galbana and comparison with related haptophyte species. Algal Research, 2020, 50, 101989. | 2.4 | 14 |
| 1803 | Chloroplast Genome Variation and Evolutionary Analysis of Olea europaea L.. Genes, 2020, 11, 879. | 1.0 | 14 |
| 1804 | Host Adaptation Predisposes Pseudomonas aeruginosa to Type VI Secretion System-Mediated Predation by the Burkholderia cepacia Complex. Cell Host and Microbe, 2020, 28, 534-547.e3. | 5.1 | 34 |
| 1805 | Evolutionary dynamics of the chloroplast genome sequences of six Colobanthus species. Scientific Reports, 2020, 10, 11522. | 1.6 | 19 |
| 1806 | A performant bridge between fixed-size and variable-size seeding. BMC Bioinformatics, 2020, 21, 328. | 1.2 | 3 |
| 1807 | Analysis of the Antifungal Properties of Bacillus velezensis B-4 Through a Bioassay and Complete-Genome Sequencing. Frontiers in Genetics, 2020, 11, 703. | 1.1 | 11 |
| 1808 | The Isolation and Genome Sequencing of Five Novel Bacteriophages From the Rumen Active Against Butyrivibrio fibrisolvens. Frontiers in Microbiology, 2020, 11, 1588. | 1.5 | 5 |
| 1809 | How Tupanvirus Degrades the Ribosomal RNA of Its Amoebal Host? The Ribonuclease T2 Track. Frontiers in Microbiology, 2020, 11, 1691. | 1.5 | 6 |
| 1810 | Characterization and Comparative Analysis of Two Rheum Complete Chloroplast Genomes. BioMed Research International, 2020, 2020, 1-11. | 0.9 | 5 |
| 1811 | Complete Chloroplast Genome of Rhipsalis baccifera, the only Cactus with Natural Distribution in the Old World: Genome Rearrangement, Intron Gain and Loss, and Implications for Phylogenetic Studies. Plants, 2020, 9, 979. | 1.6 | 9 |
| 1812 | Scalable Pairwise Whole-Genome Homology Mapping of Long Genomes with BubbZ. IScience, 2020, 23, 101224. | 1.9 | 11 |
| 1813 | Whole-genome sequencing and genomic-based acid tolerance mechanisms of Lactobacillus delbrueckii subsp. bulgaricus LJJ. Applied Microbiology and Biotechnology, 2020, 104, 7631-7642. | 1.7 | 12 |
| 1814 | Evol2Circos: A Web-Based Tool for Genome Synteny and Collinearity Analysis and its Visualization in Fishes. Journal of Heredity, 2020, 111, 486-490. | 1.0 | 4 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1815 | Influence of the polar light cycle on seasonal dynamics of an Antarctic lake microbial community. Microbiome, 2020, 8, 116. | 4.9 | 32 |
| 1816 | Genome reconstruction of white spot syndrome virus (WSSV) from archival Davidsonâ€™s-fixed paraffin embedded shrimp (Penaeus vannamei) tissue. Scientific Reports, 2020, 10, 13425. | 1.6 | 14 |
| 1817 | Characterization and expression pattern analysis of pheromone receptor-like genes in Winter Mushroom Flammulina filiformis. Archives of Microbiology, 2020, 202, 2671-2678. | 1.0 | 2 |
| 1818 | The complete plastome of Passiflora cirrhiflora A. Juss.: structural features, RNA editing sites, hotspots of nucleotide diversity and molecular markers within the subgenus Deidamioides. Revista Brasileira De Botanica, 2020, 43, 839-853. | 0.5 | 5 |
| 1819 | A novel Thermotoga strain TFO isolated from a Californian petroleum reservoir phylogenetically related to Thermotoga petrophila and T. naphthophila, two thermophilic anaerobic isolates from a Japanese reservoir: Taxonomic and genomic considerations. Systematic and Applied Microbiology, 2020, 43, 126132. | 1.2 | 6 |
| 1820 | Complete Mitochondrial Genomes Reveal Population-Level Patterns in the Widespread Red Alga Gelidiella fanii (Gelidiales, Rhodophyta). Frontiers in Marine Science, 2020, 7, . | 1.2 | 8 |
| 1821 | The complete chloroplast genome of an endangered orchid <i>Paphiopedilum spicerianum</i>. Mitochondrial DNA Part B: Resources, 2020, 5, 3594-3595. | 0.2 | 3 |
| 1822 | Origins of cultivars of Chrysanthemum â€"Evidence from the chloroplast genome and nuclear LFY gene. Journal of Systematics and Evolution, 2020, 58, 925-944. | 1.6 | 30 |
| 1823 | Mitogenomes of Two Phallus Mushroom Species Reveal Gene Rearrangement, Intron Dynamics, and Basidiomycete Phylogeny. Frontiers in Microbiology, 2020, 11, 573064. | 1.5 | 3 |
| 1824 | Colonization of a hand washing sink in a veterinary hospital by an Enterobacter hormaechei strain carrying multiple resistances to high importance antimicrobials. Antimicrobial Resistance and Infection Control, 2020, 9, 163. | 1.5 | 13 |
| 1825 | Mitochondrial evolution in the entomopathogenic fungal genus <i>Beauveria</i>. Archives of Insect Biochemistry and Physiology, 2020, 105, e21754. | 0.6 | 5 |
| 1826 | Lost and Found: Re-searching and Re-scoring Proteomics Data Aids Genome Annotation and Improves Proteome Coverage. MSystems, 2020, 5, . | 1.7 | 13 |
| 1827 | Spirochetes isolated from arthropods constitute a novel genus Entomospira genus novum within the order Spirochaetales. Scientific Reports, 2020, 10, 17053. | 1.6 | 5 |
| 1828 | A Review on Sequence Alignment Algorithms for Short Reads Based on Next-Generation Sequencing. IEEE Access, 2020, 8, 189811-189822. | 2.6 | 7 |
| 1829 | Chronological set of E. coli O157:H7 bovine strains establishes a role for repeat sequences and mobile genetic elements in genome diversification. BMC Genomics, 2020, 21, 562. | 1.2 | 3 |
| 1830 | Comparative genomics of Xanthomonas fragariae and Xanthomonas arboricola pv. fragariae reveals intra- and interspecies variations. Phytopathology Research, 2020, 2, . | 0.9 | 8 |
| 1831 | The Chloroplast Genome of<i>Salvia</i>: Genomic Characterization and Phylogenetic Analysis. International Journal of Plant Sciences, 2020, 181, 812-830. | 0.6 | 15 |
| 1832 | Improved <i>De Novo</i> Draft Genome Sequence of the Nocavionin-Producing Type Strain Nocardia terpenica IFM 0706 and Comparative Genomics with the Closely Related Strain Nocardia terpenica IFM 0406. Microbiology Resource Announcements, 2020, 9, . | 0.3 | 6 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1833 | Complete Genome and Comparative Genome Analysis of Lactobacillus reuteri YSJL-12, a Potential Probiotics Strain Isolated From Healthy Sow Fresh Feces. Evolutionary Bioinformatics, 2020, 16, 117693432094219. | 0.6 | 4 |
| 1834 | Review on the Computational Genome Annotation of Sequences Obtained by Next-Generation Sequencing. Biology, 2020, 9, 295. | 1.3 | 45 |
| 1835 | Global reprogramming of virulence and antibiotic resistance in Pseudomonas aeruginosa by a single nucleotide polymorphism in elongation factor, fusA1. Journal of Biological Chemistry, 2020, 295, 16411-16426. | 1.6 | 17 |
| 1836 | A novel therapeutic antibody screening method using bacterial high-content imaging reveals functional antibody binding phenotypes of Escherichia coli ST131. Scientific Reports, 2020, 10, 12414. | 1.6 | 9 |
| 1837 | Nucleotide substitution rates of diatom plastid encoded protein genes are positively correlated with genome architecture. Scientific Reports, 2020, 10, 14358. | 1.6 | 7 |
| 1838 | A survey of non-coding RNAs in the social and predatory myxobacterium Myxococcus xanthus DK1622. Molecular Omics, 2020, 16, 492-502. | 1.4 | 4 |
| 1839 | Sequencing and assembly of the Egyptian buffalo genome. PLoS ONE, 2020, 15, e0237087. | 1.1 | 11 |
| 1840 | Genomic Surveillance of Ceftriaxone-Resistant Escherichia coli in Western New York Suggests the Extended-Spectrum Î²-Lactamase blaCTX-M-27 Is Emerging on Distinct Plasmids in ST38. Frontiers in Microbiology, 2020, 11, 1747. | 1.5 | 16 |
| 1841 | Near-Complete Genome Sequences of a <i>Wolbachia</i> Strain Isolated from Diaphorina citri Kuwayama ( <i>Hemiptera</i> : <i>Liviidae</i> ). Microbiology Resource Announcements, 2020, 9, . | 0.3 | 5 |
| 1842 | In vitro propagation and genome sequencing of three â€˜atypicalâ€™ Ehrlichia ruminantium isolates. Onderstepoort Journal of Veterinary Research, 2020, 87, e1-e14. | 0.6 | 2 |
| 1843 | Genomic Signatures of Honey Bee Association in an Acetic Acid Symbiont. Genome Biology and Evolution, 2020, 12, 1882-1894. | 1.1 | 18 |
| 1844 | Genomic Surveillance for One Health Antimicrobial Resistance: Understanding Human, Animal, and Environmental Reservoirs and Transmission. Handbook of Environmental Chemistry, 2020, , 71-100. | 0.2 | 2 |
| 1845 | Characterization of a Protease Hyper-Productive Mutant of Bacillus pumilus by Comparative Genomic and Transcriptomic Analysis. Current Microbiology, 2020, 77, 3612-3622. | 1.0 | 4 |
| 1846 | Gammaproteobacteria mediating utilization of methyl-, sulfur- and petroleum organic compounds in deep ocean hydrothermal plumes. ISME Journal, 2020, 14, 3136-3148. | 4.4 | 36 |
| 1847 | Characterization of the Complete Mitochondrial Genomes of Two Sibling Species of Parasitic Roundworms, Haemonchus contortus and Teladorsagia circumcincta. Frontiers in Genetics, 2020, 11, 573395. | 1.1 | 13 |
| 1848 | Scalable multiple whole-genome alignment and locally collinear block construction with SibeliaZ. Nature Communications, 2020, 11, 6327. | 5.8 | 39 |
| 1849 | Mutation of hilD in a Salmonella Derby lineage linked to swine adaptation and reduced risk to human health. Scientific Reports, 2020, 10, 21539. | 1.6 | 7 |
| 1850 | Comparative Genome Analyses of 18 Verticillium dahliae Tomato Isolates Reveals Phylogenetic and Race Specific Signatures. Frontiers in Microbiology, 2020, 11, 573755. | 1.5 | 13 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1851 | Reverse Engineering Targets for Recombinant Protein Production in Corynebacterium glutamicum Inspired by a Fast-Growing Evolved Descendant. Frontiers in Bioengineering and Biotechnology, 2020, 8, 588070. | 2.0 | 2 |
| 1852 | Comparative and Functional Analyses of Two Sequenced Paenibacillus polymyxa Genomes Provides Insights Into Their Potential Genes Related to Plant Growth-Promoting Features and Biocontrol Mechanisms. Frontiers in Genetics, 2020, 11, 564939. | 1.1 | 9 |
| 1853 | Rapid Transmission of a Hyper-Virulent Meningococcal Clone Due to High Effective Contact Numbers and Super Spreaders. Frontiers in Genetics, 2020, 11, 579411. | 1.1 | 3 |
| 1854 | Diverse Horizontally-Acquired Gene Clusters Confer Sucrose Utilization to Different Lineages of the Marine Pathogen Photobacterium damselae subsp. damselae. Genes, 2020, 11, 1244. | 1.0 | 4 |
| 1855 | Nitrate Respiration in Thermus thermophilus NAR1: from Horizontal Gene Transfer to Internal Evolution. Genes, 2020, 11, 1308. | 1.0 | 5 |
| 1856 | Lysogenization of a Lactococcal Host with Three Distinct Temperate Phages Provides Homologous and Heterologous Phage Resistance. Microorganisms, 2020, 8, 1685. | 1.6 | 13 |
| 1857 | Chromosome-scale genome assembly for the duckweed Spirodela intermedia, integrating cytogenetic maps, PacBio and Oxford Nanopore libraries. Scientific Reports, 2020, 10, 19230. | 1.6 | 23 |
| 1858 | Comparative Genomics Analysis of Vibrio anguillarum Isolated from Lumpfish (Cyclopterus lumpus) in Newfoundland Reveal Novel Chromosomal Organizations. Microorganisms, 2020, 8, 1666. | 1.6 | 11 |
| 1859 | Biotic exchange leaves detectable genomic patterns in the Australian rain forest flora. Biotropica, 2020, 52, 627-635. | 0.8 | 6 |
| 1860 | Draft Genome Sequence of Adlercreutzia equolifaciens IPLA 37004, a Human Intestinal Strain That Does Not Produce Equol from Daidzein. Microbiology Resource Announcements, 2020, 9, . | 0.3 | 2 |
| 1861 | Closed Genome Sequences of 28 Foodborne Pathogens from the CFSAN Verification Set, Determined by a Combination of Long and Short Reads. Microbiology Resource Announcements, 2020, 9, . | 0.3 | 3 |
| 1862 | Whole-Genome Sequencing of Mexican Strains of Anaplasma marginale: An Approach to the Causal Agent of Bovine Anaplasmosis. International Journal of Genomics, 2020, 2020, 1-7. | 0.8 | 6 |
| 1863 | Implications of plastome evolution in the true lilies (monocot order Liliales). Molecular Phylogenetics and Evolution, 2020, 148, 106818. | 1.2 | 23 |
| 1864 | Intrinsically disordered regions are abundant in simplexvirus proteomes and display signatures of positive selection. Virus Evolution, 2020, 6, veaa028. | 2.2 | 10 |
| 1865 | Discovery and Characterization of Thermoproteus Spherical Piliferous Virus 1: a Spherical Archaeal Virus Decorated with Unusual Filaments. Journal of Virology, 2020, 94, . | 1.5 | 2 |
| 1866 | Comparative genomics of whole-cell pertussis vaccine strains from India. BMC Genomics, 2020, 21, 345. | 1.2 | 6 |
| 1867 | Genome-wide Analysis of Four Enterobacter cloacae complex type strains: Insights into Virulence and Niche Adaptation. Scientific Reports, 2020, 10, 8150. | 1.6 | 18 |
| 1868 | Telomeric and sub-telomeric regions undergo rapid turnover within a Streptomyces population. Scientific Reports, 2020, 10, 7720. | 1.6 | 15 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1869 | Past and ongoing adaptation of human cytomegalovirus to its host. PLoS Pathogens, 2020, 16, e1008476. | 2.1 | 19 |
| 1870 | Assessment of a Potential Role of Dickeya dadantii DSM 18020 as a Pectinase Producer for Utilization in Poultry Diets Based on in silico Analyses. Frontiers in Microbiology, 2020, 11, 751. | 1.5 | 4 |
| 1871 | Bacterial riboproteogenomics: the era of N-terminal proteoform existence revealed. FEMS Microbiology Reviews, 2020, 44, 418-431. | 3.9 | 12 |
| 1872 | Comprehensive dissection of dispensable genomic regions in Streptomyces based on comparative analysis approach. Microbial Cell Factories, 2020, 19, 99. | 1.9 | 14 |
| 1873 | Genome Reportâ€"A Genome Sequence Analysis of the RB51 Strain of<i>Brucella abortus</i>in the Context of Its Vaccine Properties. G3: Genes, Genomes, Genetics, 2020, 10, 1175-1181. | 0.8 | 4 |
| 1874 | Genetic variants and source of introduction of SARSâ€CoVâ€2 in South America. Journal of Medical Virology, 2020, 92, 2139-2145. | 2.5 | 33 |
| 1875 | Whole genome sequence analysis of Cupriavidus campinensis S14E4C, a heavy metal resistant bacterium. Molecular Biology Reports, 2020, 47, 3973-3985. | 1.0 | 16 |
| 1876 | Prospects of Indole derivatives as methyl transfer inhibitors: antimicrobial resistance managers. BMC Pharmacology &amp; Toxicology, 2020, 21, 33. | 1.0 | 4 |
| 1877 | Emerging Threat of Antimicrobial Resistance in Î²-Hemolytic Streptococci. Frontiers in Microbiology, 2020, 11, 797. | 1.5 | 15 |
| 1878 | Responses of mature symbiotic nodules to the whole-plant systemic nitrogen signaling. Journal of Experimental Botany, 2020, 71, 5039-5052. | 2.4 | 22 |
| 1879 | Discovery of thermophilic Bacillales using reduced-representation genotyping for identification. BMC Microbiology, 2020, 20, 114. | 1.3 | 4 |
| 1880 | Leveraging plastomes for comparative analysis and phylogenomic inference within Scutellarioideae (Lamiaceae). PLoS ONE, 2020, 15, e0232602. | 1.1 | 21 |
| 1881 | Comparative Analyses of Mitochondrial Genomes Provide Evolutionary Insights Into Nematode-Trapping Fungi. Frontiers in Microbiology, 2020, 11, 617. | 1.5 | 38 |
| 1882 | High Synteny and Sequence Identity between Genomes of Nitrosococcus oceani Strains Isolated from Different Oceanic Gyres Reveals Genome Economization and Autochthonous Clonal Evolution. Microorganisms, 2020, 8, 693. | 1.6 | 4 |
| 1883 | Comparative analysis of plastid genomes within the Campanulaceae and phylogenetic implications. PLoS ONE, 2020, 15, e0233167. | 1.1 | 11 |
| 1884 | First isolation and characterization of Brucella suis from yak. Genome, 2020, 63, 397-405. | 0.9 | 1 |
| 1885 | Tracking the evolution of the two successful CC59 methicillin-resistant Staphylococcus aureus clones in Taiwan: the divergence time of the two clades is estimated to be the 1980s. International Journal of Antimicrobial Agents, 2020, 56, 106047. | 1.1 | 4 |
| 1886 | Dual-Seq reveals genome and transcriptome of Caedibacter taeniospiralis, obligate endosymbiont of Paramecium. Scientific Reports, 2020, 10, 9727. | 1.6 | 8 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1887 | Pan-GWAS of Streptococcus agalactiae Highlights Lineage-Specific Genes Associated with Virulence and Niche Adaptation. MBio, 2020, 11, . | 1.8 | 47 |
| 1888 | Microevolution and Gain or Loss of Mobile Genetic Elements of Outbreak-Related Listeria monocytogenes in Food Processing Environments Identified by Whole Genome Sequencing Analysis. Frontiers in Microbiology, 2020, 11, 866. | 1.5 | 13 |
| 1889 | A genomic perspective of metal-resistant bacteria from gold particles: Possible survival mechanisms during gold biogeochemical cycling. FEMS Microbiology Ecology, 2020, 96, . | 1.3 | 11 |
| 1890 | The nuclear and mitochondrial genomes of Frieseomelitta varia â€“ a highly eusocial stingless bee (Meliponini) with a permanently sterile worker caste. BMC Genomics, 2020, 21, 386. | 1.2 | 15 |
| 1891 | Diversity of cyclic antimicrobial lipopeptides from Bacillus P34 revealed by functional annotation and comparative genome analysis. Microbiological Research, 2020, 238, 126515. | 2.5 | 17 |
| 1892 | In vivo dual RNA-seq reveals that neutrophil recruitment underlies differential tissue tropism of Streptococcus pneumoniae. Communications Biology, 2020, 3, 293. | 2.0 | 22 |
| 1893 | Comparative Genomics of Acinetobacter baumannii Clinical Strains From Brazil Reveals Polyclonal Dissemination and Selective Exchange of Mobile Genetic Elements Associated With Resistance Genes. Frontiers in Microbiology, 2020, 11, 1176. | 1.5 | 24 |
| 1894 | Comparative Genomic Analysis Reveals the Metabolism and Evolution of the Thermophilic Archaeal Genus Metallosphaera. Frontiers in Microbiology, 2020, 11, 1192. | 1.5 | 8 |
| 1895 | Complete genome analysis of Pantoea agglomerans-infecting bacteriophage vB_PagM_AAM22. Archives of Virology, 2020, 165, 2111-2114. | 0.9 | 3 |
| 1896 | Insights Into Chloroplast Genome Evolution Across Opuntioideae (Cactaceae) Reveals Robust Yet Sometimes Conflicting Phylogenetic Topologies. Frontiers in Plant Science, 2020, 11, 729. | 1.7 | 38 |
| 1897 | Isolation of Mycoplasma anserisalpingitidis from swan goose (Anser cygnoides) in China. BMC Veterinary Research, 2020, 16, 178. | 0.7 | 16 |
| 1898 | Beta-Lactam Sensitive Bacteria Can Acquire ESBL-Resistance via Conjugation after Long-Term Exposure to Lethal Antibiotic Concentration. Antibiotics, 2020, 9, 296. | 1.5 | 6 |
| 1899 | The complete chloroplast genome and characteristics analysis of Callistemon rigidus R.Br.. Molecular Biology Reports, 2020, 47, 5013-5024. | 1.0 | 10 |
| 1900 | Genetic and Functional Analyses of Virulence Potential of an Escherichia coli O157:H7 Strain Isolated From Super-Shedder Cattle. Frontiers in Cellular and Infection Microbiology, 2020, 10, 271. | 1.8 | 14 |
| 1901 | Plastome sequences of the subgenus Passiflora reveal highly divergent genes and specific evolutionary features. Plant Molecular Biology, 2020, 104, 21-37. | 2.0 | 13 |
| 1902 | A multiple drug-resistant Streptococcus pneumoniae of serotype 15A occurring from serotype 19A by capsular switching. Vaccine, 2020, 38, 5114-5118. | 1.7 | 5 |
| 1903 | Comparative Mitogenome Analysis Reveals Mitochondrial Genome Differentiation in Ectomycorrhizal and Asymbiotic Amanita Species. Frontiers in Microbiology, 2020, 11, 1382. | 1.5 | 42 |
| 1904 | Comparison of Chloroplast Genomes among Species of Unisexual and Bisexual Clades of the Monocot Family Araceae. Plants, 2020, 9, 737. | 1.6 | 23 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1905 | Genome relationships and LTR-retrotransposon diversity in three cultivated Capsicum L. (Solanaceae) species. BMC Genomics, 2020, 21, 237. | 1.2 | 20 |
| 1906 | The Biotherapeutic Potential of Lactobacillus reuteri Characterized Using a Target-Specific Selection Process. Frontiers in Microbiology, 2020, 11, 532. | 1.5 | 15 |
| 1907 | Toward a chimeric vaccine against multiple isolates of Mycobacteroides - An integrative approach. Life Sciences, 2020, 250, 117541. | 2.0 | 11 |
| 1908 | Comparative Genomics of Actinobacillus pleuropneumoniae Serotype 8 Reveals the Importance of Prophages in the Genetic Variability of the Species. International Journal of Genomics, 2020, 2020, 1-12. | 0.8 | 7 |
| 1909 | Closing Clostridium botulinum Group I Genomes Using a Combination of Short- and Long-Reads. Frontiers in Microbiology, 2020, 11, 239. | 1.5 | 10 |
| 1910 | Comparative Genomic Analysis Confirms Five Genetic Populations of the Select Agent, Rathayibacter toxicus. Microorganisms, 2020, 8, 366. | 1.6 | 3 |
| 1911 | Combining short and long read sequencing to characterize antimicrobial resistance genes on plasmids applied to an unauthorized genetically modified Bacillus. Scientific Reports, 2020, 10, 4310. | 1.6 | 57 |
| 1912 | Ancestral Reconstruction of Karyotypes Reveals an Exceptional Rate of Nonrandom Chromosomal Evolution in Sunflower. Genetics, 2020, 214, 1031-1045. | 1.2 | 31 |
| 1913 | Parallel Sequencing of Wolbachia wCer2 from Donor and Novel Hosts Reveals Multiple Incompatibility Factors and Genome Stability after Host Transfers. Genome Biology and Evolution, 2020, 12, 720-735. | 1.1 | 14 |
| 1914 | The draft genome of a new Verminephrobacter eiseniae strain: a nephridial symbiont of earthworms. Annals of Microbiology, 2020, 70, . | 1.1 | 3 |
| 1915 | Emergence of vancomycin-resistant Enterococcus faecium ST1421 lacking the pstS gene in Korea. European Journal of Clinical Microbiology and Infectious Diseases, 2020, 39, 1349-1356. | 1.3 | 10 |
| 1916 | Crucial Role of the Accessory Genome in the Evolutionary Trajectory of Acinetobacter baumannii Global Clone 1. Frontiers in Microbiology, 2020, 11, 342. | 1.5 | 16 |
| 1917 | New Insights Into the Plastome Evolution of the Millettioid/Phaseoloid Clade (Papilionoideae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 | 1.7 | 21 |
| 1918 | Rhizosphere assisted biodegradation of benzo(a)pyrene by cadmium resistant plant-probiotic Serratia marcescens S2I7, and its genomic traits. Scientific Reports, 2020, 10, 5279. | 1.6 | 19 |
| 1919 | Bacteriophage-Insensitive Mutants of Antimicrobial-Resistant Salmonella Enterica are Altered in their Tetracycline Resistance and Virulence in Caco-2 Intestinal Cells. International Journal of Molecular Sciences, 2020, 21, 1883. | 1.8 | 13 |
| 1920 | Genomic Stability of Composite SCCmec ACME and COMER-Like Genetic Elements in Staphylococcus epidermidis Correlates With Rate of Excision. Frontiers in Microbiology, 2020, 11, 166. | 1.5 | 12 |
| 1921 | Novel Bacteriophages Capable of Disrupting Biofilms From Clinical Strains of Aeromonas hydrophila. Frontiers in Microbiology, 2020, 11, 194. | 1.5 | 22 |
| 1922 | Complete Chloroplast Genomes of Chlorophytum comosum and Chlorophytum gallabatense: Genome Structures, Comparative and Phylogenetic Analysis. Plants, 2020, 9, 296. | 1.6 | 33 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1923 | Genomic Analysis of <i>Bacillus megaterium</i> NCT-2 Reveals Its Genetic Basis for the Bioremediation of Secondary Salinization Soil. International Journal of Genomics, 2020, 2020, 1-11. | 0.8 | 11 |
| 1924 | Horizontal gene transfer and silver nanoparticles production in a new Marinomonas strain isolated from the Antarctic psychrophilic ciliate Euplotes focardii. Scientific Reports, 2020, 10, 10218. | 1.6 | 22 |
| 1925 | The Basis for Natural Multiresistance to Phage in Pseudomonas aeruginosa. Antibiotics, 2020, 9, 339. | 1.5 | 12 |
| 1926 | Characterisation of the Pseudomonas savastanoi pv. phaseolicola population found in Eastern Australia associated with halo blight disease in Vigna radiata. Australasian Plant Pathology, 2020, 49, 515-524. | 0.5 | 3 |
| 1927 | Adaptation and Survival of Burkholderia cepacia and B. contaminans During Long-Term Incubation in Saline Solutions Containing Benzalkonium Chloride. Frontiers in Bioengineering and Biotechnology, 2020, 8, 630. | 2.0 | 14 |
| 1928 | The complete chloroplast genome sequence of <i>Rubus lambertianus</i> var. <i>glaber</i>: sequence divergence and phylogenetic application. Mitochondrial DNA Part B: Resources, 2020, 5, 1261-1262. | 0.2 | 3 |
| 1929 | Draft genome sequence of antimicrobial producing Paenibacillus alvei strain MP1 reveals putative novel antimicrobials. BMC Research Notes, 2020, 13, 280. | 0.6 | 7 |
| 1930 | Diversity of Pectobacteriaceae Species in Potato Growing Regions in Northern Morocco. Microorganisms, 2020, 8, 895. | 1.6 | 14 |
| 1931 | A novel Borrelia species, intermediate between Lyme disease and relapsing fever groups, in neotropical passerine-associated ticks. Scientific Reports, 2020, 10, 10596. | 1.6 | 32 |
| 1932 | tepR encoding a bacterial enhancerâ€binding protein orchestrates the virulence and interspecies competition of Burkholderia glumae through qsmR and a type VI secretion system. Molecular Plant Pathology, 2020, 21, 1042-1054. | 2.0 | 4 |
| 1933 | Comparative Plastid Genomics of Neotropical Bulbophyllum (Orchidaceae; Epidendroideae). Frontiers in Plant Science, 2020, 11, 799. | 1.7 | 24 |
| 1934 | Clostridium massiliamazoniense sp. nov., New Bacterial Species Isolated from Stool Sample of a Volunteer Brazilian. Current Microbiology, 2020, 77, 2008-2015. | 1.0 | 10 |
| 1935 | Comparison of the transcriptomes of different life history stages of the freshwater Rhodophyte Thorea hispida. Genomics, 2020, 112, 3978-3990. | 1.3 | 3 |
| 1936 | <i>Staphylococcus</i> Agr virulence is critical for epidermal colonization and associates with atopic dermatitis development. Science Translational Medicine, 2020, 12, . | 5.8 | 62 |
| 1937 | Complete Chloroplast Genomes of Anthurium huixtlense and Pothos scandens (Pothoideae, Araceae): Unique Inverted Repeat Expansion and Contraction Affect Rate of Evolution. Journal of Molecular Evolution, 2020, 88, 562-574. | 0.8 | 33 |
| 1938 | Molecular evolutionary and 3D protein structural analyses of Lactobacillus fermentum elongation factor Tu, a novel brain health promoting factor. Genomics, 2020, 112, 3915-3924. | 1.3 | 1 |
| 1939 | Metabolism of Soy Isoflavones by Intestinal Bacteria: Genome Analysis of an Adlercreutzia equolifaciens Strain That Does Not Produce Equol. Biomolecules, 2020, 10, 950. | 1.8 | 11 |
| 1941 | A Unique Isolation of a Lytic Bacteriophage Infected Bacillus anthracis Isolate from Pafuri, South Africa. Microorganisms, 2020, 8, 932. | 1.6 | 5 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1942 | De Novo Genome Assemblies for Three North American Bumble Bee Species: Bombus bifarius, Bombus vancouverensis, and Bombus vosnesenskii. G3: Genes, Genomes, Genetics, 2020, 10, 2585-2592. | 0.8 | 18 |
| 1943 | Comparative genome analysis provides shreds of molecular evidence for reclassification of Leuconostoc mesenteroides MTCC 10508 as a strain of Leu. suionicum. Genomics, 2020, 112, 4023-4031. | 1.3 | 13 |
| 1944 | Comparative genomics of Streptococcus parauberis: new target for molecular identification of serotype III. Applied Microbiology and Biotechnology, 2020, 104, 6211-6222. | 1.7 | 9 |
| 1945 | Comparative Genomic Analysis of 19 Clinical Isolates of Tigecycline-Resistant Acinetobacter baumannii. Frontiers in Microbiology, 2020, 11, 1321. | 1.5 | 10 |
| 1946 | A Novel Cyanobacterium Synechococcus elongatus PCC 11802 has Distinct Genomic and Metabolomic Characteristics Compared to its Neighbor PCC 11801. Scientific Reports, 2020, 10, 191. | 1.6 | 54 |
| 1947 | &lt;p&gt;Consequences Of Long-Term Bacteriaâ€™s Exposure To Silver Nanoformulations With Different PhysicoChemical Properties&lt;/p&gt;. International Journal of Nanomedicine, 2020, Volume 15, 199-213. | 3.3 | 14 |
| 1948 | Chloroplast and nuclear ribosomal cistron phylogenomics in a group of closely related sections in Salvia subg. Calosphace. Revista Brasileira De Botanica, 2020, 43, 177-191. | 0.5 | 5 |
| 1949 | First isolation of foot and mouth disease virus from wild boars in the Middle East. Transboundary and Emerging Diseases, 2020, 67, 1725-1729. | 1.3 | 3 |
| 1950 | Analysis of two Mexican Pectobacterium brasiliense strains reveals an inverted relationship between c-di-GMP levels with exopolysaccharide production and swarming motility. Microbiological Research, 2020, 235, 126427. | 2.5 | 7 |
| 1951 | Molecular evolution of chloroplast genomes in Monsteroideae (Araceae). Planta, 2020, 251, 72. | 1.6 | 59 |
| 1952 | Abundance of mobile genetic elements in an Acinetobacter lwoffii strain isolated from Transylvanian honey sample. Scientific Reports, 2020, 10, 2969. | 1.6 | 26 |
| 1953 | Statistical Mitogenome Assembly with RepeaTs. Journal of Computational Biology, 2020, 27, 1407-1421. | 0.8 | 8 |
| 1954 | Hybridization and introgression drive genome evolution of Dutch elm disease pathogens. Nature Ecology and Evolution, 2020, 4, 626-638. | 3.4 | 44 |
| 1955 | The complete mitochondrial genome of the chiltepin pepper (<i>Capsicum annuum</i> var.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Resources, 2020, 5, 683-684. | 0.2 | 12 |
| 1956 | Differential evolution in 3â€²UTRs leads to specific gene expression in Staphylococcus. Nucleic Acids Research, 2020, 48, 2544-2563. | 6.5 | 19 |
| 1957 | Functional Genomics Insights Into the Pathogenicity, Habitat Fitness, and Mechanisms Modifying Plant Development of Rhodococcus sp. PBTS1 and PBTS2. Frontiers in Microbiology, 2020, 11, 14. | 1.5 | 20 |
| 1958 | Thirty complete Streptomyces genome sequences for mining novel secondary metabolite biosynthetic gene clusters. Scientific Data, 2020, 7, 55. | 2.4 | 67 |
| 1959 | Comparative genomic analysis of Chinese human leptospirosis vaccine strain and circulating isolate. Human Vaccines and Immunotherapeutics, 2020, 16, 1345-1353. | 1.4 | 0 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1960 | Escherichia coli ST302: Genomic Analysis of Virulence Potential and Antimicrobial Resistance Mediated by Mobile Genetic Elements. Frontiers in Microbiology, 2020, 10, 3098. | 1.5 | 14 |
| 1961 | Complete chloroplast genome of Sophora alopecuroides (Papilionoideae): molecular structures, comparative genome analysis and phylogenetic analysis. Journal of Genetics, 2020, 99, 1. | 0.4 | 17 |
| 1962 | Initial Characterization of the Chloroplast Genome of Vicia sepium, an Important Wild Resource Plant, and Related Inferences About Its Evolution. Frontiers in Genetics, 2020, 11, 73. | 1.1 | 26 |
| 1963 | Antibiotic resistance, genome analysis and further safe traits of Clostridium perfringens ICVB082; a strain capable of producing an inhibitory compound directed only against a closely related pathogenic strain. Anaerobe, 2020, 62, 102177. | 1.0 | 5 |
| 1964 | The extreme plantâ€growthâ€promoting properties of <i>Pantoea phytobeneficialis</i> MSR2 revealed by functional and genomic analysis. Environmental Microbiology, 2020, 22, 1341-1355. | 1.8 | 29 |
| 1965 | Insights Obtained by Culturing Saccharibacteria With Their Bacterial Hosts. Journal of Dental Research, 2020, 99, 685-694. | 2.5 | 62 |
| 1966 | Whole genome sequencing of carbapenem-resistant Klebsiella pneumoniae: evolutionary analysis for outbreak investigation. Future Microbiology, 2020, 15, 203-212. | 1.0 | 7 |
| 1967 | Complete genome and methylome analysis of Neisseria meningitidis associated with increased serogroup Y disease. Scientific Reports, 2020, 10, 3644. | 1.6 | 2 |
| 1968 | Identifying the drivers of computationally detected correlated evolution among sites under antibiotic selection. Evolutionary Applications, 2020, 13, 781-793. | 1.5 | 3 |
| 1969 | Whole-Genome Sequencing of Lactobacillus helveticus D75 and D76 Confirms Safety and Probiotic Potential. Microorganisms, 2020, 8, 329. | 1.6 | 20 |
| 1970 | Complete genome sequence analysis of the Vibrio owensii strain SH-14 isolated from shrimp with acute hepatopancreatic necrosis disease. Archives of Microbiology, 2020, 202, 1097-1106. | 1.0 | 4 |
| 1971 | Extensive Genomic Rearrangements along with Distinct Mobilome and TALome are Associated with Extreme Pathotypes of a Rice Pathogen. Genome Biology and Evolution, 2020, 12, 3951-3956. | 1.1 | 2 |
| 1972 | Nextâ€Generation Microbial Workhorses: Comparative Genomic Analysis of Fastâ€Growing <i>Vibrio</i> Strains Reveals Their Biotechnological Potential. Biotechnology Journal, 2020, 15, e1900499. | 1.8 | 9 |
| 1973 | Isolation, Substrate Specificity, and Subunit Characterization of the Xylanosomes Produced by Oerskovia turbata JCM 3160. Current Microbiology, 2020, 77, 924-930. | 1.0 | 1 |
| 1974 | Bacteriophages Isolated from Stunted Children Can Regulate Gut Bacterial Communities in an Age-Specific Manner. Cell Host and Microbe, 2020, 27, 199-212.e5. | 5.1 | 85 |
| 1975 | Clades of huge phages from across Earthâ€™s ecosystems. Nature, 2020, 578, 425-431. | 13.7 | 331 |
| 1976 | Isolation and genomic characterization of a new mimivirus of lineage B from a Brazilian river. Archives of Virology, 2020, 165, 853-863. | 0.9 | 3 |
| 1977 | Genomic Acquisitions in Emerging Populations of <i>Xanthomonas vasicola</i> pv. <i>vasculorum</i> Infecting Corn in the United States and Argentina. Phytopathology, 2020, 110, 1161-1173. | 1.1 | 16 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 1978 | Evolutionary dynamics of chloroplast genomes in subfamily Aroideae (Araceae). Genomics, 2020, 112, 2349-2360. | 1.3 | 79 |
| 1979 | Comparative Plastid Genomics of Cryptomonas Species Reveals Fine-Scale Genomic Responses to Loss of Photosynthesis. Genome Biology and Evolution, 2020, 12, 3926-3937. | 1.1 | 27 |
| 1980 | Isolation of Four Lytic Phages Infecting Klebsiella pneumoniae K22 Clinical Isolates from Spain. International Journal of Molecular Sciences, 2020, 21, 425. | 1.8 | 19 |
| 1981 | Subchromosome-Scale Nuclear and Complete Mitochondrial Genome Characteristics of Morchella crassipes. International Journal of Molecular Sciences, 2020, 21, 483. | 1.8 | 27 |
| 1982 | Resistance Sniffer: An online tool for prediction of drug resistance patterns of Mycobacterium tuberculosis isolates using next generation sequencing data. International Journal of Medical Microbiology, 2020, 310, 151399. | 1.5 | 17 |
| 1983 | High quality 3C de novo assembly and annotation of a multidrug resistant ST-111 Pseudomonas aeruginosa genome: Benchmark of hybrid and non-hybrid assemblers. Scientific Reports, 2020, 10, 1392. | 1.6 | 32 |
| 1984 | Complete Chloroplast Genome Sequence of Chinese Lacquer Tree (<i>Toxicodendron vernicifluum</i>,) Tj ETQq0 0 0 rgBT /Overlock 10 | 0.9 | 15 |
| 1985 | Stepwise evolution and convergent recombination underlie the global dissemination of carbapenemase-producing Escherichia coli. Genome Medicine, 2020, 12, 10. | 3.6 | 40 |
| 1986 | Species-specific recruitment of transcription factors dictates toxin expression. Nucleic Acids Research, 2020, 48, 2388-2400. | 6.5 | 28 |
| 1987 | Characterization of sequence variability hotspots in Cranichideae plastomes (Orchidaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 | 1.1 | 25 |
| 1988 | Vanillin Production in <i>Pseudomonas</i> : Whole-Genome Sequencing of <i>Pseudomonas</i> sp. Strain 9.1 and Reannotation of Pseudomonas putida CalA as a Vanillin Reductase. Applied and Environmental Microbiology, 2020, 86, . | 1.4 | 17 |
| 1989 | Comprehensive analysis of the mechanisms underlying enhanced growth and root N acquisition in rice by the endophytic diazotroph, Burkholderia vietnamiensis RS1. Plant and Soil, 2020, 450, 537-555. | 1.8 | 8 |
| 1990 | Complete Genome Sequences for Two <i>Myoviridae</i> Strains Infecting Cyanobacteria in a Subarctic Lake. Microbiology Resource Announcements, 2020, 9, . | 0.3 | 3 |
| 1991 | Evolution and Genetic Diversity of Primate Cytomegaloviruses. Microorganisms, 2020, 8, 624. | 1.6 | 11 |
| 1992 | Pantoea agglomerans-Infecting Bacteriophage vB_PagS_AAS21: A Cold-Adapted Virus Representing a Novel Genus within the Family Siphoviridae. Viruses, 2020, 12, 479. | 1.5 | 5 |
| 1993 | The complete chloroplast genome of Myriophyllum spicatum reveals a 4â€kb inversion and new insights regarding plastome evolution in Haloragaceae. Ecology and Evolution, 2020, 10, 3090-3102. | 0.8 | 7 |
| 1994 | Complete genome analysis of Glutamicibacter creatinolyticus from mare abscess and comparative genomics provide insight of diversity and adaptation for Glutamicibacter. Gene, 2020, 741, 144566. | 1.0 | 14 |
| 1995 | Taxogenomic assessment and genomic characterisation of Weissella cibaria strain 92 able to metabolise oligosaccharides derived from dietary fibres. Scientific Reports, 2020, 10, 5853. | 1.6 | 15 |

| # | Article | IF | Citations |
|---|---|---|---|
| 1996 | Complete Genome Sequence of Chlamydia avium PV 4360/2, Isolated from a Feral Pigeon in Italy. Microbiology Resource Announcements, 2020, 9, . | 0.3 | 4 |
| 1997 | 2SigFinder: the combined use of small-scale and large-scale statistical testing for genomic island detection from a single genome. BMC Bioinformatics, 2020, 21, 159. | 1.2 | 29 |
| 1998 | Genomic characterization of Lactobacillus fermentum DSM 20052. BMC Genomics, 2020, 21, 328. | 1.2 | 15 |
| 1999 | Description of Three Novel Members in the Family Geobacteraceae, Oryzomonas japonicum gen. nov., sp. nov., Oryzomonas sagensis sp. nov., and Oryzomonas ruber sp. nov.. Microorganisms, 2020, 8, 634. | 1.6 | 29 |
| 2000 | Comparative Genomic and Transcriptomic Analyses of Mycobacterium kansasii Subtypes Provide New Insights Into Their Pathogenicity and Taxonomy. Frontiers in Cellular and Infection Microbiology, 2020, 10, 122. | 1.8 | 10 |
| 2001 | The complete genome of lytic Salmonella phage vB_SenM-PA13076 and therapeutic potency in the treatment of lethal Salmonella Enteritidis infections in mice. Microbiological Research, 2020, 237, 126471. | 2.5 | 41 |
| 2002 | The Organelle Genomes in the Photosynthetic Red Algal Parasite <i>Pterocladiophila hemisphaerica</i> (Florideophyceae, Rhodophyta) Have Elevated Substitution Rates and Extreme Gene Loss in the Plastid Genome. Journal of Phycology, 2020, 56, 1006-1018. | 1.0 | 7 |
| 2003 | Comparative genomic analysis and mosquito larvicidal activity of four Bacillus thuringiensis serovar israelensis strains. Scientific Reports, 2020, 10, 5518. | 1.6 | 6 |
| 2004 | Development of a workflow for identification of nuclear genotyping markers for <i>Cyclospora cayetanensis</i>. Parasite, 2020, 27, 24. | 0.8 | 13 |
| 2005 | Global clonal spread of mcr-3-carrying MDR ST34 Salmonella enterica serotype Typhimurium and monophasic 1,4,[5],12:i:â^' variants from clinical isolates. Journal of Antimicrobial Chemotherapy, 2020, 75, 1756-1765. | 1.3 | 37 |
| 2006 | Mild Stress Conditions during Laboratory Culture Promote the Proliferation of Mutations That Negatively Affect Sigma B Activity in Listeria monocytogenes. Journal of Bacteriology, 2020, 202, . | 1.0 | 22 |
| 2007 | Draft Genome Sequence of â€œ Candidatus Arthromitusâ€•UMNCA01, a Suspected Commensal Isolated from the Gut Microbiome of Commercial Turkey. Microbiology Resource Announcements, 2020, 9, . | 0.3 | 1 |
| 2008 | Draft Genome Sequence of a Serratia marcescens Strain Isolated from the Pitcher Fluids of a <i>Sarracenia</i> Pitcher Plant. Microbiology Resource Announcements, 2020, 9, . | 0.3 | 2 |
| 2009 | Draft Genome Sequences of 12 Leuconostoc carnosum Strains Isolated from Cooked Ham Packaged in a Modified Atmosphere and from Fresh Sausages. Microbiology Resource Announcements, 2020, 9, . | 0.3 | 6 |
| 2010 | The Complete Chloroplast Genome of Two Important Annual Clover Species, Trifolium alexandrinum and T. resupinatum: Genome Structure, Comparative Analyses and Phylogenetic Relationships with Relatives in Leguminosae. Plants, 2020, 9, 478. | 1.6 | 26 |
| 2011 | Complete Genome Sequence of a Legionella longbeachae Serogroup 2 Isolate Derived from a Patient with Legionnairesâ€™ Disease. Microbiology Resource Announcements, 2020, 9, . | 0.3 | 1 |
| 2012 | Draft Genome Sequences of Bifidobacterium animalis Consecutively Isolated from Healthy Japanese Individuals. Journal of Genomics, 2020, 8, 37-42. | 0.6 | 0 |
| 2013 | The Remarkable Dual-Level Diversity of Prokaryotic Flagellins. MSystems, 2020, 5, . | 1.7 | 11 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2014 | Plastome Evolution in Saxifragaceae and Multiple Plastid Capture Events Involving Heuchera and Tiarella. Frontiers in Plant Science, 2020, 11, 361. | 1.7 | 34 |
| 2015 | Whole-Genome-Sequence-Based Characterization of Extensively Drug-Resistant Acinetobacter baumannii Hospital Outbreak. MSphere, 2020, 5, . | 1.3 | 36 |
| 2016 | Exploring the success of Brazilian endemic clone Pseudomonas aeruginosa ST277 and its association with the CRISPR-Cas system type I-C. BMC Genomics, 2020, 21, 255. | 1.2 | 15 |
| 2017 | Tetracycline degradation by Klebsiella sp. strain TR5: Proposed degradation pathway and possible genes involved. Chemosphere, 2020, 253, 126729. | 4.2 | 48 |
| 2018 | Persistent contamination of raw milk by Campylobacter jejuni ST-883. PLoS ONE, 2020, 15, e0231810. | 1.1 | 25 |
| 2019 | Whole genome analysis of multidrug-resistant Citrobacter freundii B9-C2 isolated from preterm neonateâ€™s stool in the first week. Journal of Global Antimicrobial Resistance, 2020, 21, 246-251. | 0.9 | 8 |
| 2020 | Lentibacillus cibarius sp. nov., isolated from kimchi, a Korean fermented food. Journal of Microbiology, 2020, 58, 387-394. | 1.3 | 16 |
| 2021 | First detection of a plasmid located carbapenem resistant blaVIM-1 gene in E. coli isolated from meat products at retail in Belgium in 2015. International Journal of Food Microbiology, 2020, 324, 108624. | 2.1 | 16 |
| 2022 | The complete plastome sequences of five Aponogeton species (Aponogetonaceae): Insights into the structural organization and mutational hotspots. Plant Diversity, 2020, 42, 334-342. | 1.8 | 10 |
| 2023 | Gcluster: a simple-to-use tool for visualizing and comparing genome contexts for numerous genomes. Bioinformatics, 2020, 36, 3871-3873. | 1.8 | 11 |
| 2024 | Isolation and characterization of Hena1 â€“ a novel<i>Erwinia amylovora</i>bacteriophage. FEMS Microbiology Letters, 2020, 367, . | 0.7 | 11 |
| 2025 | SARSâ€CoVâ€2, an evolutionary perspective of interaction with human ACE2 reveals undiscovered amino acids necessary for complex stability. Evolutionary Applications, 2020, 13, 2168-2178. | 1.5 | 38 |
| 2026 | Molecular and Clinical Characterization of Multidrug-Resistant and Hypervirulent Klebsiella pneumoniae Strains from Liver Abscess in Taiwan. Antimicrobial Agents and Chemotherapy, 2020, 64, . | 1.4 | 21 |
| 2027 | Emergence of a Novel Salmonella enterica Serotype Reading Clonal Group Is Linked to Its Expansion in Commercial Turkey Production, Resulting in Unanticipated Human Illness in North America. MSphere, 2020, 5, . | 1.3 | 22 |
| 2028 | Complete genome sequence and annotation of the laboratory reference strain Shigella flexneri serotype 5a M90T and genome-wide transcriptional start site determination. BMC Genomics, 2020, 21, 285. | 1.2 | 7 |
| 2029 | Temporal Dynamics of Salmonella enterica subsp. enterica Serovar Agona Isolates From a Recurrent Multistate Outbreak. Frontiers in Microbiology, 2020, 11, 478. | 1.5 | 14 |
| 2030 | Correlations among oligonucleotide repeats, nucleotide substitutions, and insertionâ€“deletion mutations in chloroplast genomes of plant family Malvaceae. Journal of Systematics and Evolution, 2021, 59, 388-402. | 1.6 | 43 |
| 2031 | Incorporating the plasmidome into antibiotic resistance surveillance in animal agriculture. Plasmid, 2021, 113, 102529. | 0.4 | 2 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2032 | Acquisition of a genomic resistance island (AbGRI5) from global clone 2 through homologous recombination in a clinical <i>Acinetobacter baumannii</i> isolate. Journal of Antimicrobial Chemotherapy, 2021, 76, 65-69. | 1.3 | 13 |
| 2033 | Genetics and regulation of nitrogen fixation in Paenibacillus brasilensis PB24. Microbiological Research, 2021, 243, 126647. | 2.5 | 6 |
| 2034 | Complete genome reconstruction and genetic analysis of Taura syndrome virus of shrimp from archival Davidson's-fixed paraffin embedded tissue. Virology, 2021, 553, 117-121. | 1.1 | 7 |
| 2035 | Deciphering the origin of<i>Aspergillus flavus</i>NRRL21882, the active biocontrol agent of Aflaâ€Guard<sup>Â®</sup>. Letters in Applied Microbiology, 2021, 72, 509-516. | 1.0 | 11 |
| 2036 | Whole genome sequencing and genome annotation of Dermacoccus abyssi strain HZAU 226 isolated from spoiled eggs. Genomics, 2021, 113, 1199-1206. | 1.3 | 5 |
| 2037 | Genotyping Dickeya dianthicola Causing Potato Blackleg and Soft Rot Outbreak Associated With Inoculum Geography in the United States. Plant Disease, 2021, 105, PDIS-10-20-2138. | 0.7 | 5 |
| 2038 | High Sequence Divergence but Limited Architectural Rearrangements in Organelle Genomes of Cyanophora (Glaucophyta) Species. Journal of Eukaryotic Microbiology, 2021, 68, e12831. | 0.8 | 0 |
| 2039 | Whole-genome Sequencing and Mining of Protease Coding Genes in Bacillus paralicheniformis MKU3, and its Degradomics in Feather Meal Medium. Current Microbiology, 2021, 78, 206-217. | 1.0 | 3 |
| 2040 | SNPâ€based genotyping and wholeâ€genome sequencing reveal previously unknown genetic diversity in <i>Xanthomonas vasicola</i> pv. <i>musacearum</i>, causal agent of banana xanthomonas wilt, in its presumed Ethiopian origin. Plant Pathology, 2021, 70, 534-543. | 1.2 | 3 |
| 2041 | Development of a realâ€time PCR assay for detection and quantification of <i>Streptococcus iniae</i> using the lactate permease gene. Journal of Fish Diseases, 2021, 44, 53-61. | 0.9 | 14 |
| 2042 | A single nucleotide polymorphism in an IgA1 protease gene determines <i>Streptococcus pneumoniae</i> adaptation to the middle ear during otitis media. Pathogens and Disease, 2021, 79, . | 0.8 | 5 |
| 2043 | Phylogeny of <i>Orthotrichum</i> s.l. and <i>Ulota</i> s.l. (Orthotrichaceae, Bryophyta): Insights into stomatal evolution. Journal of Systematics and Evolution, 2022, 60, 876-900. | 1.6 | 3 |
| 2044 | CRISPR-Cas systems restrict horizontal gene transfer in <i>Pseudomonas aeruginosa</i>. ISME Journal, 2021, 15, 1420-1433. | 4.4 | 59 |
| 2045 | Development of genomic resources for the genus Celtis (Cannabaceae) based on genome skimming data. Plant Diversity, 2021, 43, 43-53. | 1.8 | 13 |
| 2046 | Chloroplast genome evolution in the Dracunculus clade (Aroideae, Araceae). Genomics, 2021, 113, 183-192. | 1.3 | 27 |
| 2047 | Mosaic genome evolution and phylogenetics of Chrysodeixis includens nucleopolyhedrovirus (ChinNPV) and virulence of seven new isolates from the Brazilian states of Minas Gerais and Mato Grosso. Archives of Virology, 2021, 166, 125-138. | 0.9 | 1 |
| 2048 | Phylogeny of Veneridae (Bivalvia) based on mitochondrial genomes. Zoologica Scripta, 2021, 50, 58-70. | 0.7 | 13 |
| 2049 | Life and Death of Selfish Genes: Comparative Genomics Reveals the Dynamic Evolution of Cytoplasmic Incompatibility. Molecular Biology and Evolution, 2021, 38, 2-15. | 3.5 | 72 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2050 | Comparative genome analysis of 12 Shigella sonnei strains: virulence, resistance, and their interactions. International Microbiology, 2021, 24, 83-91. | 1.1 | 1 |
| 2051 | Myxosporea (Myxozoa, Cnidaria) Lack DNA Cytosine Methylation. Molecular Biology and Evolution, 2021, 38, 393-404. | 3.5 | 12 |
| 2052 | Draft Genome of Fusarium oxysporum f. sp. cubense Strain Tropical Race-4 Infecting Cavendish (AAA) Group of Banana in India. Plant Disease, 2021, 105, 481-483. | 0.7 | 17 |
| 2053 | Phageome Analysis of Bifidobacteria-Rich Samples. Methods in Molecular Biology, 2021, 2278, 71-85. | 0.4 | 0 |
| 2054 | Complete Genome Sequence of <i>Francisella</i> sp. Strain LA11-2445 (FDC406), a Novel <i>Francisella</i> Species Isolated from a Human Skin Lesion. Microbiology Resource Announcements, 2021, 10, . | 0.3 | 0 |
| 2055 | New insights into the evolutionary characteristic between the New World and Old World Lupinus species using complete chloroplast genomes. International Journal of Transgender Health, 2021, 14, 414-427. | 1.1 | 2 |
| 2056 | Genome Sequences of 104 Escherichia coli O157:H7 Isolates from Pigs, Cattle, and Pork Production Environments in Alberta, Canada. Microbiology Resource Announcements, 2021, 10, . | 0.3 | 1 |
| 2057 | Phylogenomic and evolutionary dynamics of inverted repeats across Angelica plastomes. BMC Plant Biology, 2021, 21, 26. | 1.6 | 32 |
| 2058 | Mechanisms of aerobic dechlorination of hexachlorobenzene and pentachlorophenol by &lt;i&gt;Nocardioides&lt;/i&gt; sp. PD653. Journal of Pesticide Sciences, 2021, 46, 373-381. | 0.8 | 3 |
| 2059 | Proof of the triple prerequisite conditions which are essential for carbapenem resistance development in Klebsiella pneumoniae by using radiation-mediated mutagenesis. FEMS Microbiology Letters, 2021, 368, . | 0.7 | 0 |
| 2060 | Comparative genomic analysis of Polypodiaceae chloroplasts reveals fine structural features and dynamic insertion sequences. BMC Plant Biology, 2021, 21, 31. | 1.6 | 14 |
| 2061 | Genetic Sequence Alignment Computing for Ensuring Cyber Security of the IoT Systems. Advances in Sustainability Science and Technology, 2021, , 235-252. | 0.4 | 2 |
| 2062 | Genome analysis of the metabolically versatile <i>Pseudomonas umsongensis</i> GO16: the genetic basis for PET monomer upcycling into polyhydroxyalkanoates. Microbial Biotechnology, 2021, 14, 2463-2480. | 2.0 | 35 |
| 2063 | <i>Bifidobacterium dentium</i> N8 with potential probiotic characteristics prevents LPS-induced intestinal barrier injury by alleviating the inflammatory response and regulating the tight junction in Caco-2 cell monolayers. Food and Function, 2021, 12, 7171-7184. | 2.1 | 31 |
| 2064 | The mitogenomes of two saprophytic Boletales species (Coniophora) reveals intron dynamics and accumulation of plasmid-derived and non-conserved genes. Computational and Structural Biotechnology Journal, 2021, 19, 401-414. | 1.9 | 23 |
| 2065 | Culex quinquefasciatus carrying Wolbachia is less susceptible to entomopathogenic bacteria. Scientific Reports, 2021, 11, 1094. | 1.6 | 9 |
| 2066 | Geno-informatics for Prediction of Virulence and Drug Resistance in Bacterial Pathogens. , 2021, , 3-18. |  | 0 |
| 2067 | Comparative Chloroplast Genomics of Corydalis Species (Papaveraceae): Evolutionary Perspectives on Their Unusual Large Scale Rearrangements. Frontiers in Plant Science, 2020, 11, 600354. | 1.7 | 30 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2068 | Genomic Analysis of Antimicrobial Resistance and Resistance Plasmids in Salmonella Serovars from Poultry in Nigeria. Antibiotics, 2021, 10, 99. | 1.5 | 29 |
| 2069 | The Effect of Alignment on Peoples Ability to Judge Event Sequence Similarity. IEEE Transactions on Visualization and Computer Graphics, 2021, PP, 1-1. | 2.9 | 0 |
| 2070 | Uncovering dynamic evolution in the plastid genome of seven Ligusticum species provides insights into species discrimination and phylogenetic implications. Scientific Reports, 2021, 11, 988. | 1.6 | 10 |
| 2071 | Draft Genome Sequence of Pseudomonas sp. Strain T2.31D-1, Isolated from a Drilling Core Sample Obtained 414 Meters below Surface in the Iberian Pyrite Belt. Microbiology Resource Announcements, 2021, 10, . | 0.3 | 3 |
| 2072 | Whole plastomes are not enough: phylogenomic and morphometric exploration at multiple demographic levels of the bee orchid clade <i>Ophrys</i> sect. <i>Sphegodes</i>. Journal of Experimental Botany, 2021, 72, 654-681. | 2.4 | 15 |
| 2073 | Genetic and evolutionary analyses of plastomes of the subfamily Cactoideae (Cactaceae) indicate relaxed protein biosynthesis and tRNA import from cytosol. Revista Brasileira De Botanica, 2021, 44, 97-116. | 0.5 | 7 |
| 2074 | Assembly, Annotation, and Comparative Analysis of Bifidobacterial Genomes. Methods in Molecular Biology, 2021, 2278, 31-44. | 0.4 | 0 |
| 2075 | Comparative Genomics, from the Annotated Genome to Valuable Biological Information: A Case Study. Methods in Molecular Biology, 2021, 2242, 91-112. | 0.4 | 0 |
| 2076 | Potential Whole-Cell Biosensors for Detection of Metal Using MerR Family Proteins from Enterobacter sp. YSU and Stenotrophomonas maltophilia OR02. Micromachines, 2021, 12, 142. | 1.4 | 2 |
| 2077 | Morphological and genomic evidence for a new species of Corallorhiza (Orchidaceae Epidendroideae) from SW China. Plant Diversity, 2021, 43, 409-419. | 1.8 | 1 |
| 2078 | Genomic sequencing of different sequevars of Ralstonia solanacearum belonging to the Moko ecotype. Genetics and Molecular Biology, 2021, 44, e20200172. | 0.6 | 5 |
| 2080 | A biological and genomic comparison of a drug-resistant and a drug-susceptible strain of <i>Candida auris</i> isolated from Beijing, China. Virulence, 2021, 12, 1388-1399. | 1.8 | 11 |
| 2081 | Comprehensive genomic analysis reveals virulence factors and antibiotic resistance genes in Pantoea agglomerans KM1, a potential opportunistic pathogen. PLoS ONE, 2021, 16, e0239792. | 1.1 | 21 |
| 2082 | Comparative mitochondrial genome analysis reveals intron dynamics and gene rearrangements in two Trametes species. Scientific Reports, 2021, 11, 2569. | 1.6 | 13 |
| 2083 | Genomic Characterization of Multidrug-Resistant Escherichia coli BH100 Sub-strains. Frontiers in Microbiology, 2020, 11, 549254. | 1.5 | 5 |
| 2084 | Genome-wide genetic marker analysis and genotyping of Escherichia fergusonii strain OTSVEF-60. Brazilian Journal of Microbiology, 2021, 52, 989-1004. | 0.8 | 14 |
| 2085 | Rapid divergence of the male reproductive proteins in the<i>Drosophila dunni</i>group and implications for postmating incompatibilities between species. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 4 |
| 2086 | Complete Genome Sequence of Campylobacter hepaticus USA52, Associated with Chicken Spotty Liver Disease. Microbiology Resource Announcements, 2021, 10, . | 0.3 | 2 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2087 | A comparison of fourteen fully characterized mammalian-associated <i>Campylobacter fetus</i> isolates suggests that loss of defense mechanisms contribute to high genomic plasticity and subspecies evolution. PeerJ, 2021, 9, e10586. | 0.9 | 5 |
| 2088 | Comparative Genomic Analysis of Three Pseudomonas Species Isolated from the Eastern Oyster (Crassostrea virginica) Tissues, Mantle Fluid, and the Overlying Estuarine Water Column. Microorganisms, 2021, 9, 490. | 1.6 | 7 |
| 2089 | Comprehensive genomics depict accessory genes encoding pathogenicity and biofilm determinants in <i>Enterococcus faecalis</i>. Future Microbiology, 2021, 16, 143-157. | 1.0 | 2 |
| 2091 | Comparative Genomics of Mycobacterium avium Subspecies Paratuberculosis Sheep Strains. Frontiers in Veterinary Science, 2021, 8, 637637. | 0.9 | 7 |
| 2093 | Portable CRISPR-Cas9 <sup>N</sup> System for Flexible Genome Engineering in Lactobacillus acidophilus, Lactobacillus gasseri, and Lactobacillus paracasei. Applied and Environmental Microbiology, 2021, 87, . | 1.4 | 18 |
| 2094 | Co-Bridges: Pair-wise Visual Connection and Comparison for Multi-item Data Streams. IEEE Transactions on Visualization and Computer Graphics, 2021, 27, 1612-1622. | 2.9 | 11 |
| 2095 | Zinc limitation in Klebsiella pneumoniae profiled by quantitative proteomics influences transcriptional regulation and cation transporter-associated capsule production. BMC Microbiology, 2021, 21, 43. | 1.3 | 5 |
| 2096 | Detection and identification of Xanthomonas campestris pv. campestris and pv. raphani by multiplex polymerase chain reaction using specific primers. Applied Microbiology and Biotechnology, 2021, 105, 1991-2002. | 1.7 | 3 |
| 2097 | Whole Genome Sequencing and Antimicrobial Resistance of Staphylococcus aureus from Surgical Site Infections in Ghana. Pathogens, 2021, 10, 196. | 1.2 | 4 |
| 2098 | Multiple Displacement Amplification as a Solution for Low Copy Number Plasmid Sequencing. Frontiers in Microbiology, 2021, 12, 617487. | 1.5 | 2 |
| 2100 | Comparative Analyses of Euonymus Chloroplast Genomes: Genetic Structure, Screening for Loci With Suitable Polymorphism, Positive Selection Genes, and Phylogenetic Relationships Within Celastrineae. Frontiers in Plant Science, 2020, 11, 593984. | 1.7 | 25 |
| 2101 | Dissemination of Extended-Spectrum-Î²-Lactamase-Producing <i>Enterobacter cloacae</i> Complex from a Hospital to the Nearby Environment in Guadeloupe (French West Indies): ST114 Lineage Coding for a Successful IncHI2/ST1 Plasmid. Antimicrobial Agents and Chemotherapy, 2021, 65, . | 1.4 | 9 |
| 2102 | Harnessing CRISPR-Cas9 for Genome Editing in Streptococcus pneumoniae D39V. Applied and Environmental Microbiology, 2021, 87, . | 1.4 | 6 |
| 2103 | Characterization of a pericentric inversion in plateau fence lizards (<i>Sceloporus tristichus</i>): evidence from chromosome-scale genomes. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 8 |
| 2104 | A novel DNA chromatography method to discriminate Mycobacterium abscessus subspecies and macrolide susceptibility. EBioMedicine, 2021, 64, 103187. | 2.7 | 16 |
| 2105 | Genomic Characterization Provides an Insight into the Pathogenicity of the Poplar Canker Bacterium Lonsdalea populi. Genes, 2021, 12, 246. | 1.0 | 0 |
| 2106 | Identification and characterization of a spreadable IncI1 plasmid harbouring a blaCTX-M-15 gene in an Italian human isolate of Salmonella serovar Napoli. Plasmid, 2021, 114, 102566. | 0.4 | 3 |
| 2107 | In-Silico Pangenomics of SARS-CoV-2 Isolates Reveal Evidence for Subtle Adaptive Expression Strategies, Continued Clonal Evolution, and Sub-Clonal Emergences, Despite Genome Stability. Microbiology Research, 2021, 12, 204-233. | 0.8 | 4 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2108 | Characterization of multidrug-resistant Acinetobacter baumannii strain ATCC BAA1605 using whole-genome sequencing. BMC Research Notes, 2021, 14, 83. | 0.6 | 8 |
| 2109 | Whole-Genome Sequencing and Comparative Genomics of Three Helicobacter pylori Strains Isolated from the Stomach of a Patient with Adenocarcinoma. Pathogens, 2021, 10, 331. | 1.2 | 5 |
| 2111 | The plastome of Phaius hainanensis (Orchidaceae): an endangered species endemic to Hainan province, China. Mitochondrial DNA Part B: Resources, 2021, 6, 1253-1255. | 0.2 | 0 |
| 2112 | The first eleven mitochondrial genomes from the ectomycorrhizal fungal genus (Boletus) reveal intron loss and gene rearrangement. International Journal of Biological Macromolecules, 2021, 172, 560-572. | 3.6 | 38 |
| 2114 | Analysis of Secreted Proteins and Potential Virulence via the ICEs-Mediated Pathway of the Foodborne Pathogen Vibrio parahaemolyticus. Frontiers in Microbiology, 2021, 12, 612166. | 1.5 | 3 |
| 2115 | A bifunctional enzyme belonging to cytochrome P450 family involved in the O-dealkylation and N-dealkoxymethylation toward chloroacetanilide herbicides in Rhodococcus sp. B2. Microbial Cell Factories, 2021, 20, 61. | 1.9 | 8 |
| 2116 | Complete Annotated Genome Sequence of the Salmonella enterica Serovar Typhimurium LT7 Strain STK003, Historically Used in Gene Transfer Studies. Microbiology Resource Announcements, 2021, 10, . | 0.3 | 1 |
| 2117 | Chloroplast genome sequence of Chongming lima bean (Phaseolus lunatus L.) and comparative analyses with other legume chloroplast genomes. BMC Genomics, 2021, 22, 194. | 1.2 | 26 |
| 2119 | The complete chloroplast genome of Stauntonia chinensis and compared analysis revealed adaptive evolution of subfamily Lardizabaloideae species in China. BMC Genomics, 2021, 22, 161. | 1.2 | 26 |
| 2120 | Field evaluation of PGP Bacillus sp. strain D5 native to Crocus sativus, in traditional and non traditional areas, and mining of PGP genes from its genome. Scientific Reports, 2021, 11, 5454. | 1.6 | 24 |
| 2121 | Francisellosis of Yesso scallops Mizuhopecten yessoensis in Japan is caused by a novel type of Francisella halioticida. Diseases of Aquatic Organisms, 2021, 144, 9-19. | 0.5 | 2 |
| 2122 | Complete chloroplast genome sequence of Adenophora racemosa (Campanulaceae): Comparative analysis with congeneric species. PLoS ONE, 2021, 16, e0248788. | 1.1 | 9 |
| 2123 | Draft Genome Sequence of Saccharomyces cerevisiae LW2591Y, a Laboratory Strain for <i>In Vivo</i> Multigene Assemblies. Microbiology Resource Announcements, 2021, 10, . | 0.3 | 1 |
| 2124 | Comparative genome analysis of three Group A Streptococcus dysgalactiae subsp. equisimilis strains isolated in Japan. Journal of Medical Microbiology, 2021, 70, . | 0.7 | 1 |
| 2125 | Draft Genome of Proteus mirabilis Serogroup O18 Elaborating Phosphocholine-Decorated O Antigen. Frontiers in Cellular and Infection Microbiology, 2021, 11, 620010. | 1.8 | 3 |
| 2126 | Draft Genome Resource of a Novel Virulent <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> Race 1 Strain (VCG 0124) Infecting Cavendish (AAA) Group of Banana in India. Plant Disease, 2021, 105, 2708-2710. | 0.7 | 5 |
| 2127 | Expression of fungal biosynthetic gene clusters in S. cerevisiae for natural product discovery. Synthetic and Systems Biotechnology, 2021, 6, 20-22. | 1.8 | 6 |
| 2128 | Comparative analysis of the complete chloroplast genome of seven Nymphaea species. Aquatic Botany, 2021, 170, 103353. | 0.8 | 13 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2129 | Authentication of Aspergillus parasiticus strains in the genome database of the National Center for Biotechnology Information. BMC Research Notes, 2021, 14, 111. | 0.6 | 5 |
| 2130 | The Distribution of Onion Virulence Gene Clusters Among Pantoea spp.. Frontiers in Plant Science, 2021, 12, 643787. | 1.7 | 12 |
| 2131 | Insights into Acinetobacter baumannii fatty acid synthesis 3-oxoacyl-ACP reductases. Scientific Reports, 2021, 11, 7050. | 1.6 | 9 |
| 2132 | Analysis of a Methanogen and an Actinobacterium Dominating the Thermophilic Microbial Community of an Electromethanogenic Biocathode. Archaea, 2021, 2021, 1-13. | 2.3 | 4 |
| 2133 | Alvis: a tool for contig and read ALignment VISualisation and chimera detection. BMC Bioinformatics, 2021, 22, 124. | 1.2 | 14 |
| 2134 | Nitric oxide (NO) elicits aminoglycoside tolerance in Escherichia coli but antibiotic resistance gene carriage and NO sensitivity have not co-evolved. Archives of Microbiology, 2021, 203, 2541-2550. | 1.0 | 7 |
| 2135 | New Genotype of Yersinia pestis Found in Live Rodents in Yunnan Province, China. Frontiers in Microbiology, 2021, 12, 628335. | 1.5 | 5 |
| 2136 | High Rates of Genome Rearrangements and Pathogenicity of Shigella spp.. Frontiers in Microbiology, 2021, 12, 628622. | 1.5 | 13 |
| 2137 | Complete Genome Sequence of Bifidobacterium longum subsp. longum JCM7052. Microbiology Resource Announcements, 2021, 10, . | 0.3 | 1 |
| 2138 | Molecular characterization of <i>Neisseria gonorrhoeae</i> isolates collected through a national surveillance programme in Japan, 2013: evidence of the emergence of a ceftriaxone-resistant strain from a ceftriaxone-susceptible lineage. Journal of Antimicrobial Chemotherapy, 2021, 76, 1769-1775. | 1.3 | 8 |
| 2139 | Antiviral Resistance and Phage Counter Adaptation to Antibiotic-Resistant Extraintestinal Pathogenic <i>Escherichia coli</i>. MBio, 2021, 12, . | 1.8 | 23 |
| 2140 | Genomic diversity and molecular epidemiology of Pasteurella multocida. PLoS ONE, 2021, 16, e0249138. | 1.1 | 36 |
| 2142 | Isolation and Characterization of a Virulent Bacteriophage for Controlling Salmonella Enteritidis Growth in Ready-to-Eat Mixed-Ingredient Salads. Journal of Food Protection, 2021, 84, 1629-1639. | 0.8 | 8 |
| 2144 | Third-generation sequencing revises the molecular karyotype for <i>Toxoplasma gondii</i> and identifies emerging copy number variants in sexual recombinants. Genome Research, 2021, 31, 834-851. | 2.4 | 19 |
| 2145 | Genomic features underlying the evolutionary transitions of <i>Apibacter</i> to honey bee gut symbionts. Insect Science, 2022, 29, 259-275. | 1.5 | 13 |
| 2146 | Identification and Characterization of a Novel Genomic Island Harboring Cadmium and Arsenic Resistance Genes in Listeria welshimeri. Biomolecules, 2021, 11, 560. | 1.8 | 7 |
| 2147 | Draft Genome Sequence of <i>Bacillus</i> sp. Strain IGA-FME-2, Isolated from the Bulk Soil of Soybean (Glycine max L.) in Northeast China. Microbiology Resource Announcements, 2021, 10, . | 0.3 | 0 |
| 2148 | A Novel Structure Harboring blaCTX-M-27 on IncF Plasmids in Escherichia coli Isolated from Swine in China. Antibiotics, 2021, 10, 387. | 1.5 | 8 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2149 | Insights into genomic evolution from the chromosomal and mitochondrial genomes of Ustilaginoidea virens. Phytopathology Research, 2021, 3, . | 0.9 | 9 |
| 2150 | Microbial community characterization of shrimp survivors to AHPND challenge test treated with an effective shrimp probiotic (Vibrio diabolicus). Microbiome, 2021, 9, 88. | 4.9 | 36 |
| 2151 | Combination Therapy of Phage vB_KpnM_P-KP2 and Gentamicin Combats Acute Pneumonia Caused by K47 Serotype Klebsiella pneumoniae. Frontiers in Microbiology, 2021, 12, 674068. | 1.5 | 24 |
| 2152 | Population genomics and antimicrobial resistance dynamics of Escherichia coli in wastewater and river environments. Communications Biology, 2021, 4, 457. | 2.0 | 20 |
| 2153 | Association between the blaCTX-M-14-harboring Escherichia coli Isolated from Weasels and Domestic Animals Reared on a University Campus. Antibiotics, 2021, 10, 432. | 1.5 | 6 |
| 2154 | The Development of Bacteriophage Resistance in Vibrio alginolyticus Depends on a Complex Metabolic Adaptation Strategy. Viruses, 2021, 13, 656. | 1.5 | 6 |
| 2155 | Quantitative Control of Early Flowering in White Lupin (Lupinus albus L.). International Journal of Molecular Sciences, 2021, 22, 3856. | 1.8 | 4 |
| 2156 | Whole genome sequencing of a clinical drug resistant Candida albicans isolate reveals known and novel mutations in genes involved in resistance acquisition mechanisms. Journal of Medical Microbiology, 2021, 70, . | 0.7 | 7 |
| 2157 | Phylogenetic origin of two Japanese Torreya taxa found in two regions with strongly contrasting snow depth. Journal of Plant Research, 2021, 134, 907-919. | 1.2 | 3 |
| 2158 | Complete genome sequence of the Pseudomonas oleovorans strain ODT-83 isolated from oyster. Archives of Microbiology, 2021, 203, 3117-3124. | 1.0 | 2 |
| 2159 | Occurrence and Transmission of <i>bla</i> <sub>NDM</sub> -Carrying <i>Enterobacteriaceae</i> from Geese and the Surrounding Environment on a Commercial Goose Farm. Applied and Environmental Microbiology, 2021, 87, . | 1.4 | 13 |
| 2160 | Genomic Insight of Alicyclobacillus mali FL18 Isolated From an Arsenic-Rich Hot Spring. Frontiers in Microbiology, 2021, 12, 639697. | 1.5 | 17 |
| 2161 | Plastid and nuclear phylogenomic incongruences and biogeographic implications of <i>Magnolia</i> s.l. (Magnoliaceae). Journal of Systematics and Evolution, 2022, 60, 1-15. | 1.6 | 29 |
| 2162 | Prevalence and Genetic Analysis of Chromosomal mcr-3/7 in Aeromonas From U.S. Animal-Derived Samples. Frontiers in Microbiology, 2021, 12, 667406. | 1.5 | 12 |
| 2163 | Complete chloroplast genome of Myracrodruon urundeuva and its phylogenetics relationships in Anacardiaceae family. Physiology and Molecular Biology of Plants, 2021, 27, 801-814. | 1.4 | 7 |
| 2164 | Microbiome assembly for sulfonamide subsistence and the transfer of genetic determinants. ISME Journal, 2021, 15, 2817-2829. | 4.4 | 10 |
| 2165 | Genomic-Led Discovery of a Novel Glycopeptide Antibiotic by <i>Nonomuraea coxensis</i> DSM 45129. ACS Chemical Biology, 2021, 16, 915-928. | 1.6 | 16 |
| 2167 | Trends in Molecular Diagnosis and Diversity Studies for Phytosanitary Regulated Xanthomonas. Microorganisms, 2021, 9, 862. | 1.6 | 22 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2168 | Complete Chloroplast Genome of Clethra fargesii Franch., an Original Sympetalous Plant from Central China: Comparative Analysis, Adaptive Evolution, and Phylogenetic Relationships. Forests, 2021, 12, 441. | 0.9 | 22 |
| 2169 | Divergence times and plastid phylogenomics within the intronâ€rich order Erythropeltales (Compsopogonophyceae, Rhodophyta). Journal of Phycology, 2021, 57, 1035-1044. | 1.0 | 3 |
| 2171 | SSG-LUGIA: Single Sequence based Genome Level Unsupervised Genomic Island Prediction Algorithm. Briefings in Bioinformatics, 2021, 22, . | 3.2 | 3 |
| 2172 | Complete Genome Sequence of Chlamydia abortus MRI-10/19, Isolated from a Sheep Vaccinated with the Commercial Live <i>C. abortus</i> 1B Vaccine Strain. Microbiology Resource Announcements, 2021, 10, . | 0.3 | 2 |
| 2173 | Closed Genome Sequence of a Salmonella enterica Serotype Senftenberg Strain Carrying the <i>mcr-9</i> Gene Isolated from Broken Chicken Eggshells in Trinidad and Tobago. Microbiology Resource Announcements, 2021, 10, e0146520. | 0.3 | 7 |
| 2174 | Re-examination of two diatom reference genomes using long-read sequencing. BMC Genomics, 2021, 22, 379. | 1.2 | 22 |
| 2175 | Extensive Comparative Genomic Analysis of Enterococcus faecalis and Enterococcus faecium Reveals a Direct Association between the Absence of CRISPRâ€“Cas Systems, the Presence of Anti-Endonuclease (ardA) and the Acquisition of Vancomycin Resistance in E. faecium. Microorganisms, 2021, 9, 1118. | 1.6 | 6 |
| 2177 | Genomeâ€informed approach to identify genetic determinants of Flavobacterium psychrophilum phage susceptibility. Environmental Microbiology, 2021, 23, 4185-4199. | 1.8 | 8 |
| 2178 | Adaptive laboratory evolution accelerated glutarate production by Corynebacterium glutamicum. Microbial Cell Factories, 2021, 20, 97. | 1.9 | 19 |
| 2179 | The pESI mega-plasmid conferring virulence and multiple-drug resistance is detected in Salmonella Infantis genome from Brazil. Infection, Genetics and Evolution, 2021, 95, 104934. | 1.0 | 10 |
| 2180 | Whole-Genome Analysis of Mycobacterium avium subsp. paratuberculosis IS900Insertions Reveals Strain Type-Specific Modalities. Frontiers in Microbiology, 2021, 12, 660002. | 1.5 | 7 |
| 2181 | Comparative Analysis of Mitochondrial Genome Features among Four Clonostachys Species and Insight into Their Systematic Positions in the Order Hypocreales. International Journal of Molecular Sciences, 2021, 22, 5530. | 1.8 | 7 |
| 2183 | Novel chromosomal insertions of ISEcp1-blaCTX-M-15 and diverse antimicrobial resistance genes in Zambian clinical isolates of Enterobacter cloacae and Escherichia coli. Antimicrobial Resistance and Infection Control, 2021, 10, 79. | 1.5 | 24 |
| 2184 | A chromosome-level genome of a Kordofan melon illuminates the origin of domesticated watermelons. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 3.3 | 37 |
| 2185 | Phylogenomics and biogeography of <i>Wisteria</i>: Implications on plastome evolution among inverted repeatâ€lacking clade (IRLC) legumes. Journal of Systematics and Evolution, 2022, 60, 253-265. | 1.6 | 10 |
| 2186 | Characterization of the Complete Mitochondrial Genome of Basidiomycete Yeast Hannaella oryzae: Intron Evolution, Gene Rearrangement, and Its Phylogeny. Frontiers in Microbiology, 2021, 12, 646567. | 1.5 | 25 |
| 2187 | Identification of Three Type II Toxin-Antitoxin Systems in Model Bacterial Plant Pathogen Dickeya dadantii 3937. International Journal of Molecular Sciences, 2021, 22, 5932. | 1.8 | 4 |
| 2188 | Genomic Island Prediction via Chi-Square Test and Random Forest Algorithm. Computational and Mathematical Methods in Medicine, 2021, 2021, 1-9. | 0.7 | 32 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2189 | Complete genome sequence of the newly discovered temperate Clostridioides difficile bacteriophage phiCDKH01 of the family Siphoviridae. Archives of Virology, 2021, 166, 2305-2310. | 0.9 | 8 |
| 2190 | Comparative plastome analysis of <i>Blumea</i>, with implications for genome evolution and phylogeny of Asteroideae. Ecology and Evolution, 2021, 11, 7810-7826. | 0.8 | 29 |
| 2191 | Genomic sequencing of a frog virus 3 strain from cultured American bullfrogs (Lithobates) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 Td | 0.9 | 4 |
| 2193 | Relationship of the Pine Growth Promoting Pantoea eucalypti FBS135 with Type Strains P. eucalypti LMG 24197T and P. vagans 24199T. Life, 2021, 11, 608. | 1.1 | 3 |
| 2194 | Chitosan flocculation associated with biofilms of C. saccharolyticus and C. owensensis enhances biomass retention in a CSTR. International Journal of Hydrogen Energy, 2021, 46, 21338-21347. | 3.8 | 2 |
| 2195 | The global emergence of a novel <i>Streptococcus suis</i> clade associated with human infections. EMBO Molecular Medicine, 2021, 13, e13810. | 3.3 | 33 |
| 2196 | How Bacteria Change after Exposure to Silver Nanoformulations: Analysis of the Genome and Outer Membrane Proteome. Pathogens, 2021, 10, 817. | 1.2 | 1 |
| 2197 | Genomic Analysis of Prophages Recovered from Listeria monocytogenes Lysogens Found in Seafood and Seafood-Related Environment. Microorganisms, 2021, 9, 1354. | 1.6 | 5 |
| 2198 | Whole genome data from Curtobacterium flaccumfaciens pv. flaccumfaciens strains associated with tan spot of mungbean and soybean reveal diverse plasmid profiles. Molecular Plant-Microbe Interactions, 2021, 34, 1216-1222. | 1.4 | 7 |
| 2199 | Comparative Genomics of Closely Related Tetragenococcus halophilus Strains Elucidate the Diversity and Microevolution of CRISPR Elements. Frontiers in Microbiology, 2021, 12, 687985. | 1.5 | 5 |
| 2200 | Molecular characterization of antimicrobial resistance in Klebsiella pneumoniae isolated from Brazilian dairy herds. Journal of Dairy Science, 2021, 104, 7210-7224. | 1.4 | 8 |
| 2201 | The proximity of Hydrocotyle umbellata L. with araliaceae as evident from plastome and phylotranscriptomic analyses. Journal of King Saud University - Science, 2021, 33, 101412. | 1.6 | 0 |
| 2202 | Horizontal Gene Transfer of Genes Encoding Copper-Containing Membrane-Bound Monooxygenase (CuMMO) and Soluble Di-iron Monooxygenase (SDIMO) in Ethane- and Propane-Oxidizing <i>Rhodococcus</i> Bacteria. Applied and Environmental Microbiology, 2021, 87, e0022721. | 1.4 | 5 |
| 2203 | Functional and genomic characterization of Komagataeibacter uvaceti FXV3, a multiple stress resistant bacterium producing increased levels of cellulose. Biotechnology Reports (Amsterdam,) Tj ETQq1 1 0.784314 rgBT /Overlock 1 | 2.1 | 10 |
| 2204 | Phylogenomic Analyses of Hepatica Species and Comparative Analyses Within Tribe Anemoneae (Ranunculaceae). Frontiers in Plant Science, 2021, 12, 638580. | 1.7 | 2 |
| 2205 | Investigation of Plasmids Among Clinical Staphylococcus aureus and Staphylococcus haemolyticus Isolates From Egypt. Frontiers in Microbiology, 2021, 12, 659116. | 1.5 | 11 |
| 2206 | Variability of the response of human vaginal Lactobacillus crispatus to 17Î²-estradiol. Scientific Reports, 2021, 11, 11533. | 1.6 | 5 |
| 2207 | Genome Scale Analysis Reveals IscR Directly and Indirectly Regulates Virulence Factor Genes in Pathogenic Yersinia. MBio, 2021, 12, e0063321. | 1.8 | 4 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2208 | Mitogenomics and Evolutionary History of Rodent Whipworms (Trichuris spp.) Originating from Three Biogeographic Regions. Life, 2021, 11, 540. | 1.1 | 2 |
| 2209 | Genomic Rearrangements and Sequence Evolution across Brown Algal Organelles. Genome Biology and Evolution, 2021, 13, . | 1.1 | 12 |
| 2210 | Evolution of Interbacterial Antagonism in Bee Gut Microbiota Reflects Host and Symbiont Diversification. MSystems, 2021, 6, . | 1.7 | 13 |
| 2211 | Molecular Clocks and Archeogenomics of a Late Period Egyptian Date Palm Leaf Reveal Introgression from Wild Relatives and Add Timestamps on the Domestication. Molecular Biology and Evolution, 2021, 38, 4475-4492. | 3.5 | 14 |
| 2212 | Genomic and Phenotypic Characterization of Chloracidobacterium Isolates Provides Evidence for Multiple Species. Frontiers in Microbiology, 2021, 12, 704168. | 1.5 | 3 |
| 2213 | High-Quality Genome Reconstruction of Candida albicans CHN1 Using Nanopore and Illumina Sequencing and Hybrid Assembly. Microbiology Resource Announcements, 2021, 10, e0029921. | 0.3 | 3 |
| 2214 | Comparative Chloroplast Genomics of Litsea Lam. (Lauraceae) and Its Phylogenetic Implications. Forests, 2021, 12, 744. | 0.9 | 13 |
| 2216 | Phenotypic and genomic hallmarks of a novel, potentially pathogenic rapidly growing Mycobacterium species related to the Mycobacterium fortuitum complex. Scientific Reports, 2021, 11, 13011. | 1.6 | 6 |
| 2217 | Staphylococcus saprophyticus From Clinical and Environmental Origins Have Distinct Biofilm Composition. Frontiers in Microbiology, 2021, 12, 663768. | 1.5 | 12 |
| 2219 | Genome Analysis of a Verrucomicrobial Endosymbiont With a Tiny Genome Discovered in an Antarctic Lake. Frontiers in Microbiology, 2021, 12, 674758. | 1.5 | 18 |
| 2220 | Molecular Evolution and Adaptation of Livestock-Associated Methicillin-Resistant Staphylococcus aureus (LA-MRSA) Sequence Type 9. MSystems, 2021, 6, e0049221. | 1.7 | 36 |
| 2222 | The Virulence of S. marcescens Strains Isolated From Contaminated Blood Products Is Divergent in the C. elegans Infection Model. Frontiers in Genetics, 2021, 12, 667062. | 1.1 | 1 |
| 2223 | Detection of CTX-M-27 Î²-Lactamase Genes on Two Distinct Plasmid Types in ST38 Escherichia coli from Three U.S. States. Antimicrobial Agents and Chemotherapy, 2021, 65, e0082521. | 1.4 | 11 |
| 2224 | Forward genetics in Wolbachia: Regulation of Wolbachia proliferation by the amplification and deletion of an addictive genomic island. PLoS Genetics, 2021, 17, e1009612. | 1.5 | 24 |
| 2225 | Grand Challenges in Bioinformatics Data Visualization. Frontiers in Bioinformatics, 2021, 1, . | 1.0 | 18 |
| 2226 | Stable high-density and maternally inherited Wolbachia infections in Anopheles moucheti and Anopheles demeilloni mosquitoes. Current Biology, 2021, 31, 2310-2320.e5. | 1.8 | 49 |
| 2227 | Full-Genome Sequences of Alphacoronaviruses and Astroviruses from Myotis and Pipistrelle Bats in Denmark. Viruses, 2021, 13, 1073. | 1.5 | 15 |
| 2228 | Genome reduction and relaxed selection is associated with the transition to symbiosis in the basidiomycete genus Podaxis. IScience, 2021, 24, 102680. | 1.9 | 9 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2230 | Rubrolone production by Dactylosporangium vinaceum: biosynthesis, modulation and possible biological function. Applied Microbiology and Biotechnology, 2021, 105, 5541-5551. | 1.7 | 5 |
| 2231 | A Novel Polyvalent Bacteriophage vB_EcoM_swi3 Infects Pathogenic Escherichia coli and Salmonella enteritidis. Frontiers in Microbiology, 2021, 12, 649673. | 1.5 | 14 |
| 2233 | Comparative and phylogenetic analyses of the chloroplast genomes of species of Paeoniaceae. Scientific Reports, 2021, 11, 14643. | 1.6 | 19 |
| 2234 | A chimeric nuclease substitutes a phage CRISPR-Cas system to provide sequence-specific immunity against subviral parasites. ELife, 2021, 10, . | 2.8 | 31 |
| 2235 | Pangenomic Analysis of Dickeya dianthicola Strains Related to the Outbreak of Blackleg and Soft Rot of Potato in USA. Plant Disease, 2021, , PDIS03210587RE. | 0.7 | 5 |
| 2236 | Chloroplast Genome Sequencing, Comparative Analysis, and Discovery of Unique Cytoplasmic Variants in Pomegranate (Punica granatum L.). Frontiers in Genetics, 2021, 12, 704075. | 1.1 | 10 |
| 2237 | C-protein Î±-antigen modulates the lantibiotic thusin resistance in Streptococcus agalactiae. Antonie Van Leeuwenhoek, 2021, 114, 1595-1607. | 0.7 | 1 |
| 2239 | Mycobacterium tuberculosis complex lineage 5 exhibits high levels of within-lineage genomic diversity and differing gene content compared to the type strain H37Rv. Microbial Genomics, 2021, 7, . | 1.0 | 9 |
| 2240 | The Conservation of Chloroplast Genome Structure and Improved Resolution of Infrafamilial Relationships of Crassulaceae. Frontiers in Plant Science, 2021, 12, 631884. | 1.7 | 16 |
| 2241 | Experimental and Genomic Evaluation of the Oestrogen Degrading Bacterium Rhodococcus equi ATCC13557. Frontiers in Microbiology, 2021, 12, 670928. | 1.5 | 2 |
| 2243 | Structures of the alkanesulfonate monooxygenase MsuD provide insight into Câ€"S bond cleavage, substrate scope, and an unexpected role for the tetramer. Journal of Biological Chemistry, 2021, 297, 100823. | 1.6 | 5 |
| 2244 | A two-component monooxygenase for continuous denitration and dechlorination of chlorinated 4-nitrophenol in Ensifer sp. strain 22-1. Environmental Research, 2021, 198, 111216. | 3.7 | 9 |
| 2246 | Evolutionary Insights Into Two Widespread Ectomycorrhizal Fungi (Pisolithus) From Comparative Analysis of Mitochondrial Genomes. Frontiers in Microbiology, 2021, 12, 583129. | 1.5 | 2 |
| 2247 | Global biogeography of chemosynthetic symbionts reveals both localized and globally distributed symbiont groups. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 3.3 | 15 |
| 2249 | Current status of structural variation studies in plants. Plant Biotechnology Journal, 2021, 19, 2153-2163. | 4.1 | 65 |
| 2250 | Clostridium culturomicium sp. nov. and Clostridium jeddahitimonense sp. nov., novel members of the Clostridium genus isolated from the stool of an obese Saudi Arabian. Current Microbiology, 2021, 78, 3586-3595. | 1.0 | 3 |
| 2251 | The <i>Pseudoalteromonas</i> multipartite genome: distribution and expression of pangene categories, and a hypothesis for the origin and evolution of the chromid. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 6 |
| 2252 | Complete Genome Sequence of vB_EcoP_SU7, a Podoviridae Coliphage with the Rare C3 Morphotype. Microorganisms, 2021, 9, 1576. | 1.6 | 6 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2253 | Comparative chloroplast genome analysis of Impatiens species (Balsaminaceae) in the karst area of China: insights into genome evolution and phylogenomic implications. BMC Genomics, 2021, 22, 571. | 1.2 | 27 |
| 2254 | The Emergence and Molecular Characteristics of New Delhi Metallo Î²-Lactamase-Producing Escherichia coli From Ducks in Guangdong, China. Frontiers in Microbiology, 2021, 12, 677633. | 1.5 | 7 |
| 2255 | Draft Genome Sequence of Enterococcus mundtii SCPM-O-B-8398 (E28), Isolated from Fermented Milk in the Moscow Region, Russian Federation. Microbiology Resource Announcements, 2021, 10, e0027721. | 0.3 | 0 |
| 2256 | Repeated exposure of nosocomial pathogens to silver does not select for silver resistance but does impact ciprofloxacin susceptibility. Acta Biomaterialia, 2021, 134, 760-773. | 4.1 | 1 |
| 2257 | Rapid strain-specific identification of two Lactobacillus rhamnosus strains using PCR based on gene family analysis. LWT - Food Science and Technology, 2021, 146, 111395. | 2.5 | 10 |
| 2258 | Novel genomic islands and a new vanD-subtype in the first sporadic VanD-type vancomycin resistant enterococci in Norway. PLoS ONE, 2021, 16, e0255187. | 1.1 | 6 |
| 2259 | Genome Characterization, Comparison and Phylogenetic Analysis of Complete Mitochondrial Genome of Evolvulus alsinoides Reveals Highly Rearranged Gene Order in Solanales. Life, 2021, 11, 769. | 1.1 | 10 |
| 2260 | Complete Genome Sequence of Pseudomonas amygdali pv. tabaci Strain 6605, a Causal Agent of Tobacco Wildfire Disease. Microbiology Resource Announcements, 2021, 10, e0040521. | 0.3 | 2 |
| 2261 | Plastid phylogenomics and biogeography of the genus <i>Monochoria</i> (Pontederiaceae). Journal of Systematics and Evolution, 2021, 59, 1027-1039. | 1.6 | 6 |
| 2262 | The first complete genome sequence of species Shewanella decolorationis, from a bioremediation competent strain Ni1-3. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 2 |
| 2263 | The mitochondrial genome of <i>Ophiostoma himal-ulmi</i> and comparison with other fungi causing Dutch elm disease. Canadian Journal of Microbiology, 2021, 67, 584-598. | 0.8 | 5 |
| 2264 | Plastid genomes and phylogenomics of liverworts (Marchantiophyta): Conserved genome structure but highest relative plastid substitution rate in land plants. Molecular Phylogenetics and Evolution, 2021, 161, 107171. | 1.2 | 12 |
| 2265 | The Sisal Virome: Uncovering the Viral Diversity of Agave Varieties Reveals New and Organ-Specific Viruses. Microorganisms, 2021, 9, 1704. | 1.6 | 5 |
| 2266 | Genomic-Assisted Marker Development Suitable for CsCvy-1 Selection in Cucumber Breeding. Frontiers in Plant Science, 2021, 12, 691576. | 1.7 | 4 |
| 2267 | The plastome sequence of Bactris gasipaes and evolutionary analysis in tribe Cocoseae (Arecaceae). PLoS ONE, 2021, 16, e0256373. | 1.1 | 7 |
| 2268 | Genome-Wide Analysis of Four Pathotypes of Wheat Rust Pathogen (Puccinia graminis) Reveals Structural Variations and Diversifying Selection. Journal of Fungi (Basel, Switzerland), 2021, 7, 701. | 1.5 | 2 |
| 2269 | A widely diverged locus involved in locomotor adaptation in <i>Heliconius</i> butterflies. Science Advances, 2021, 7, . | 4.7 | 9 |
| 2270 | Comparative Genome Analysis Provides Molecular Evidence for Reclassification of the Photosynthetic Bacterium Rhodobacter sphaeroides EBL0706 as a Strain of Luteovulum azotoformans. Microorganisms, 2021, 9, 1754. | 1.6 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2271 | The Insights into Mitochondrial Genomes of Sunflowers. Plants, 2021, 10, 1774. | 1.6 | 7 |
| 2272 | Plastome Evolution in the Hyperdiverse Genus Euphorbia (Euphorbiaceae) Using Phylogenomic and Comparative Analyses: Large-Scale Expansion and Contraction of the Inverted Repeat Region. Frontiers in Plant Science, 2021, 12, 712064. | 1.7 | 16 |
| 2273 | The complete chloroplast genome of <i>Rhodobryum laxelimbatum</i> (Hampe ex Ochi) Z. Iwatsuki and T. J. Koponen. Mitochondrial DNA Part B: Resources, 2021, 6, 2632-2634. | 0.2 | 0 |
| 2274 | Genomic Characterization of Multidrug-Resistant Salmonella Serovars Derby and Rissen From the Pig Value Chain in Vietnam. Frontiers in Veterinary Science, 2021, 8, 705044. | 0.9 | 7 |
| 2275 | Comparative analysis of plastomes in Oxalidaceae: Phylogenetic relationships and potential molecular markers. Plant Diversity, 2021, 43, 281-291. | 1.8 | 12 |
| 2276 | Genome-Resolved Metagenomic Analyses Reveal the Presence of a Putative Bacterial Endosymbiont in an Avian Nasal Mite (Rhinonyssidae; Mesostigmata). Microorganisms, 2021, 9, 1734. | 1.6 | 1 |
| 2277 | Identification of a Family of <i>Vibrio</i> Type III Secretion System Effectors That Contain a Conserved Serine/Threonine Kinase Domain. MSphere, 2021, 6, e0059921. | 1.3 | 6 |
| 2278 | Comparative Genomic Analyses of Flavobacterium psychrophilum Isolates Reveals New Putative Genetic Determinants of Virulence Traits. Microorganisms, 2021, 9, 1658. | 1.6 | 5 |
| 2279 | Virulent Drexlervirial Bacteriophage MSK, Morphological and Genome Resemblance With Rtp Bacteriophage Inhibits the Multidrug-Resistant Bacteria. Frontiers in Microbiology, 2021, 12, 706700. | 1.5 | 5 |
| 2280 | The chloroplast genome of Prunus zhengheensis: Genome comparative and phylogenetic relationships analysis. Gene, 2021, 793, 145751. | 1.0 | 6 |
| 2281 | Pathogenicity and genomic features of vapN-harboring Rhodococcus equi isolated from human patients. International Journal of Medical Microbiology, 2021, 311, 151519. | 1.5 | 15 |
| 2282 | Comparative Chloroplast Genomics in Phyllanthaceae Species. Diversity, 2021, 13, 403. | 0.7 | 6 |
| 2283 | Comparison between genome sequences of Chilean <i>Tenacibaculum dicentrarchi</i> isolated from red conger eel (<i>Genypterus chilensis</i>) and Atlantic salmon (<i>Salmo salar</i>) focusing on bacterial virulence determinants. Journal of Fish Diseases, 2021, 44, 1843-1860. | 0.9 | 11 |
| 2284 | Reduction trend of mcr-1 circulation in Emilia-Romagna Region, Italy. European Journal of Clinical Microbiology and Infectious Diseases, 2021, 40, 2585-2592. | 1.3 | 7 |
| 2285 | Genome analyses of four Wolbachia strains and associated mitochondria of Rhagoletis cerasi expose cumulative modularity of cytoplasmic incompatibility factors and cytoplasmic hitchhiking across host populations. BMC Genomics, 2021, 22, 616. | 1.2 | 4 |
| 2286 | Characterization and Dynamics of Intracellular Gene Transfer in Plastid Genomes of Viola (Violaceae) and Order Malpighiales. Frontiers in Plant Science, 2021, 12, 678580. | 1.7 | 5 |
| 2287 | Plastid phylogenomics of Pleurothallidinae (Orchidaceae): Conservative plastomes, new variable markers, and comparative analyses of plastid, nuclear, and mitochondrial data. PLoS ONE, 2021, 16, e0256126. | 1.1 | 1 |
| 2289 | Multiple-Drug Resistant Nasopharyngeal <i>Streptococcus pneumoniae</i> Isolated in Russia: Serotypes, Antimicrobial Susceptibility, and Molecular Characterization of the Emergent Serotype 13/ST2754 Lineage. Microbial Drug Resistance, 2022, 28, 39-47. | 0.9 | 4 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2290 | Carboxylicivirga marinus sp. nov., Isolated From Marine Sediment, and Genome Insight of the Genus Carboxylicivirga. Frontiers in Marine Science, 2021, 8, . | 1.2 | 9 |
| 2291 | Isolation, characterization and comparison of lytic Epseptimavirus phages targeting Salmonella. Food Research International, 2021, 147, 110480. | 2.9 | 12 |
| 2293 | Genetic Variation in Host-Specific Competitiveness of the Symbiont Rhizobium leguminosarum Symbiovar viciae. Frontiers in Plant Science, 2021, 12, 719987. | 1.7 | 4 |
| 2294 | Wholeâ€genome sequencing reveals forgotten lineages and recurrent hybridizations within the kelp genus <i>Alaria</i> (Phaeophyceae). Journal of Phycology, 2021, 57, 1721-1738. | 1.0 | 10 |
| 2295 | The complete genome of 2,6-dichlorobenzamide (BAM) degrader Aminobacter sp. MSH1 suggests a polyploid chromosome, phylogenetic reassignment, and functions of plasmids. Scientific Reports, 2021, 11, 18943. | 1.6 | 5 |
| 2296 | Molecular Confirmation of Ranavirus Infection in Amphibians From Chad, Africa. Frontiers in Veterinary Science, 2021, 8, 733939. | 0.9 | 2 |
| 2297 | Lineage-Specific Variation in IR Boundary Shift Events, Inversions, and Substitution Rates among Caprifoliaceae s.l. (Dipsacales) Plastomes. International Journal of Molecular Sciences, 2021, 22, 10485. | 1.8 | 4 |
| 2298 | Whole-genome sequence data of the proteolytic and bacteriocin producing strain Enterococcus faecalis PK23 isolated from the traditional Halitzia cheese produced in Cyprus. Data in Brief, 2021, 38, 107437. | 0.5 | 4 |
| 2299 | Genomic Analysis of the 1-Aminocyclopropane-1-Carboxylate Deaminase-Producing Pseudomonas thivervalensis SC5 Reveals Its Multifaceted Roles in Soil and in Beneficial Interactions With Plants. Frontiers in Microbiology, 2021, 12, 752288. | 1.5 | 12 |
| 2300 | Antimicrobial plant secondary metabolites, MDR transporters and antimicrobial resistance in cereal-associated lactobacilli: is there a connection?. Food Microbiology, 2022, 102, 103917. | 2.1 | 12 |
| 2301 | Draft Genome Sequence of <i>Salegentibacter</i> sp. Strain BDJ18, a Plankton-Associated Bacterium in the Northeast Atlantic Ocean. Microbiology Resource Announcements, 2021, 10, e0062821. | 0.3 | 0 |
| 2302 | Genomic analysis revealed conserved acid tolerance mechanisms from native microâ€organisms in fermented feed. Journal of Applied Microbiology, 2022, 132, 1152-1165. | 1.4 | 2 |
| 2303 | Phylogenomics, CAZyome and core secondary metabolome of Streptomyces albus species. Molecular Genetics and Genomics, 2021, 296, 1299-1311. | 1.0 | 5 |
| 2304 | Genomic Stability and Genetic Defense Systems in<i>Dolosigranulum pigrum</i>, a Candidate Beneficial Bacterium from the Human Microbiome. MSystems, 2021, 6, e0042521. | 1.7 | 11 |
| 2305 | Complete Genome Sequencing of Leptospira interrogans Isolates from Malaysia Reveals Massive Genome Rearrangement but High Conservation of Virulence-Associated Genes. Pathogens, 2021, 10, 1198. | 1.2 | 4 |
| 2306 | Genomic characterization of Enterobacter xiangfangensis STP-3: Application to real time petroleum oil sludge bioremediation. Microbiological Research, 2021, 253, 126882. | 2.5 | 8 |
| 2307 | Engineering of a robust Escherichia coli chassis and exploitation for large-scale production processes. Metabolic Engineering, 2021, 67, 75-87. | 3.6 | 15 |
| 2308 | The chloroplast genome of Amygdalus L. (Rosaceae) reveals the phylogenetic relationship and divergence time. BMC Genomics, 2021, 22, 645. | 1.2 | 14 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2309 | A Unifying Framework for Analysis of Spatial-Temporal Event Sequence Similarity and Its Applications. ISPRS International Journal of Geo-Information, 2021, 10, 594. | 1.4 | 1 |
| 2310 | Complete Genome Sequence of Weissella confusa LM1 and Comparative Genomic Analysis. Frontiers in Microbiology, 2021, 12, 749218. | 1.5 | 6 |
| 2311 | Genome sequencing of the neotype strain CBS 554.65 reveals the MAT1â€"2 locus of Aspergillus niger. BMC Genomics, 2021, 22, 679. | 1.2 | 5 |
| 2312 | Morphological and Genomic Features of the New Klosneuvirinae Isolate Fadolivirus IHUMI-VV54. Frontiers in Microbiology, 2021, 12, 719703. | 1.5 | 9 |
| 2313 | Comprehensive genomic analysis of Bacillus velezensis AL7 reveals its biocontrol potential against Verticillium wilt of cotton. Molecular Genetics and Genomics, 2021, 296, 1287-1298. | 1.0 | 13 |
| 2315 | Complete Plastome of Three Korean Asarum (Aristolochiaceae): Confirmation Tripartite Structure within Korean Asarum and Comparative Analyses. Plants, 2021, 10, 2056. | 1.6 | 2 |
| 2317 | Escherichia coli Nissle 1917 secondary metabolism: aryl polyene biosynthesis and phosphopantetheinyl transferase crosstalk. Applied Microbiology and Biotechnology, 2021, 105, 7785-7799. | 1.7 | 3 |
| 2318 | Genetic Characterization of <i>Clostridium botulinum</i> Isolated from the First Case of Infant Botulism in Korea. Annals of Laboratory Medicine, 2021, 41, 489-492. | 1.2 | 2 |
| 2319 | Description of Stenotrophomonas sepilia sp. nov., isolated from blood culture of a hospitalized patient as a new member of Stenotrophomonas maltophilia complex. New Microbes and New Infections, 2021, 43, 100920. | 0.8 | 6 |
| 2320 | Inactivation of SARS-CoV-2 by Simulated Sunlight on Contaminated Surfaces. Microbiology Spectrum, 2021, 9, e0033321. | 1.2 | 18 |
| 2321 | Genome collinearity analysis illuminates the evolution of donkey chromosome 1 and horse chromosome 5 in perissodactyls: A comparative study. BMC Genomics, 2021, 22, 665. | 1.2 | 3 |
| 2322 | Comparative Genomic Understanding of Gram-Positive Plant Growth-Promoting <i>Leifsonia</i>. Phytobiomes Journal, 2021, 5, 263-274. | 1.4 | 2 |
| 2323 | The complete chloroplast genome and characteristics analysis of Musa basjoo Siebold. Molecular Biology Reports, 2021, 48, 7113-7125. | 1.0 | 3 |
| 2324 | Whole genome sequencing of Enterobacter mori, an emerging pathogen of kiwifruit and the potential genetic adaptation to pathogenic lifestyle. AMB Express, 2021, 11, 129. | 1.4 | 4 |
| 2325 | Comparative genetic analyses provide clues about capsule switching in Streptococcus suis 2 strains with different virulence levels and genetic backgrounds. Microbiological Research, 2021, 250, 126814. | 2.5 | 8 |
| 2326 | Global Expansion of Linezolid-Resistant Coagulase-Negative Staphylococci. Frontiers in Microbiology, 2021, 12, 661798. | 1.5 | 14 |
| 2327 | The Characterization of a Novel Phage, pPa_SNUABM_DT01, Infecting Pseudomonas aeruginosa. Microorganisms, 2021, 9, 2040. | 1.6 | 7 |
| 2328 | Aspergillus fumigatus versus Genus Aspergillus: Conservation, Adaptive Evolution and Specific Virulence Genes. Microorganisms, 2021, 9, 2014. | 1.6 | 4 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2329 | Plastomes from tribe Plantagineae (Plantaginaceae) reveal infrageneric structural synapormorphies and localized hypermutation for Plantago and functional loss of ndh genes from Littorella. Molecular Phylogenetics and Evolution, 2021, 162, 107217. | 1.2 | 23 |
| 2330 | Genomic and Phenotypic Analysis of Heat and Sanitizer Resistance in Escherichia coli from Beef in Relation to the Locus of Heat Resistance. Applied and Environmental Microbiology, 2021, 87, e0157421. | 1.4 | 8 |
| 2331 | Limosilactobacillus caccae sp. nov., a new bacterial species isolated from the human gut microbiota. FEMS Microbiology Letters, 2021, 368, . | 0.7 | 1 |
| 2332 | Bacterial Long-Range Warfare: Aerial Killing of Legionella pneumophila by Pseudomonas fluorescens. Microbiology Spectrum, 2021, 9, e0040421. | 1.2 | 6 |
| 2333 | Genetic Analysis of mcr-1-Carrying Plasmids From Gram-Negative Bacteria in a Dutch Tertiary Care Hospital: Evidence for Intrapatient and Interspecies Transmission Events. Frontiers in Microbiology, 2021, 12, 727435. | 1.5 | 7 |
| 2334 | Mitochondrial genes are involved in the fertility transformation of the thermosensitive male-sterile line YS3038 in wheat. Molecular Breeding, 2021, 41, 1. | 1.0 | 3 |
| 2335 | Whole-Genome Assessment of Clinical Acinetobacter baumannii Isolates Uncovers Potentially Novel Factors Influencing Carbapenem Resistance. Frontiers in Microbiology, 2021, 12, 714284. | 1.5 | 3 |
| 2336 | Potentiating effects of leaderless enterocin DD14 in combination with methicillin on clinical methicillin-resistant Staphylococcus aureus S1 strain. Microbiological Research, 2021, 252, 126864. | 2.5 | 12 |
| 2337 | Characterization of a Streptococcus species isolated from Siganus guttatus in South China. Aquaculture, 2021, 545, 737163. | 1.7 | 0 |
| 2338 | Metabolism analysis of 17Î±-ethynylestradiol by Pseudomonas citronellolis SJTE-3 and identification of the functional genes. Journal of Hazardous Materials, 2022, 423, 127045. | 6.5 | 8 |
| 2339 | Biofilm formation by Non-O157 Shiga toxin-producing Escherichia coli in monocultures and co-cultures with meat processing surface bacteria. Food Microbiology, 2022, 102, 103902. | 2.1 | 10 |
| 2340 | Mitochondrial genome of Bulinus truncatus (Gastropoda: Lymnaeoidea): Implications for snail systematics and schistosome epidemiology. Current Research in Parasitology and Vector-borne Diseases, 2021, 1, 100017. | 0.7 | 6 |
| 2341 | Phylogenomics of the <i>Maverick</i> Virus-Like Mobile Genetic Elements of Vertebrates. Molecular Biology and Evolution, 2021, 38, 1731-1743. | 3.5 | 22 |
| 2342 | Factors enforcing the species boundary between the human pathogens Cryptococcus neoformans and Cryptococcus deneoformans. PLoS Genetics, 2021, 17, e1008871. | 1.5 | 13 |
| 2343 | Genome-Based Analyses of Fitness Effects and Compensatory Changes Associated with Acquisition of blaCMY-, blaCTX-M-, and blaOXA-48/VIM-1-Containing Plasmids in Escherichia coli. Antibiotics, 2021, 10, 90. | 1.5 | 9 |
| 2344 | A Bioinformatic Pipeline for Improved Genome Analysis and Clustering of Isolates during Outbreaks of Legionnaires' Disease. Journal of Clinical Microbiology, 2021, 59, . | 1.8 | 3 |
| 2345 | Core and Accessory Genome Analysis of Vibrio mimicus. Microorganisms, 2021, 9, 191. | 1.6 | 6 |
| 2346 | Precision long-read metagenomics sequencing for food safety by detection and assembly of Shiga toxin-producing Escherichia coli in irrigation water. PLoS ONE, 2021, 16, e0245172. | 1.1 | 28 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2348 | A New Asset for Pathogen Informatics â€“ the Enteropathogen Resource Integration Center (ERIC), an NIAID Bioinformatics Resource Center for Biodefense and Emerging/Re-emerging Infectious Disease. Advances in Experimental Medicine and Biology, 2007, 603, 28-42. | 0.8 | 9 |
| 2349 | Sequence Comparison Without Alignment: The SpaM Approaches. Methods in Molecular Biology, 2021, 2231, 121-134. | 0.4 | 10 |
| 2350 | Informatics for Infectious Disease Research and Control. , 2010, , 1-26. | | 1 |
| 2351 | Large-Scale Multiple Sequence Alignment and Phylogeny Estimation. Computational Biology, 2013, , 85-146. | 0.1 | 14 |
| 2352 | Comparative Analyses of Extrachromosomal Bacterial Replicons, Identification of Chromids, and Experimental Evaluation of Their Indispensability. Methods in Molecular Biology, 2015, 1231, 15-29. | 0.4 | 7 |
| 2353 | Analysis of Genome Rearrangement by Block-Interchanges. Methods in Molecular Biology, 2007, 396, 121-134. | 0.4 | 1 |
| 2354 | Genome Rearrangement by the Double Cut and Join Operation. Methods in Molecular Biology, 2008, 452, 385-416. | 0.4 | 13 |
| 2355 | In Sffamily Identification of Genes in Bacteriophage DNA. Methods in Molecular Biology, 2009, 502, 57-89. | 0.4 | 25 |
| 2356 | Bioinformatics for Analysis of Poxvirus Genomes. Methods in Molecular Biology, 2012, 890, 233-258. | 0.4 | 8 |
| 2357 | Heuristic Alignment Methods. Methods in Molecular Biology, 2014, 1079, 29-43. | 0.4 | 4 |
| 2358 | Horizontal Gene Transfer in Fungi. Grand Challenges in Biology and Biotechnology, 2020, , 317-332. | 2.4 | 3 |
| 2359 | The Bacterial Guide to Designing a Diversified Gene Portfolio. , 2020, , 51-87. | | 15 |
| 2360 | Sibelia: A Scalable and Comprehensive Synteny Block Generation Tool for Closely Related Microbial Genomes. Lecture Notes in Computer Science, 2013, , 215-229. | 1.0 | 74 |
| 2361 | The characteristics and genome analysis of vB_ApiP_XC38, a novel phage infecting Acinetobacter pittii. Virus Genes, 2020, 56, 498-507. | 0.7 | 7 |
| 2362 | Metal resistant bacteria on gold particles: Implications of how anthropogenic contaminants could affect natural gold biogeochemical cycling. Science of the Total Environment, 2020, 727, 138698. | 3.9 | 9 |
| 2363 | Identification, characterization, and phylogenetic analysis of eight new inducible prophages in Lactobacillus. Virus Research, 2020, 286, 198003. | 1.1 | 11 |
| 2364 | Verrucomicrobia use hundreds of enzymes to digest the algal polysaccharide fucoidan. Nature Microbiology, 2020, 5, 1026-1039. | 5.9 | 182 |
| 2365 | Detection of mcr-1-Carrying Escherichia coli Causing Bloodstream Infection in a New York City Hospital: Avian Origins, Human Concerns?. Open Forum Infectious Diseases, 2017, 4, ofx115. | 0.4 | 20 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2366 | Characterization of the Ï†CTX-like Pseudomonas aeruginosa phage Dobby isolated from the kidney stone microbiota. Access Microbiology, 2019, 1, . | 0.2 | 11 |
| 2367 | Isolation and characterization of Kingella negevensis sp. nov., a novel Kingella species detected in a healthy paediatric population. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2370-2376. | 0.8 | 34 |
| 2368 | Pectobacterium polaris sp. nov., isolated from potato (Solanum tuberosum). International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 5222-5229. | 0.8 | 100 |
| 2369 | Whole-genome sequence analysis of the Mycobacterium avium complex and proposal of the transfer of Mycobacterium yongonense to Mycobacterium intracellulare subsp. yongonense subsp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1998-2005. | 0.8 | 25 |
| 2370 | Marinobacter maroccanus sp. nov., a moderately halophilic bacterium isolated from a saline soil. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 227-234. | 0.8 | 12 |
| 2371 | Borrelia maritima sp. nov., a novel species of the Borrelia burgdorferi sensu lato complex, occupying a basal position to North American species. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 849-856. | 0.8 | 27 |
| 2372 | Francisella opportunistica sp. nov., isolated from human blood and cerebrospinal fluid. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1145-1151. | 0.8 | 16 |
| 2373 | Reclassification of Francisella noatunensis subsp. orientalis Ottem et al. 2009 as Francisella orientalis sp. nov., Francisella noatunensis subsp. chilensis subsp. nov. and emended description of Francisella noatunensis. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2034-2048. | 0.8 | 38 |
| 2374 | Elucidating the genetic diversity of Phthorimaea operculella granulovirus (PhopGV). Journal of General Virology, 2019, 100, 679-690. | 1.3 | 7 |
| 2375 | Genetic environment of the KPC gene in Acinetobacter baumannii ST2 clone from Puerto Rico and genomic insights into its drug resistance. Journal of Medical Microbiology, 2016, 65, 784-792. | 0.7 | 38 |
| 2376 | Defining the role of pneumococcal neuraminidases and O-glycosidase in pneumococcal haemolytic uraemic syndrome. Journal of Medical Microbiology, 2016, 65, 975-984. | 0.7 | 14 |
| 2377 | Molecular characteristics of Streptococcus agalactiae strains deficient in alpha-like protein encoding genes. Journal of Medical Microbiology, 2017, 66, 26-33. | 0.7 | 8 |
| 2378 | Manual curation and reannotation of the genomes of Clostridium difficile 630Î"erm and C. difficile 630. Journal of Medical Microbiology, 2017, 66, 286-293. | 0.7 | 117 |
| 2379 | Repeated local emergence of carbapenem-resistant Acinetobacter baumannii in a single hospital ward. Microbial Genomics, 2016, 2, e000050. | 1.0 | 65 |
| 2380 | Whole-genome sequencing of a quarter-century melioidosis outbreak in temperate Australia uncovers a region of low-prevalence endemicity. Microbial Genomics, 2016, 2, e000067. | 1.0 | 23 |
| 2381 | Phase variable DNA repeats in Neisseria gonorrhoeae influence transcription, translation, and protein sequence variation. Microbial Genomics, 2016, 2, e000078. | 1.0 | 11 |
| 2382 | Taxonogenomics reveal multiple novel genomospecies associated with clinical isolates of Stenotrophomonas maltophilia. Microbial Genomics, 2018, 4, . | 1.0 | 24 |
| 2383 | A genomic view of experimental intraspecies and interspecies transformation of a rifampicin-resistance allele into Neisseria meningitidis. Microbial Genomics, 2018, 4, . | 1.0 | 10 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2384 | The characterization of mobile colistin resistance (mcr) genes among 33â€¯000 Salmonella enterica genomes from routine public health surveillance in England. Microbial Genomics, 2020, 6, . | 1.0 | 16 |
| 2385 | Transposable elements contribute to the genome plasticity of Ralstonia solanacearum species complex. Microbial Genomics, 2020, 6, . | 1.0 | 13 |
| 2386 | Analysis of complete Campylobacter concisus genomes identifies genomospecies features, secretion systems and novel plasmids and their association with severe ulcerative colitis. Microbial Genomics, 2020, 6, . | 1.0 | 13 |
| 2387 | Epigenomics, genomics, resistome, mobilome, virulome and evolutionary phylogenomics of carbapenem-resistant Klebsiella pneumoniae clinical strains. Microbial Genomics, 2020, 6, . | 1.0 | 24 |
| 2388 | Novel genomic rearrangements mediated by multiple genetic elements in Streptococcus pyogenes M23ND confer potential for evolutionary persistence. Microbiology (United Kingdom), 2016, 162, 1346-1359. | 0.7 | 6 |
| 2389 | Evolution of bacteria seen through their essential genes: the case of Pseudomonas aeruginosa and Azotobacter vinelandii. Microbiology (United Kingdom), 2019, 165, 976-984. | 0.7 | 6 |
| 2390 | Genome sequence comparison and superinfection between two related Pseudomonas aeruginosa phages, D3112 and MP22. Microbiology (United Kingdom), 2007, 153, 2885-2895. | 0.7 | 56 |
| 2444 | Bacillus anthracis. , 0, , 165-183. |  | 1 |
| 2445 | Clostridium perfringens. , 0, , 213-221. |  | 1 |
| 2446 | Identification of Genes Required for Glucan Exopolysaccharide Production in Lactobacillus johnsonii Suggests a Novel Biosynthesis Mechanism. Applied and Environmental Microbiology, 2020, 86, . | 1.4 | 13 |
| 2447 | Draft Genome Sequence of <i>Xenophilus</i> sp., a Novel Bacterium Isolated from the Skin of a Southern Leopard Frog ( <i>Rana sphenocephala</i> ) in Florida, USA. Genome Announcements, 2017, 5, . | 0.8 | 1 |
| 2448 | Genome Sequence of â€œ <i>Candidatus</i> Nitrosocosmicus franklandusâ€•C13, a Terrestrial Ammonia-Oxidizing Archaeon. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 11 |
| 2449 | High-Quality Draft Genome Sequence and Annotation of the Basidiomycete Yeast Sporisorium graminicola CBS10092, a Producer of Mannosylerythritol Lipids. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 6 |
| 2450 | Complete Genome Sequence of Subcluster 5.2 <i>Synechococcus</i> sp. Strain CB0101, Isolated from the Chesapeake Bay. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 5 |
| 2451 | Draft Genome Sequence of Agrobacterium fabrum ARqua1. Microbiology Resource Announcements, 2020, 9, . | 0.3 | 4 |
| 2452 | Complete Genome Sequences of Four Salmonella enterica Strains Associated with Pistachios Assembled Using a Combination of Short- and Long-Read Sequencing. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 4 |
| 2453 | Complete Genome Sequences of Three Mycoplasma anserisalpingitis ( Mycoplasma sp. 1220) Strains. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 6 |
| 2454 | Phylogenomic characterization of ranaviruses isolated from cultured fish and amphibians in Thailand. Facets, 2020, 5, 963-979. | 1.1 | 5 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2455 | Comparative analyses of Legionella species identifies genetic features of strains causing LegionnairesÂ¿ disease. Genome Biology, 2014, 15, 505. | 13.9 | 62 |
| 2456 | Comparative chloroplast genomics of the genus Taxodium. BMC Genomics, 2020, 21, 114. | 1.2 | 23 |
| 2457 | Proteins involved in the biosynthesis of lipophosphoglycan in Leishmania: a comparative genomic and evolutionary analysis. Parasites and Vectors, 2020, 13, 44. | 1.0 | 9 |
| 2458 | NovoGraph: Human genome graph construction from multiple long-read de novo assemblies. F1000Research, 2018, 7, 1391. | 0.8 | 5 |
| 2459 | Chloroplast Genome Sequence Annotation of <i>Dendrobium nobile</i> (Asparagales: Orchidaceae), an Endangered Medicinal Orchid from Northeast India. PLOS Currents, 2017, 9, . | 1.4 | 2 |
| 2460 | A Methodological Framework for the Reconstruction of Contiguous Regions of Ancestral Genomes and Its Application to Mammalian Genomes. PLoS Computational Biology, 2008, 4, e1000234. | 1.5 | 108 |
| 2461 | Diversity and distribution of nuclease bacteriocins in bacterial genomes revealed using Hidden Markov Models. PLoS Computational Biology, 2017, 13, e1005652. | 1.5 | 52 |
| 2462 | MUMmer4: A fast and versatile genome alignment system. PLoS Computational Biology, 2018, 14, e1005944. | 1.5 | 1,412 |
| 2463 | Localized Plasticity in the Streamlined Genomes of Vinyl Chloride Respiring Dehalococcoides. PLoS Genetics, 2009, 5, e1000714. | 1.5 | 162 |
| 2464 | Virus Satellites Drive Viral Evolution and Ecology. PLoS Genetics, 2015, 11, e1005609. | 1.5 | 49 |
| 2465 | Genetic diversity of the Plasmodium falciparum GTP-cyclohydrolase 1, dihydrofolate reductase and dihydropteroate synthetase genes reveals new insights into sulfadoxine-pyrimethamine antimalarial drug resistance. PLoS Genetics, 2020, 16, e1009268. | 1.5 | 15 |
| 2466 | Haemophilus ducreyi Cutaneous Ulcer Strains Are Nearly Identical to Class I Genital Ulcer Strains. PLoS Neglected Tropical Diseases, 2015, 9, e0003918. | 1.3 | 26 |
| 2467 | Complete Genomic Characterization of a Pathogenic A.II Strain of Francisella tularensis Subspecies tularensis. PLoS ONE, 2007, 2, e947. | 1.1 | 46 |
| 2468 | An Anomalous Type IV Secretion System in Rickettsia Is Evolutionarily Conserved. PLoS ONE, 2009, 4, e4833. | 1.1 | 89 |
| 2469 | Metagenomic Sequencing of an In Vitro-Simulated Microbial Community. PLoS ONE, 2010, 5, e10209. | 1.1 | 200 |
| 2470 | The Genome of a Bacillus Isolate Causing Anthrax in Chimpanzees Combines Chromosomal Properties of B. cereus with B. anthracis Virulence Plasmids. PLoS ONE, 2010, 5, e10986. | 1.1 | 157 |
| 2471 | progressiveMauve: Multiple Genome Alignment with Gene Gain, Loss and Rearrangement. PLoS ONE, 2010, 5, e11147. | 1.1 | 3,652 |
| 2472 | Anchor-Based Whole Genome Phylogeny (ABWGP): A Tool for Inferring Evolutionary Relationship among Closely Related Microorganims. PLoS ONE, 2010, 5, e14159. | 1.1 | 10 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2473 | New Implications on Genomic Adaptation Derived from the Helicobacter pylori Genome Comparison. PLoS ONE, 2011, 6, e17300. | 1.1 | 15 |
| 2474 | Phage Encoded H-NS: A Potential Achilles Heel in the Bacterial Defence System. PLoS ONE, 2011, 6, e20095. | 1.1 | 59 |
| 2475 | Metabolic Versatility and Antibacterial Metabolite Biosynthesis Are Distinguishing Genomic Features of the Fire Blight Antagonist Pantoea vagans C9-1. PLoS ONE, 2011, 6, e22247. | 1.1 | 56 |
| 2476 | The Genome Sequence of the North-European Cucumber (Cucumis sativus L.) Unravels Evolutionary Adaptation Mechanisms in Plants. PLoS ONE, 2011, 6, e22728. | 1.1 | 112 |
| 2477 | Pseudomonas syringae pv. actinidiae Draft Genomes Comparison Reveal Strain-Specific Features Involved in Adaptation and Virulence to Actinidia Species. PLoS ONE, 2011, 6, e27297. | 1.1 | 137 |
| 2478 | Genome-Wide Analysis of the Emerging Infection with Mycobacterium avium Subspecies paratuberculosis in the Arabian Camels (Camelus dromedarius). PLoS ONE, 2012, 7, e31947. | 1.1 | 69 |
| 2479 | Isolation and Characterization of Cytotoxic, Aggregative Citrobacter freundii. PLoS ONE, 2012, 7, e33054. | 1.1 | 63 |
| 2480 | Comparative Genome Analysis of the High Pathogenicity Salmonella Typhimurium Strain UK-1. PLoS ONE, 2012, 7, e40645. | 1.1 | 23 |
| 2481 | Characterization and Differential Gene Expression between Two Phenotypic Phase Variants in Salmonella enterica Serovar Typhimurium. PLoS ONE, 2012, 7, e43592. | 1.1 | 19 |
| 2482 | In Vivo Capsular Switch in Streptococcus pneumoniae â€" Analysis by Whole Genome Sequencing. PLoS ONE, 2012, 7, e47983. | 1.1 | 22 |
| 2483 | Identification of Wolbachia Strains in Mosquito Disease Vectors. PLoS ONE, 2012, 7, e49922. | 1.1 | 33 |
| 2484 | Capturing the Biofuel Wellhead and Powerhouse: The Chloroplast and Mitochondrial Genomes of the Leguminous Feedstock Tree Pongamia pinnata. PLoS ONE, 2012, 7, e51687. | 1.1 | 73 |
| 2485 | Genome Analysis and Phylogenetic Relatedness of Gallibacterium anatis Strains from Poultry. PLoS ONE, 2013, 8, e54844. | 1.1 | 32 |
| 2486 | Phylogenetics and Differentiation of Salmonella Newport Lineages by Whole Genome Sequencing. PLoS ONE, 2013, 8, e55687. | 1.1 | 63 |
| 2487 | Pseudomonas syringae pv. actinidiae from Recent Outbreaks of Kiwifruit Bacterial Canker Belong to Different Clones That Originated in China. PLoS ONE, 2013, 8, e57464. | 1.1 | 143 |
| 2488 | The Complete Genome and Phenome of a Community-Acquired Acinetobacter baumannii. PLoS ONE, 2013, 8, e58628. | 1.1 | 93 |
| 2489 | Multiple Single-Cell Genomes Provide Insight into Functions of Uncultured Deltaproteobacteria in the Human Oral Cavity. PLoS ONE, 2013, 8, e59361. | 1.1 | 44 |
| 2490 | Complete Sequence and Analysis of Plastid Genomes of Two Economically Important Red Algae: Pyropia haitanensis and Pyropia yezoensis. PLoS ONE, 2013, 8, e65902. | 1.1 | 68 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2491 | Comparative Genome Analysis of Enterobacter cloacae. PLoS ONE, 2013, 8, e74487. | 1.1 | 72 |
| 2492 | Detection of Homologous Recombination Events in Bacterial Genomes. PLoS ONE, 2013, 8, e75230. | 1.1 | 3 |
| 2493 | A Genomic Redefinition of Pseudomonas avellanae species. PLoS ONE, 2013, 8, e75794. | 1.1 | 40 |
| 2494 | GenomeFingerprinter: The Genome Fingerprint and the Universal Genome Fingerprint Analysis for Systematic Comparative Genomics. PLoS ONE, 2013, 8, e77912. | 1.1 | 1 |
| 2495 | Architecture and Gene Repertoire of the Flexible Genome of the Extreme Acidophile Acidithiobacillus caldus. PLoS ONE, 2013, 8, e78237. | 1.1 | 68 |
| 2496 | The Genome Sequence of the Fungal Pathogen Fusarium virguliforme That Causes Sudden Death Syndrome in Soybean. PLoS ONE, 2014, 9, e81832. | 1.1 | 50 |
| 2497 | Unusual Large-Scale Chromosomal Rearrangements in Mycobacterium tuberculosis Beijing B0/W148 Cluster Isolates. PLoS ONE, 2014, 9, e84971. | 1.1 | 23 |
| 2498 | Genomic Evolution of 11 Type Strains within Family Planctomycetaceae. PLoS ONE, 2014, 9, e86752. | 1.1 | 18 |
| 2499 | Whole Genome Analysis of a Community-Associated Methicillin-Resistant Staphylococcus aureus ST59 Isolate from a Case of Human Sepsis and Severe Pneumonia in China. PLoS ONE, 2014, 9, e89235. | 1.1 | 19 |
| 2500 | Direct Amplification, Sequencing and Profiling of Chlamydia trachomatis Strains in Single and Mixed Infection Clinical Samples. PLoS ONE, 2014, 9, e99290. | 1.1 | 24 |
| 2501 | Genome Sequence of Candidatus Nitrososphaera evergladensis from Group I.1b Enriched from Everglades Soil Reveals Novel Genomic Features of the Ammonia-Oxidizing Archaea. PLoS ONE, 2014, 9, e101648. | 1.1 | 87 |
| 2502 | Virulence and Draft Genome Sequence Overview of Multiple Strains of the Swine Pathogen Haemophilus parasuis. PLoS ONE, 2014, 9, e103787. | 1.1 | 37 |
| 2503 | Large-Scale Phylogenetic Classification of Fungal Chitin Synthases and Identification of a Putative Cell-Wall Metabolism Gene Cluster in Aspergillus Genomes. PLoS ONE, 2014, 9, e104920. | 1.1 | 18 |
| 2504 | Complete Chloroplast Genome Sequence of Omani Lime (Citrus aurantiifolia) and Comparative Analysis within the Rosids. PLoS ONE, 2014, 9, e113049. | 1.1 | 60 |
| 2505 | A Role for Tn6029 in the Evolution of the Complex Antibiotic Resistance Gene Loci in Genomic Island 3 in Enteroaggregative Hemorrhagic Escherichia coli O104:H4. PLoS ONE, 2015, 10, e0115781. | 1.1 | 43 |
| 2506 | Interrogation of the Burkholderia pseudomallei Genome to Address Differential Virulence among Isolates. PLoS ONE, 2014, 9, e115951. | 1.1 | 29 |
| 2507 | Comparative Analysis of Super-Shedder Strains of Escherichia coli O157:H7 Reveals Distinctive Genomic Features and a Strongly Aggregative Adherent Phenotype on Bovine Rectoanal Junction Squamous Epithelial Cells. PLoS ONE, 2015, 10, e0116743. | 1.1 | 36 |
| 2508 | Discovery of Putative Small Non-Coding RNAs from the Obligate Intracellular Bacterium Wolbachia pipientis. PLoS ONE, 2015, 10, e0118595. | 1.1 | 13 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2509 | The Complete Chloroplast and Mitochondrial Genomes of the Green Macroalga Ulva sp. UNA00071828 (Ulvophyceae, Chlorophyta). PLoS ONE, 2015, 10, e0121020. | 1.1 | 66 |
| 2510 | Initial Evidence for Adaptive Selection on the NADH Subunit Two of Freshwater Dolphins by Analyses of Mitochondrial Genomes. PLoS ONE, 2015, 10, e0123543. | 1.1 | 28 |
| 2511 | Genetically and Phenotypically Distinct Pseudomonas aeruginosa Cystic Fibrosis Isolates Share a Core Proteomic Signature. PLoS ONE, 2015, 10, e0138527. | 1.1 | 37 |
| 2512 | Analysis of the Complete Chloroplast Genome of a Medicinal Plant, Dianthus superbus var. longicalyncinus, from a Comparative Genomics Perspective. PLoS ONE, 2015, 10, e0141329. | 1.1 | 58 |
| 2513 | Genomic and Gene-Expression Comparisons among Phage-Resistant Type-IV Pilus Mutants of Pseudomonas syringae pathovar phaseolicola. PLoS ONE, 2015, 10, e0144514. | 1.1 | 11 |
| 2514 | Identifying Likely Transmission Pathways within a 10-Year Community Outbreak of Tuberculosis by High-Depth Whole Genome Sequencing. PLoS ONE, 2016, 11, e0150550. | 1.1 | 24 |
| 2515 | Bacillus pumilus SAFR-032 Genome Revisited: Sequence Update and Re-Annotation. PLoS ONE, 2016, 11, e0157331. | 1.1 | 21 |
| 2516 | Comparative Genomics and Metabolic Analysis Reveals Peculiar Characteristics of Rhodococcus opacus Strain M213 Particularly for Naphthalene Degradation. PLoS ONE, 2016, 11, e0161032. | 1.1 | 21 |
| 2517 | Comparative Genomics of Acetobacterpasteurianus Ab3, an Acetic Acid Producing Strain Isolated from Chinese Traditional Rice Vinegar Meiguichu. PLoS ONE, 2016, 11, e0162172. | 1.1 | 12 |
| 2518 | Experimental Evolution of Mycobacterium tuberculosis in Human Macrophages Results in Low-Frequency Mutations Not Associated with Selective Advantage. PLoS ONE, 2016, 11, e0167989. | 1.1 | 6 |
| 2519 | Genomic sequence of 'Candidatus Liberibacter solanacearum' haplotype C and its comparison with haplotype A and B genomes. PLoS ONE, 2017, 12, e0171531. | 1.1 | 39 |
| 2520 | The quantitative impact of read mapping to non-native reference genomes in comparative RNA-Seq studies. PLoS ONE, 2017, 12, e0180904. | 1.1 | 9 |
| 2521 | Comparative pathogenomics of Clostridium tetani. PLoS ONE, 2017, 12, e0182909. | 1.1 | 36 |
| 2522 | Identification and genomic comparison of temperate bacteriophages derived from emetic Bacillus cereus. PLoS ONE, 2017, 12, e0184572. | 1.1 | 20 |
| 2523 | Treatment with high-dose antidepressants severely exacerbates the pathological outcome of experimental Escherichia coli infections in poultry. PLoS ONE, 2017, 12, e0185914. | 1.1 | 7 |
| 2524 | Genomic diversity of Taylorella equigenitalis introduced into the United States from 1978 to 2012. PLoS ONE, 2018, 13, e0194253. | 1.1 | 2 |
| 2525 | Ancestry of the AUTS2 familyâ€"A novel group of polycomb-complex proteins involved in human neurological disease. PLoS ONE, 2020, 15, e0232101. | 1.1 | 4 |
| 2526 | Dissemination and Mechanism for the MCR-1 Colistin Resistance. PLoS Pathogens, 2016, 12, e1005957. | 2.1 | 205 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2527 | Automated transcription start site prediction for comparative Transcriptomics using the SuperGenome. EMBnet Journal, 2013, 19, 19. | 0.2 | 4 |
| 2528 | Fusaricidins in Paenibacillus polymyxa A21 and their antagonistic activity against Botrytis cinerea on tomato. Frontiers of Agricultural Science and Engineering, 2018, . | 0.9 | 2 |
| 2529 | The complete chloroplast genome of Papaver setigerum and comparative analyses in Papaveraceae. Genetics and Molecular Biology, 2020, 43, e20190272. | 0.6 | 12 |
| 2530 | Molecular Detection of Salmonella enterica subsp. arizonae by Quantitative PCR. Avian Diseases, 2020, 64, 305-309. | 0.4 | 3 |
| 2531 | Chromatiblock: scalable whole-genome visualization of structural differences in prokaryotes. Journal of Open Source Software, 2020, 5, 2451. | 2.0 | 1 |
| 2532 | Low Coverage Whole Genome Sequencing Yields the Complete Mitogenome of Hypselodoris bullocki and Hypselodoris apolegma (Mollusca: Chromodorididae). Journal of Coastal Research, 2019, 97, 23. | 0.1 | 3 |
| 2533 | Characterization of the Chloroplast Genome Facilitated the Transformation of Parachlorella kessleri-I, A Potential Marine Alga for Biofuel Production. Current Genomics, 2020, 21, 610-623. | 0.7 | 4 |
| 2534 | Constraints of Drug Resistance in Mycobacterium tuberculosis - Prospects for Pharmacological Reversion of Susceptibility to Antibiotics. The Open Conference Proceedings Journal, 2017, 8, 33-43. | 0.6 | 3 |
| 2535 | Two multi-fragment recombination events resulted in the Î²-lactam-resistant serotype 11A-ST6521 related to Spain9V-ST156 pneumococcal clone spreading in south-western Europe, 2008 to 2016. Eurosurveillance, 2020, 25, . | 3.9 | 12 |
| 2536 | mcr-Colistin Resistance Genes Mobilized by IncX4, IncHI2, and IncI2 Plasmids in Escherichia coli of Pigs and White Stork in Spain. Frontiers in Microbiology, 2019, 10, 3072. | 1.5 | 57 |
| 2537 | Genome-Wide Association Studies for the Detection of Genetic Variants Associated With Daptomycin and Ceftaroline Resistance in Staphylococcus aureus. Frontiers in Microbiology, 2021, 12, 639660. | 1.5 | 11 |
| 2538 | Genomic Insight into Pediococcus acidilactici HN9, a Potential Probiotic Strain Isolated from the Traditional Thai-Style Fermented Beef Nhang. Microorganisms, 2021, 9, 50. | 1.6 | 18 |
| 2539 | Complete Genome Sequence of Ovine Mycobacterium avium subsp. paratuberculosis Strain JIII-386 (MAP-S/type III) and Its Comparison to MAP-S/type I, MAP-C, and M. avium Complex Genomes. Microorganisms, 2021, 9, 70. | 1.6 | 13 |
| 2540 | Isolation and Characterization of Salmonella Jumbo-Phage pSal-SNUABM-04. Viruses, 2021, 13, 27. | 1.5 | 20 |
| 2541 | The complete mitochondrial genome sequence of Scolopendra mutilans L. Koch, 1878 (Scolopendromorpha, Scolopendridae), with a comparative analysis of other centipede genomes. ZooKeys, 2020, 925, 73-88. | 0.5 | 7 |
| 2542 | In silico Analysis of Chlorobium Genomes Divulge Insights into the Lifestyle of the Bacteria. Research Journal of Microbiology, 2008, 3, 600-613. | 0.2 | 4 |
| 2543 | Comparative genome analysis of 15 clinical <em>Shigella flexneri</em> strains regarding virulence and antibiotic resistance. AIMS Microbiology, 2019, 5, 205-222. | 1.0 | 9 |
| 2544 | Isolation and characterization of the &lt;em&gt;Staphylococcus aureus&lt;/em&gt; bacteriophage vB_SauS_SA2. AIMS Microbiology, 2019, 5, 285-307. | 1.0 | 14 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2545 | Non-contiguous finished genome sequence and description of Paenibacillus senegalensis sp. nov.. Standards in Genomic Sciences, 2012, 7, 70-81. | 1.5 | 47 |
| 2546 | Diversified lineages and drug-resistance profiles of clinical isolates of Mycobacterium tuberculosis complex in Malaysia. International Journal of Mycobacteriology, 2019, 8, 320. | 0.3 | 3 |
| 2547 | GI&lt;sub&gt;FeGSH&lt;/sub&gt;: A New Genomic Island Might Explain the Differences in &lt;i&gt;Brucella&lt;/i&gt; Virulence. Open Journal of Animal Sciences, 2017, 07, 141-148. | 0.2 | 4 |
| 2548 | Decoding the Genomic Architecture of Mammalian and Plant Genomes: Synteny Blocks and Large-scale Duplications. Communications in Information and Systems, 2010, 10, 1-22. | 0.3 | 2 |
| 2549 | A noviceâ€™s guide to analyzing NGS-derived organelle and metagenome data. Algae, 2016, 31, 137-154. | 0.9 | 17 |
| 2550 | Comparative Genome Analysis of Rathayibacter tritici NCPPB 1953 with Rathayibacter toxicus Strains Can Facilitate Studies on Mechanisms of Nematode Association and Host Infection. Plant Pathology Journal, 2017, 33, 370-381. | 0.7 | 6 |
| 2551 | Functional annotations in bacterial genomes based on small RNA signatures. Bioinformation, 2008, 2, 284-295. | 0.2 | 4 |
| 2553 | Expansion of the fatty acyl reductase gene family shaped pheromone communication in Hymenoptera. ELife, 2019, 8, . | 2.8 | 26 |
| 2554 | Pantonâ€“Valentine leucocidin is the key determinant of Staphylococcus aureus pyomyositis in a bacterial GWAS. ELife, 2019, 8, . | 2.8 | 56 |
| 2555 | Phage integration alters the respiratory strategy of its host. ELife, 2019, 8, . | 2.8 | 24 |
| 2556 | Post-acute COVID-19 associated with evidence of bystander T-cell activation and a recurring antibiotic-resistant bacterial pneumonia. ELife, 2020, 9, . | 2.8 | 26 |
| 2557 | AliTVâ€”interactive visualization of whole genome comparisons. PeerJ Computer Science, 0, 3, e116. | 2.7 | 80 |
| 2558 | Plastome structure and adaptive evolution of <i>Calanthe</i> s.l. species. PeerJ, 2020, 8, e10051. | 0.9 | 15 |
| 2559 | Isolation and evolutionary analyses of porcine epidemic diarrhea virus in Asia. PeerJ, 2020, 8, e10114. | 0.9 | 11 |
| 2560 | Biases in genome reconstruction from metagenomic data. PeerJ, 2020, 8, e10119. | 0.9 | 32 |
| 2561 | Phylogenetic relationships and taxonomic position of genus<i>Hyperacrius</i>(Rodentia: Arvicolinae) from Kashmir based on evidences from analysis of mitochondrial genome and study of skull morphology. PeerJ, 2020, 8, e10364. | 0.9 | 3 |
| 2562 | Augmenting transcriptome assembly by combining<i>de novo</i>and genome-guided tools. PeerJ, 2013, 1, e133. | 0.9 | 19 |
| 2563 | Gall-ID: tools for genotyping gall-causing phytopathogenic bacteria. PeerJ, 2016, 4, e2222. | 0.9 | 37 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2564 | Chromosomal rearrangements and protein globularity changes in<i>Mycobacterium tuberculosis</i>isolates from cerebrospinal fluid. PeerJ, 2016, 4, e2484. | 0.9 | 5 |
| 2565 | <i>Legionella</i>shows a diverse secondary metabolism dependent on a broad spectrum Sfp-type phosphopantetheinyl transferase. PeerJ, 2016, 4, e2720. | 0.9 | 5 |
| 2566 | The complete chloroplast genome sequence of<i>Helwingia himalaica</i>(Helwingiaceae, Aquifoliales) and a chloroplast phylogenomic analysis of the Campanulidae. PeerJ, 2016, 4, e2734. | 0.9 | 10 |
| 2567 | Evolutionary origins of the emergent ST796 clone of vancomycin resistant<i>Enterococcus faecium</i>. PeerJ, 2017, 5, e2916. | 0.9 | 46 |
| 2568 | Plastomes of the green algae <i>Hydrodictyon reticulatum</i> and <i>Pediastrum duplex</i> (Sphaeropleales, Chlorophyceae). PeerJ, 2017, 5, e3325. | 0.9 | 8 |
| 2569 | Chloroplast genome expansion by intron multiplication in the basal psychrophilic euglenoid<i>Eutreptiella pomquetensis</i>. PeerJ, 2017, 5, e3725. | 0.9 | 11 |
| 2570 | Complete genome sequence and comparative genomics of the golden pompano (<i>Trachinotus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 | 0.9 | 33 |
| 2571 | Strain-level genetic diversity of<i>Methylophaga nitratireducenticrescens</i>confers plasticity to denitrification capacity in a methylotrophic marine denitrifying biofilm. PeerJ, 2018, 6, e4679. | 0.9 | 9 |
| 2572 | TarSynFlow, a workflow for bacterial genome comparisons that revealed genes putatively involved in the probiotic character of<i>Shewanella putrefaciens</i>strain Pdp11. PeerJ, 2019, 7, e6526. | 0.9 | 3 |
| 2573 | The complete chloroplast genome of <i>Fagus crenata</i> (subgenus <i>Fagus</i>) and comparison with <i>F. engleriana</i> (subgenus <i>Engleriana</i>). PeerJ, 2019, 7, e7026. | 0.9 | 16 |
| 2574 | Mitochondrial genomics of human pathogenic parasite<i>Leishmania</i>(<i>Viannia</i>)<i>panamensis</i>. PeerJ, 2019, 7, e7235. | 0.9 | 13 |
| 2575 | The sugarcane mitochondrial genome: assembly, phylogenetics and transcriptomics. PeerJ, 2019, 7, e7558. | 0.9 | 15 |
| 2576 | Detection and identification of<i>Xanthomonas</i>pathotypes associated with citrus diseases using comparative genomics and multiplex PCR. PeerJ, 2019, 7, e7676. | 0.9 | 10 |
| 2577 | Plastome of mycoheterotrophic<i>Burmannia itoana</i>Mak. (Burmanniaceae) exhibits extensive degradation and distinct rearrangements. PeerJ, 2019, 7, e7787. | 0.9 | 5 |
| 2578 | <scp>L</scp>-cysteine transporter-PCR to detect hydrogen sulfide-producing <i>Campylobacter fetus</i>. PeerJ, 2019, 7, e7820. | 0.9 | 9 |
| 2579 | Development of molecular markers for invasive alien plants in Korea: a case study of a toxic weed, <i>Cenchrus longispinus</i> L., based on next generation sequencing data. PeerJ, 2019, 7, e7965. | 0.9 | 2 |
| 2580 | Characteristics of the complete mitochondrial genome of the monotypic genus Arctictis (Family:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 | 0.9 | 3 |
| 2581 | ÂComplete plastid genome sequences of two species of the Neotropical genus <i>Brunellia</i> (Brunelliaceae). PeerJ, 2020, 8, e8392. | 0.9 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2582 | Pan-Genome Analysis of Effectors in Korean Strains of the Soybean Pathogen Xanthomonas citri pv. glycines. Microorganisms, 2021, 9, 2065. | 1.6 | 4 |
| 2583 | Characterization of chloroplast genome of the marine diatom <i>Chaetoceros gracilis</i>. Mitochondrial DNA Part B: Resources, 2021, 6, 3159-3161. | 0.2 | 0 |
| 2584 | Third generation cephalosporin resistance in clinical non-typhoidal Salmonella enterica in Germany and emergence of bla CTX-M-harbouring pESI plasmids. Microbial Genomics, 2021, 7, . | 1.0 | 11 |
| 2585 | Complete Genome Sequence of the Marine-Derived Bacterium Streptomyces sp. Strain GMY02. Microbiology Resource Announcements, 2021, 10, e0068121. | 0.3 | 1 |
| 2586 | Emergence of 16S rRNA methyltransferases among carbapenemase-producing Enterobacterales in Spain studied by whole-genome sequencing. International Journal of Antimicrobial Agents, 2022, 59, 106456. | 1.1 | 11 |
| 2587 | The complete mitochondrial genome of Ophiocordyceps gracilis and its comparison with related species. IMA Fungus, 2021, 12, 31. | 1.7 | 7 |
| 2588 | Transition of Serotype 35B Pneumococci From Commensal to Prevalent Virulent Strain in Children. Frontiers in Cellular and Infection Microbiology, 2021, 11, 744742. | 1.8 | 3 |
| 2589 | Establishment of a near-contiguous genome sequence of the citric acid producing yeast Yarrowia lipolytica DSM 3286 with resolution of rDNA clusters and telomeres. NAR Genomics and Bioinformatics, 2021, 3, lqab085. | 1.5 | 4 |
| 2590 | Genomic Changes and Genetic Divergence of Vibrio alginolyticus Under Phage Infection Stress Revealed by Whole-Genome Sequencing and Resequencing. Frontiers in Microbiology, 2021, 12, 710262. | 1.5 | 3 |
| 2591 | Fish genomics and its impact on fundamental and applied research of vertebrate biology. Reviews in Fish Biology and Fisheries, 2022, 32, 357-385. | 2.4 | 7 |
| 2592 | Phage Therapy Related Microbial Succession Associated with Successful Clinical Outcome for a Recurrent Urinary Tract Infection. Viruses, 2021, 13, 2049. | 1.5 | 33 |
| 2593 | Whole-Genome Sequencing Analysis of a stx-Negative EscherichiaÂcoli O63:H6 Isolate Associated with Hemolytic Uremic Syndrome. Diagnostics, 2021, 11, 1823. | 1.3 | 2 |
| 2594 | Minimalistic mycoplasmas harbor different functional toxin-antitoxin systems. PLoS Genetics, 2021, 17, e1009365. | 1.5 | 7 |
| 2595 | Identification and genomic analysis of Mycobacterium ulcerans ecovar Liflandii from the farmed Chinese tongue sole, Cynoglossus semilaevis GÃ¼nther. Aquaculture, 2022, 548, 737614. | 1.7 | 4 |
| 2596 | Dynamic impact of virome on colitis and colorectal cancer: Immunity, inflammation, prevention and treatment. Seminars in Cancer Biology, 2022, 86, 943-954. | 4.3 | 17 |
| 2597 | Complete genomes of the eukaryotic poultry parasite Histomonas meleagridis: linking sequence analysis with virulence / attenuation. BMC Genomics, 2021, 22, 753. | 1.2 | 17 |
| 2599 | Genomic sequence data of bacterial isolates from pistachio trees and other woody plants in California are inconsistent with a role of Rhodococcus as the causative agent of Pistachio Bushy Top Syndrome. PhytoFrontiers, 0, , . | 0.8 | 0 |
| 2600 | Probiotic effects of the Bacillus velezensis GY65 strain in the mandarin fish, Siniperca chuatsi. Aquaculture Reports, 2021, 21, 100902. | 0.7 | 10 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2601 | Genome analysis of an OXA-48-producing carbapenem- and colistin-resistant Klebsiella pneumoniae sequence type 11 clone isolated from an inpatient. Gene Reports, 2021, 25, 101394. | 0.4 | 1 |
| 2602 | First report of two foodborne Salmonella enterica subsp. enterica serovar Bovismorbificans isolates carrying a novel mega-plasmid harboring blaDHA-1 and qnrB4 genes. International Journal of Food Microbiology, 2021, 360, 109439. | 2.1 | 5 |
| 2603 | MEDITE: A Unilingual Textual Aligner. Lecture Notes in Computer Science, 2006, , 458-469. | 1.0 | 2 |
| 2604 | Rough Computational Annotation and Hierarchical Conserved Area Viewing Tool for Genomes Using Multiple Relation Graph.. Journal of Life Science, 2008, 18, 565-571. | 0.2 | 0 |
| 2605 | Alignment and Analysis of Closely Related Genomes. Lecture Notes in Computer Science, 2009, , 343-352. | 1.0 | 0 |
| 2606 | Pangenomic Reverse Vaccinology. , 2010, , 203-221. |  | 1 |
| 2607 | Practical Multiple Sequence Alignment. , 2010, , 21-43. |  | 0 |
| 2608 | Overview: The Impact of Microbial Genomics on Food Safety. , 2011, , 1-27. |  | 0 |
| 2609 | Functional Inference in Microbial Genomics Based on Large-Scale Comparative Analysis. , 2011, , 55-92. |  | 0 |
| 2610 | Hidden Breakpoints in Genome Alignments. Lecture Notes in Computer Science, 2012, , 391-403. | 1.0 | 0 |
| 2611 | Identification of Genomic Islands by Pattern Discovery. , 2012, , 166-181. |  | 0 |
| 2612 | Organization, expression and evolution of flagellar genesin &lt;i&gt;Rhodobacter sphaeroides &lt;/i&gt;2.4.1. Open Journal of Genetics, 2012, 02, 5-10. | 0.1 | 0 |
| 2613 | Contribution of Transcription Factor Binding Site Motif Variants to Condition-Specific Gene Expression Patterns in Budding Yeast. PLoS ONE, 2012, 7, e32274. | 1.1 | 0 |
| 2614 | Sequence Homology Handling. Computational Biology, 2013, , 301-334. | 0.1 | 1 |
| 2615 | Visualization in Biology and Medicine. Mathematics and Visualization, 2014, , 247-263. | 0.4 | 0 |
| 2616 | Alternaria Comparative Genomics: The Secret Life of Rots. , 2014, , 45-63. |  | 3 |
| 2617 | Application of Genome Studies of Coffee Rust. Advances in Intelligent Systems and Computing, 2014, , 133-139. | 0.5 | 1 |
| 2618 | Aggregation of Similarity Measures for Ortholog Detection: Validation with Measures Based on Rough Set Theory. Computacion Y Sistemas, 2014, 18, . | 0.2 | 1 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2623 | In Silico Signature Prediction Modeling in Cytolethal Distending Toxin-Producing Escherichia coli Strains. Genomics and Informatics, 2017, 15, 69. | 0.4 | 1 |
| 2642 | NovoGraph: Genome graph construction from multiple long-read de novo assemblies. F1000Research, 2018, 7, 1391. | 0.8 | 8 |
| 2644 | Analysis of the genome of the bacteria Bacillus amyloliquefaciens BIM B-439D. , 2018, 62, 592-600. | 0.0 | 1 |
| 2648 | Multiple Chromosomes in Bacteria: Low Level of Evolutionary Constraint Drives the Rapid Genetic Divergence of Chromosome II. Advances in Microbiology, 2019, 09, 656-677. | 0.3 | 0 |
| 2653 | Adaptation of metal and antibiotic resistant traits in novel Î²-Proteobacterium<i>Achromobacter xylosoxidans</i>BHW-15. PeerJ, 2019, 7, e6537. | 0.9 | 5 |
| 2655 | An orthogonal amber initiator tRNA functions similarly across diverse <em>Escherichia coli</em> laboratory strains. Matters, 0, , . | 1.0 | 0 |
| 2657 | The completely assembled genome of a strain from the New Zealand <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> (PSA) outbreak. Acta Horticulturae, 2019, , 23-28. | 0.1 | 1 |
| 2659 | Draft Genome Sequence of <i>Brevundimonas</i> sp. Strain T2.26MG-97, Isolated from a Rock Core Sample from 492.6 Meters Deep on the Subsurface of the Iberian Pyrite Belt. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 1 |
| 2660 | Complete Genome Sequence of a Pseudomonas aeruginosa Isolate from a Kidney Stone. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 3 |
| 2661 | Genomic differences among carriage and invasive nontypeable pneumococci circulating in South Africa. Microbial Genomics, 2019, 5, . | 1.0 | 0 |
| 2664 | Draft Genome Sequence of Bacillus safensis RP10, Isolated from Soil in the Atacama Desert, Chile. Microbiology Resource Announcements, 2019, 8, . | 0.3 | 2 |
| 2673 | Lumen and mucosa-associated<i>Lactobacillus rhamnosus</i>from the intestinal tract of organ donors. Gut Microbiome, 2020, 1, . | 0.8 | 1 |
| 2683 | Complete Genome Sequences of Diverse Uropathogenic Staphylococcus saprophyticus Isolates from a College Health Center. Microbiology Resource Announcements, 2020, 9, . | 0.3 | 0 |
| 2684 | An Explorative Tool for Mutation Tracking in the Spike Glycoprotein of SARS-CoV-2. , 2021, , . |  | 0 |
| 2686 | Whole genome global insight of antibiotic resistance gene repertoire and virulome of high - risk multidrug-resistant Uropathogenic Escherichia coli. Microbial Pathogenesis, 2021, 161, 105256. | 1.3 | 12 |
| 2687 | Complete Genome Analysis of Undecylprodigiosin Pigment Biosynthesizing Marine Streptomyces Species Displaying Potential Bioactive Applications. Microorganisms, 2021, 9, 2249. | 1.6 | 5 |
| 2688 | Mitochondrial genomes do not appear to regulate flowering pattern / reproductive strategy in Cannabis sativa. AoB PLANTS, 2022, 14, plab068. | 1.2 | 1 |
| 2689 | Characterization and adaptation of Caldicellulosiruptor strains to higher sugar concentrations, targeting enhanced hydrogen production from lignocellulosic hydrolysates. Biotechnology for Biofuels, 2021, 14, 210. | 6.2 | 4 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2691 | Comparative genome analyses of Mycobacteroides immunogenum reveals two potential novel subspecies. Microbial Genomics, 2020, 6, . | 1.0 | 5 |
| 2692 | Swine Conjunctivitis Associated with a Novel Mycoplasma Species Closely Related to Mycoplasma hyorhinis. Pathogens, 2021, 10, 13. | 1.2 | 5 |
| 2693 | Complete chloroplast genome comparisons for Pityopsis (Asteraceae). PLoS ONE, 2020, 15, e0241391. | 1.1 | 7 |
| 2696 | Genomic and Phenotypic Diversity of Carbapenemase-Producing Enterobacteriaceae Isolates from Bacteremia in China: A Multicenter Epidemiological, Microbiological, and Genetic Study. Engineering, 2022, 12, 90-100. | 3.2 | 15 |
| 2697 | Culicoidibacter larvae gen. nov., sp. nov., from the gastrointestinal tract of the biting midge (Culicoides sonorensis) larva, belongs to a novel lineage Culicoidibacteraceae fam. nov., Culicoidibacterales ord. nov. and Culicoidibacteria classis nov. of the phylum Firmicutes. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6482-6490. | 0.8 | 14 |
| 2698 | Helicobacter pylori diversification during chronic infection within a single host generates sub-populations with distinct phenotypes. PLoS Pathogens, 2020, 16, e1008686. | 2.1 | 7 |
| 2699 | Sequencing of Complete Chloroplast Genomes. Methods in Molecular Biology, 2021, 2222, 89-105. | 0.4 | 0 |
| 2700 | Bioinspired Intrusion Detection in ITC Infrastructures. Lecture Notes in Networks and Systems, 2021, , 10-22. | 0.5 | 5 |
| 2701 | Sequence Alignment Algorithms for Intrusion Detection in the Internet of Things. Nonlinear Phenomena in Complex Systems, 2020, 23, 397-404. | 0.1 | 8 |
| 2702 | Bovine abortion by a vaccine strain of Bacillus anthracis. Ciencia Rural, 2020, 50, . | 0.3 | 0 |
| 2703 | Phenotypic and Genotypic Characterisation of Clinical Isolates of Nosocomial Infections. Eurasian Journal of Applied Biotechnology, 2020, , . | 0.0 | 1 |
| 2704 | Comparative Analyses and Phylogenetic Relationships between Cryptomeria fortunei and Related Species Based on Complete Chloroplast Genomes. Phyton, 2020, 89, 957-986. | 0.4 | 1 |
| 2705 | Draft genome sequences of &lt;i&gt;Enterococcus durans&lt;/i&gt; EDD2 strain associated with honeybees. AIMS Agriculture and Food, 2020, 5, 288-291. | 0.8 | 1 |
| 2706 | Complete genome sequence of a methicillin-resistant Staphylococcus schleiferi strain from canine otitis externa in Korea. Journal of Veterinary Science, 2020, 21, e11. | 0.5 | 3 |
| 2707 | Comparative Genome Analysis of Psychrobacillus Strain PB01, Isolated from an Iceberg. Journal of Microbiology and Biotechnology, 2020, 30, 237-243. | 0.9 | 6 |
| 2709 | Whole-Genome Sequence of Drug-Resistant Mycobacterium tuberculosis Strain S7, Isolated from a Patient with Pulmonary Tuberculosis. Microbiology Resource Announcements, 2020, 9, . | 0.3 | 1 |
| 2711 | Bactericidal Effect of Pseudomonas oryziphila sp. nov., a Novel Pseudomonas Species Against Xanthomonas oryzae Reduces Disease Severity of Bacterial Leaf Streak of Rice. Frontiers in Microbiology, 2021, 12, 759536. | 1.5 | 12 |
| 2712 | Complete Genome Sequence of Bacillus velezensis GMEKP1, Isolated from a Natural Bamboo Hive of Stingless Bees. Microbiology Resource Announcements, 2021, 10, e0065921. | 0.3 | 0 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2714 | Different gene rearrangements of the genus Dardanus (Anomura: Diogenidae) and insights into the phylogeny of Paguroidea. Scientific Reports, 2021, 11, 21833. | 1.6 | 7 |
| 2716 | Re-classification of Streptomyces venezuelae strains and mining secondary metabolite biosynthetic gene clusters. IScience, 2021, 24, 103410. | 1.9 | 2 |
| 2717 | Complete Genome Sequence of Rickettsia parkeri Strain Black Gap. Microbiology Resource Announcements, 2021, 10, e0062321. | 0.3 | 1 |
| 2718 | Comprehensive analysis of complete mitochondrial genome of Sapindus mukorossi Gaertn.: an important industrial oil tree species in China. Industrial Crops and Products, 2021, 174, 114210. | 2.5 | 16 |
| 2721 | Identification of Genomic Islands by Pattern Discovery. , 0, , 742-758. |  | 0 |
| 2722 | Merging Multi-Version Texts: a Generic Solution to the Overlap Problem. Balisage Series on Markup Technologies, 0, , . | 0.0 | 4 |
| 2723 | Omics-based comparative analysis of putative mobile genetic elements in Lactococcus lactis. FEMS Microbiology Letters, 2019, 366, i105-i113. | 0.7 | 1 |
| 2724 | Draft Genome Sequence of Shewanella sp. Strain T2.3D-1.1, Isolated from 121.8 Meters Deep in the Subsurface of the Iberian Pyrite Belt. Microbiology Resource Announcements, 2020, 9, . | 0.3 | 2 |
| 2725 | Draft Genome Sequence of Escherichia coli Strain Tj, Isolated from the Varzob River in Tajikistan. Microbiology Resource Announcements, 2020, 9, . | 0.3 | 1 |
| 2729 | Symbiosis islands of Loteae-nodulating Mesorhizobium comprise three radiating lineages with concordant nod gene complements and nodulation host-range groupings. Microbial Genomics, 2020, 6, . | 1.0 | 7 |
| 2733 | Development of PCR-Based Molecular Marker for Detection of Xanthomonas campestris pv. campestris Race 6, the Causative Agent of Black Rot of Brassicas. Plant Pathology Journal, 2020, 36, 418-427. | 0.7 | 7 |
| 2736 | Complete Plastome of Carlina acaulis and Implications on Systematics of the Tribe Cardueae (Asteraceae). Annales Botanici Fennici, 2021, 58, . | 0.0 | 0 |
| 2737 | Genomic evidence for stability of the Bacillus Calmetteâ€GuÃ©rin (BCG) vaccine strain (Pasteur 1173P2) from different batches in Iran. Journal of Applied Microbiology, 2021, , . | 1.4 | 0 |
| 2738 | Accurate long-read de novo assembly evaluation with Inspector. Genome Biology, 2021, 22, 312. | 3.8 | 46 |
| 2739 | Extensive Genome Exploration of Clostridium botulinum Group III Field Strains. Microorganisms, 2021, 9, 2347. | 1.6 | 9 |
| 2740 | Phylogeny of Maleae (Rosaceae) Based on Complete Chloroplast Genomes Supports the Distinction of Aria, Chamaemespilus and Torminalis as Separate Genera, Different from Sorbus sp.. Plants, 2021, 10, 2534. | 1.6 | 8 |
| 2741 | Deciphering the Molecular Basis for Attenuation of Flavobacterium columnare Strain Fc1723 Used as Modified Live Vaccine against Columnaris Disease. Vaccines, 2021, 9, 1370. | 2.1 | 3 |
| 2742 | Genomic characterization and production of antimicrobial lipopeptides by Bacillus velezensis P45 growing on feather by-products. Journal of Applied Microbiology, 2022, 132, 2067-2079. | 1.4 | 4 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2743 | Comparative Chloroplast Genome Analyses of the Winter-Blooming Eastern Asian Endemic Genus Chimonanthus (Calycanthaceae) With Implications For Its Phylogeny and Diversification. Frontiers in Genetics, 2021, 12, 709996. | 1.1 | 1 |
| 2744 | Prediction and Analysis in silico of Genomic Islands in Aeromonas hydrophila. Frontiers in Microbiology, 2021, 12, 769380. | 1.5 | 2 |
| 2745 | Paralysiella testudinis gen. nov., sp. nov., isolated from the cloaca of a toad-headed turtle (Mesoclemmys nasuta). International Journal of Systematic and Evolutionary Microbiology, 2021, 71, . | 0.8 | 9 |
| 2748 | Remarkably coherent population structure for a dominant Antarctic Chlorobium species. Microbiome, 2021, 9, 231. | 4.9 | 5 |
| 2749 | Mitochondrial genomes of two parasitic Cuscuta species lack clear evidence of horizontal gene transfer and retain unusually fragmented ccmFC genes. BMC Genomics, 2021, 22, 816. | 1.2 | 11 |
| 2750 | The Gene Rearrangement, Loss, Transfer, and Deep Intronic Variation in Mitochondrial Genomes of Conidiobolus. Frontiers in Microbiology, 2021, 12, 765733. | 1.5 | 5 |
| 2751 | Comparative Genomics Analyses Support the Reclassification of Bisgaard Taxon 40 as Mergibacter gen. nov., With Mergibacter septicus sp. nov. as Type Species: Novel Insights Into the Phylogeny and Virulence Factors of a Pasteurellaceae Family Member Associated With Mortality Events in Seabirds. Frontiers in Microbiology, 2021, 12, 667356. | 1.5 | 4 |
| 2754 | Comparative genomics and phylogenetic relationships of two endemic and endangered species (Handeliodendron bodinieri and Eurycorymbus cavaleriei) of two monotypic genera within Sapindales. BMC Genomics, 2022, 23, 27. | 1.2 | 12 |
| 2755 | Characterization, genome analysis and in vitro activity of a novel phage vB_EcoA_RDN8.1 active against multi-drug resistant and extensively drug-resistant biofilm-forming uropathogenic Escherichia coli isolates, India. Journal of Applied Microbiology, 2022, 132, 3387-3404. | 1.4 | 5 |
| 2756 | Mobile Genetic Elements Drive Antimicrobial Resistance Gene Spread in Pasteurellaceae Species. Frontiers in Microbiology, 2021, 12, 773284. | 1.5 | 11 |
| 2757 | Regulation of Heterogenous LexA Expression in Staphylococcus aureus by an Antisense RNA Originating from Transcriptional Read-Through upon Natural Mispairings in the sbrB Intrinsic Terminator. International Journal of Molecular Sciences, 2022, 23, 576. | 1.8 | 1 |
| 2758 | Plasmids Bring Additional Capabilities to Caulobacter Isolates. Current Microbiology, 2022, 79, 45. | 1.0 | 0 |
| 2759 | Plastome structure, evolution, and phylogeny of Selaginella. Molecular Phylogenetics and Evolution, 2022, 169, 107410. | 1.2 | 11 |
| 2760 | Comparative Genomic and Phylogenetic Analysis of Spike and Nucleocapsid Proteins of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and 9 Other Taxonomically Related Coronaviruses using in-Silico Tools. Vantage: Journal of Thermatic Analysis, 2020, 1, 46-81. | 0.0 | 0 |
| 2762 | Genome analysis of Lysinibacillus sphaericus isolate 6.2 pathogenic to Culex quinquefasciatus Say, 1823 (Diptera: Culicidae). Biodiversitas, 2021, 22, . | 0.2 | 0 |
| 2763 | Genetic characteristics of an amikacin-resistant Brucella abortus strain first isolated from Marmota himalayana. Microbial Pathogenesis, 2022, 164, 105402. | 1.3 | 3 |
| 2764 | Genomic insights into the plant-associated lifestyle of Kosakonia radicincitans MUSA4, a diazotrophic plant-growth-promoting bacterium. Systematic and Applied Microbiology, 2022, 45, 126303. | 1.2 | 6 |
| 2765 | Phage JS02, a putative temperate phage, a novel biofilm-degrading agent for Staphylococcus aureus. Letters in Applied Microbiology, 2022, 75, 643-654. | 1.0 | 9 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2766 | Complete sequence of classic F-type plasmid pRK100 shows unique conservation over time and geographic location. Plasmid, 2022, 119-120, 102618. | 0.4 | 0 |
| 2767 | A Novel Method to Create Efficient Phage Cocktails via Use of Phage-Resistant Bacteria. Applied and Environmental Microbiology, 2022, 88, aem0232321. | 1.4 | 16 |
| 2768 | Identification of candidate type 3 effectors that determine host specificity associated with emerging Ralstonia pseudosolanacearum strains. European Journal of Plant Pathology, 2022, 163, 35-50. | 0.8 | 9 |
| 2770 | Genome diversity of domesticated Acinetobacter baumannii ATCC 19606T strains. Microbial Genomics, 2022, 8, . | 1.0 | 7 |
| 2771 | Complete de novo assembly of Wolbachia endosymbiont of Diaphorina citri Kuwayama (Hemiptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 | 1.6 | 14 |
| 2772 | Novel insights into Pinus species plastids genome through phylogenetic relationships and repeat sequence analysis. PLoS ONE, 2022, 17, e0262040. | 1.1 | 3 |
| 2773 | A PARTHENOGENESIS allele from apomictic dandelion can induce egg cell division without fertilization in lettuce. Nature Genetics, 2022, 54, 84-93. | 9.4 | 56 |
| 2774 | Complete Chloroplast Genome Sequence of Fagus longipetiolata Seemen (Fagaceae): Genome Structure, Adaptive Evolution, and Phylogenetic Relationships. Life, 2022, 12, 92. | 1.1 | 15 |
| 2775 | Systematics of <i>Mukdenia</i> and <i>Oresitrophe</i> (Saxifragaceae): Insights from genome skimming data. Journal of Systematics and Evolution, 2023, 61, 99-114. | 1.6 | 3 |
| 2776 | Structural and evolutive features of the Plinia phitrantha and P. cauliflora plastid genomes and evolutionary relationships within tribe Myrteae (Myrtaceae). Genetics and Molecular Biology, 2022, 45, e20210193. | 0.6 | 0 |
| 2777 | Characterization and validation of an alternative reference bacterium Korean Pharmacopoeia Staphylococcus aureus strain. Journal of Microbiology, 2022, 60, 187-191. | 1.3 | 1 |
| 2778 | Modular evolution of secretion systems and virulence plasmids in a bacterial species complex. BMC Biology, 2022, 20, 16. | 1.7 | 16 |
| 2780 | Chloroplast Genome Evolution in Four Montane Zingiberaceae Taxa in China. Frontiers in Plant Science, 2021, 12, 774482. | 1.7 | 16 |
| 2781 | Selective Isolation of Eggerthella lenta from Human Faeces and Characterisation of the Species Prophage Diversity. Microorganisms, 2022, 10, 195. | 1.6 | 9 |
| 2783 | Complete chloroplast genomes of Rubus species (Rosaceae) and comparative analysis within the genus. BMC Genomics, 2022, 23, 32. | 1.2 | 17 |
| 2784 | The first complete plastome of Mimusops coriacea (A. DC.) Miq. (Sapotaceae). Genetics and Molecular Biology, 2022, 45, e20210174. | 0.6 | 0 |
| 2785 | Complete Genome Sequences of Mycobacterium chimaera Strains 850 and 852, Isolated from Heater-Cooler Unit Water. Microbiology Resource Announcements, 2022, 11, e0102121. | 0.3 | 2 |
| 2786 | Plastome phylogenomics of Allaeanthus, Broussonetia and Malaisia (Dorstenieae, Moraceae) and the origin of B.ÂÃ— kazinoki. Journal of Plant Research, 2022, 135, 203-220. | 1.2 | 4 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2787 | The Complete Mitogenome of Elymus sibiricus and Insights Into Its Evolutionary Pattern Based on Simple Repeat Sequences of Seed Plant Mitogenomes. Frontiers in Plant Science, 2021, 12, 802321. | 1.7 | 21 |
| 2788 | Genomic Features and Pervasive Negative Selection in <i>Rhodanobacter</i> Strains Isolated from Nitrate and Heavy Metal Contaminated Aquifer. Microbiology Spectrum, 2022, 10, e0259121. | 1.2 | 8 |
| 2789 | The complete chloroplast genome sequencing analysis revealed an unusual IRs reduction in three species of subfamily Zygophylloideae. PLoS ONE, 2022, 17, e0263253. | 1.1 | 11 |
| 2790 | Comparative Genomic Analysis of Pathogenic Factors of Pectobacterium Species Isolated in South Korea Using Whole-Genome Sequencing. Plant Pathology Journal, 2022, 38, 12-24. | 0.7 | 1 |
| 2791 | Persistence and Dissemination Capacities of a blaNDM-5-Harboring IncX-3 Plasmid in Escherichia coli Isolated from an Urban River in Montpellier, France. Antibiotics, 2022, 11, 196. | 1.5 | 4 |
| 2792 | The plastome of Melocactus glaucescens Buining &amp; Brederoo reveals unique evolutionary features and loss of essential tRNA genes. Planta, 2022, 255, 57. | 1.6 | 5 |
| 2793 | Dissemination Routes of Carbapenem and Pan-Aminoglycoside Resistance Mechanisms in Hospital and Urban Wastewater Canalizations of Ghana. MSystems, 2022, 7, e0101921. | 1.7 | 7 |
| 2794 | Complete genome assembly of the levanâ€positive strain <scp>PVFi1</scp> of <i>Pseudomonas savastanoi</i> pv. <i>savastanoi</i> isolated from olive knots in Central Italy. Environmental Microbiology Reports, 2022, 14, 274-285. | 1.0 | 7 |
| 2795 | The complete chloroplast genome sequence of Cicer echinospermum, genome organization and comparison with related species. Scientia Horticulturae, 2022, 296, 110912. | 1.7 | 7 |
| 2796 | Evolutionary classification of tumor- and root-inducing plasmids based on T-DNAs and virulence regions. Molecular Phylogenetics and Evolution, 2022, 169, 107388. | 1.2 | 5 |
| 2798 | The Complete Chloroplast Genome Sequence of Cicer bijugum, Genome Organization, and Comparison with Related Species. Current Genomics, 2022, 23, 50-65. | 0.7 | 3 |
| 2799 | Endogenous CRISPR-Cas Systems in Group I Clostridium botulinum and Clostridium sporogenes Do Not Directly Target the Botulinum Neurotoxin Gene Cluster. Frontiers in Microbiology, 2021, 12, 787726. | 1.5 | 8 |
| 2800 | Comparison of Magnoliaceae Plastomes: Adding Neotropical Magnolia to the Discussion. Plants, 2022, 11, 448. | 1.6 | 7 |
| 2801 | The First Mitochondrial Genome of Ciborinia camelliae and Its Position in the Sclerotiniaceae Family. Frontiers in Fungal Biology, 2022, 2, . | 0.9 | 4 |
| 2802 | Long-Read Sequencing Reveals Genetic Adaptation of Bartonella Adhesin A Among Different Bartonella henselae Isolates. Frontiers in Microbiology, 2022, 13, 838267. | 1.5 | 9 |
| 2803 | Dual RNA sequencing reveals dendritic cell reprogramming in response to typhoidal Salmonella invasion. Communications Biology, 2022, 5, 111. | 2.0 | 11 |
| 2804 | Analysis of the Complete Plastomes of 31 Species of Hoya Group: Insights Into Their Comparative Genomics and Phylogenetic Relationships. Frontiers in Plant Science, 2021, 12, 814833. | 1.7 | 12 |
| 2805 | Defining the mutation sites in chickpea nodulation mutants PM233 and PM405. BMC Plant Biology, 2022, 22, 66. | 1.6 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2806 | Identification of Type VI Secretion Systems Effector Proteins That Contribute to Interbacterial Competition in Salmonella Dublin. Frontiers in Microbiology, 2022, 13, 811932. | 1.5 | 9 |
| 2807 | Aspergillus flavus La3279, a component strain of the Aflasafeâ„¢ biocontrol product, contains a partial aflatoxin biosynthesis gene cluster followed by a genomic region highly variable among A. flavus isolates. International Journal of Food Microbiology, 2022, 366, 109559. | 2.1 | 7 |
| 2808 | GEnView: a gene-centric, phylogeny-based comparative genomics pipeline for bacterial genomes and plasmids. Bioinformatics, 2022, 38, 1727-1728. | 1.8 | 6 |
| 2809 | Complete plastid genome of L. (Surianaceae) and its implications in phylogenetic reconstruction of Fabales. Journal of Genetics, 2019, 98, . | 0.4 | 0 |
| 2810 | Complete chloroplast genome of (Papilionoideae): molecular structures, comparative genome analysis and phylogenetic analysis. Journal of Genetics, 2020, 99, . | 0.4 | 7 |
| 2811 | Complete Genome Sequence of Four Strains of <i>Leptospira borgpetersenii</i> serovar Hardjo isolated from Cattle in the Central United States. Journal of Genomics, 2022, 10, 45-48. | 0.6 | 4 |
| 2812 | Trans-Regional and Cross-Host Spread of &lt;i&gt;mcr&lt;/i&gt;-Carrying Plasmids Revealed by Complete Plasmid Sequences â€" 44 Countries, 1998â^'2020. China CDC Weekly, 2022, 4, 242-248. | 1.0 | 6 |
| 2813 | Comparative mitochondrial genome analyses reveal conserved gene arrangement but massive expansion/contraction in two closely related Exserohilum pathogens. Computational and Structural Biotechnology Journal, 2022, 20, 1456-1469. | 1.9 | 4 |
| 2814 | The first de novo genome assembly and sex marker identification of Pluang Chomphu fish (Tor tambra) from Southern Thailand. Computational and Structural Biotechnology Journal, 2022, 20, 1470-1480. | 1.9 | 2 |
| 2815 | Phenotypic and Genomic Diversification in Complex Carbohydrate-Degrading Human Gut Bacteria. MSystems, 2022, 7, e0094721. | 1.7 | 40 |
| 2816 | Genome Mining and Analysis of PKS Genes in Eurotium cristatum E1 Isolated from Fuzhuan Brick Tea. Journal of Fungi (Basel, Switzerland), 2022, 8, 193. | 1.5 | 3 |
| 2817 | Isolation and Characterization of Levoglucosan-Metabolizing Bacteria. Applied and Environmental Microbiology, 2022, 88, AEM0186821. | 1.4 | 6 |
| 2818 | Comparative Genome Analysis of Two Bacillus pumilus Strains Producing High Level of Extracellular Hydrolases. Genes, 2022, 13, 409. | 1.0 | 8 |
| 2819 | Characterization and genomic analysis of a Demerecviridae phage SP76 with lytic multiple-serotypes of Salmonella. Archives of Microbiology, 2022, 204, 175. | 1.0 | 1 |
| 2821 | Experimental evaluation of ecological principles to understand and modulate the outcome of bacterial strain competition in gut microbiomes. ISME Journal, 2022, 16, 1594-1604. | 4.4 | 24 |
| 2822 | Population Dynamics of a Two Phagesâ€"One Host Infection System Using Escherichia coli Strain ECOR57 and Phages vB_EcoP_SU10 and vB_EcoD_SU57. Pharmaceuticals, 2022, 15, 268. | 1.7 | 2 |
| 2823 | Oxytetracycline and Streptomycin Resistance Genes in Xanthomonas arboricola pv. pruni, the Causal Agent of Bacterial Spot in Peach. Frontiers in Microbiology, 2022, 13, 821808. | 1.5 | 13 |
| 2824 | Decoding the Gene Variants of Two Native Probiotic Lactiplantibacillus plantarum Strains through Whole-Genome Resequencing: Insights into Bacterial Adaptability to Stressors and Antimicrobial Strength. Genes, 2022, 13, 443. | 1.0 | 6 |

| # | Article | IF | Citations |
|---|---|---|---|
| 2825 | The Use of Long-Read Sequencing Technologies in Infection Control: Horizontal Transfer of a blaCTX-M-27 Containing IncFII Plasmid in a Patient Screening Sample. Microorganisms, 2022, 10, 491. | 1.6 | 5 |
| 2826 | Phylogenomic and comparative analyses of Coffeeae alliance (Rubiaceae): deep insights into phylogenetic relationships and plastome evolution. BMC Plant Biology, 2022, 22, 88. | 1.6 | 17 |
| 2827 | Genomic and Phenotypic Characterization of the Nontoxigenic Clostridioides difficile Strain CCUG37785 and Demonstration of Its Therapeutic Potential for the Prevention of C. difficile Infection. Microbiology Spectrum, 2022, 10, e0178821. | 1.2 | 7 |
| 2828 | The <i>Bacillus</i> phage <scp>SPÎ²</scp> and its relatives: a temperate phage model system reveals new strains, species, prophage integration loci, conserved proteins and lysogeny management components. Environmental Microbiology, 2022, 24, 2098-2118. | 1.8 | 19 |
| 2829 | The Importance of Shiga Toxin-Producing Escherichia coli O145:NM[H28]/H28 Infections in Argentina, 1998â€"2020. Microorganisms, 2022, 10, 582. | 1.6 | 6 |
| 2830 | Use of Nanopore Sequencing to Characterise the Genomic Architecture of Mobile Genetic Elements Encoding blaCTX-M-15 in Escherichia coli Causing Travellersâ€™ Diarrhoea. Frontiers in Microbiology, 2022, 13, 862234. | 1.5 | 4 |
| 2831 | A mobile restrictionâ€"modification system provides phage defence and resolves an epigenetic conflict with an antagonistic endonuclease. Nucleic Acids Research, 2022, 50, 3348-3361. | 6.5 | 17 |
| 2834 | Complete Chloroplast Genomes and Comparative Analyses of Three Ornamental Impatiens Species. Frontiers in Genetics, 2022, 13, 816123. | 1.1 | 4 |
| 2835 | Complete Genome Assemblies of All Xanthomonas translucens Pathotype Strains Reveal Three Genetically Distinct Clades. Frontiers in Microbiology, 2021, 12, 817815. | 1.5 | 19 |
| 2836 | Ensifer meliloti L6-AK89, an Effective Inoculant of Medicago lupulina Varieties: Phenotypic and Deep-Genome Screening. Agronomy, 2022, 12, 766. | 1.3 | 8 |
| 2837 | The Space-Exposed Kombucha Microbial Community Member Komagataeibacter oboediens Showed Only Minor Changes in Its Genome After Reactivation on Earth. Frontiers in Microbiology, 2022, 13, 782175. | 1.5 | 5 |
| 2838 | CovDif, a Tool to Visualize the Conservation between SARS-CoV-2 Genomes and Variants. Viruses, 2022, 14, 561. | 1.5 | 1 |
| 2840 | Environmental Potential for Microbial 1,4-Dioxane Degradation Is Sparse despite Mobile Elements Playing a Role in Trait Distribution. Applied and Environmental Microbiology, 2022, 88, e0209121. | 1.4 | 8 |
| 2841 | Successful Intra- but Not Inter-species Recombination of msr(D) in Neisseria subflava. Frontiers in Microbiology, 2022, 13, 855482. | 1.5 | 1 |
| 2842 | <i>In Vitro</i> Evolution of Specific Phages Infecting the Fish Pathogen <i>Flavobacterium psychrophilum</i>. Phage, 2022, 3, 28-37. | 0.8 | 1 |
| 2843 | Comparative Genomic Analysis Reveals Intestinal Habitat Adaptation of LigilactobacillusÂequi Rich in Prophage and Degrading Cellulase. Molecules, 2022, 27, 1867. | 1.7 | 1 |
| 2844 | Identification of the Genes of the Plant Pathogen Pseudomonas syringae MB03 Required for the Nematicidal Activity Against Caenorhabditis elegans Through an Integrated Approach. Frontiers in Microbiology, 2022, 13, 826962. | 1.5 | 3 |
| 2845 | Characterization of strain-specific Bacillus cereus swimming motility and flagella by means of specific antibodies. PLoS ONE, 2022, 17, e0265425. | 1.1 | 3 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2846 | Independent Size Expansions and Intron Proliferation in Red Algal Plastid and Mitochondrial Genomes. Genome Biology and Evolution, 2022, 14, . | 1.1 | 5 |
| 2847 | Comparative genomic analysis of vertebrate mitochondrial reveals a differential of rearrangements rate between taxonomic class. Scientific Reports, 2022, 12, 5479. | 1.6 | 13 |
| 2848 | Complex mitogenomic rearrangements within the Pectinidae (Mollusca: Bivalvia). Bmc Ecology and Evolution, 2022, 22, 29. | 0.7 | 6 |
| 2849 | A comparative study on the genomes, transcriptomes, and metabolic properties of Escherichia coli strains Nissle 1917, BL21(DE3), and MG1655. Engineering Microbiology, 2022, 2, 100012. | 2.2 | 9 |
| 2850 | A high-quality reference genome for the fish pathogen Streptococcus iniae. Microbial Genomics, 2022, 8, . | 1.0 | 0 |
| 2851 | Screening of Potential Vibrio cholerae Bacteriophages for Cholera Therapy: A Comparative Genomic Approach. Frontiers in Microbiology, 2022, 13, 803933. | 1.5 | 4 |
| 2852 | Isolation of a Colistin-Susceptible MDR <i>Pantoea calida</i> Harboring the <i>mcr-9</i> Gene Suggests the Silent Spread of the Resistance Factor. Microbial Drug Resistance, 2022, 28, 408-412. | 0.9 | 2 |
| 2853 | Tracking habitat or testing its suitability? Similar distributional patterns can hide very different histories of persistence versus nonequilibrium dynamics. Evolution; International Journal of Organic Evolution, 2022, 76, 1209-1228. | 1.1 | 3 |
| 2854 | Genomic evolution and adaptation of arthropod-associated Rickettsia. Scientific Reports, 2022, 12, 3807. | 1.6 | 25 |
| 2855 | Genomic, biochemical, and phylogenetic evaluation of bacteria isolated from deep-sea sediment harboring methane hydrates. Archives of Microbiology, 2022, 204, 205. | 1.0 | 0 |
| 2856 | The complete plastomes of seven Peucedanum plants: comparative and phylogenetic analyses for the Peucedanum genus. BMC Plant Biology, 2022, 22, 101. | 1.6 | 25 |
| 2857 | Comparative analysis of complete Ilex (Aquifoliaceae) chloroplast genomes: insights into evolutionary dynamics and phylogenetic relationships. BMC Genomics, 2022, 23, 203. | 1.2 | 11 |
| 2858 | Lytic Phages against ST11 K47 Carbapenem-Resistant Klebsiella pneumoniae and the Corresponding Phage Resistance Mechanisms. MSphere, 2022, 7, e0008022. | 1.3 | 7 |
| 2859 | Comparative Draft Genomes of Leishmania orientalis Isolate PCM2 (Formerly Named Leishmania) Tj ETQq1 1 0.784314 rgBT /Overlock 1<br>Biology, 2022, 11, 515. | 1.3 | 6 |
| 2861 | Black pepper and tarragon essential oils suppress the lipolytic potential and the type II secretion system of P. psychrophila KM02. Scientific Reports, 2022, 12, 5487. | 1.6 | 2 |
| 2862 | Detection and characterisation of 16S rRNA methyltransferase-producing Pseudomonas aeruginosa from the UK and Republic of Ireland from 2003â€"2015. International Journal of Antimicrobial Agents, 2022, 59, 106550. | 1.1 | 8 |
| 2863 | Whole genome sequence analysis of Salmonella Typhi in Papua New Guinea reveals an established population of genotype 2.1.7 sensitive to antimicrobials. PLoS Neglected Tropical Diseases, 2022, 16, e0010306. | 1.3 | 6 |
| 2864 | Isolation and Characterization of Lytic Bacteriophages Targeting Diverse <i>Enterobacter</i> spp. Clinical Isolates. Phage, 2022, 3, 50-58. | 0.8 | 1 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2865 | Genetic Diversity of Antimicrobial Resistance and Key Virulence Features in Two Extensively Drug-Resistant Acinetobacter baumannii Isolates. International Journal of Environmental Research and Public Health, 2022, 19, 2870. | 1.2 | 4 |
| 2867 | Population genomics of the grapevine pathogen Eutypa lata reveals evidence for population expansion and intraspecific differences in secondary metabolite gene clusters. PLoS Genetics, 2022, 18, e1010153. | 1.5 | 10 |
| 2868 | Comparative and phylogenetic analyses of six Kenya Polystachya (Orchidaceae) species based on the complete chloroplast genome sequences. BMC Plant Biology, 2022, 22, 177. | 1.6 | 37 |
| 2869 | Rates of evolutionary change of resident Escherichia coli O157:H7 differ within the same ecological niche. BMC Genomics, 2022, 23, 275. | 1.2 | 3 |
| 2870 | Comparative Genomic Analysis of a Pantonâ€"Valentine Leukocidin-Positive ST22 Community-Acquired Methicillin-Resistant Staphylococcus aureus from Pakistan. Antibiotics, 2022, 11, 496. | 1.5 | 6 |
| 2871 | Genome Wide Analysis of the Potato Soft Rot Pathogen Pectobacterium carotovorum Strain ICMP 5702 to Predict Novel Insights into Its Genetic Features. Plant Pathology Journal, 2022, 38, 102-114. | 0.7 | 1 |
| 2872 | Safety Assessment of Lactiplantibacillus plantarum TWK10 Based on Whole-Genome Sequencing, Phenotypic, and Oral Toxicity Analysis. Microorganisms, 2022, 10, 784. | 1.6 | 9 |
| 2873 | Bifidobacterium longum subsp. longum K5 alleviates inflammatory response and prevents intestinal barrier injury induced by LPS in vitro based on comparative genomics. Journal of Functional Foods, 2022, 92, 105030. | 1.6 | 10 |
| 2874 | Comparative mitochondrial genomes of the Rhus gall aphid Kaburagia rhusicola subspecies with variable gall shapes. Gene, 2022, 824, 146379. | 1.0 | 0 |
| 2875 | Genetic characterization and comparative genomics of a multi drug resistant (MDR) Escherichia coli SCM-21 isolated from a subclinical case of bovine mastitis. Comparative Immunology, Microbiology and Infectious Diseases, 2022, 85, 101799. | 0.7 | 6 |
| 2876 | Isolation and genomic analysis of temperate phage 5W targeting multidrug-resistant Acinetobacter baumannii. Archives of Microbiology, 2022, 204, 58. | 1.0 | 9 |
| 2877 | A dual endosymbiosis supports nutritional adaptation to hematophagy in the invasive tick Hyalomma marginatum. ELife, 2021, 10, . | 2.8 | 32 |
| 2878 | Genomic diversity of antimicrobial resistance in non-typhoidal Salmonella in Victoria, Australia. Microbial Genomics, 2021, 7, . | 1.0 | 2 |
| 2879 | Analyses of Chloroplast Genome of Eutrema japonicum Provide New Insights into the Evolution of Eutrema Species. Agronomy, 2021, 11, 2546. | 1.3 | 5 |
| 2880 | Increased Pathogenicity of the Nematophagous Fungus Drechmeria coniospora Following Long-Term Laboratory Culture. Frontiers in Fungal Biology, 2021, 2, . | 0.9 | 0 |
| 2881 | Comparative Chloroplast Genomics of Sophora Species: Evolution and Phylogenetic Relationships in the Early-Diverging Legume Subfamily Papilionoideae (Fabaceae). Frontiers in Plant Science, 2021, 12, 778933. | 1.7 | 7 |
| 2882 | Genomic comparison and phenotypic profiling of small colony variants of Burkholderia pseudomallei. PLoS ONE, 2021, 16, e0261382. | 1.1 | 1 |
| 2883 | Proteome and secretome profiling of zinc availability in Cryptococcus neoformans identifies Wos2 as a subtle influencer of fungal virulence determinants. BMC Microbiology, 2021, 21, 341. | 1.3 | 6 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 2884 | Prochlorococcus have low global mutation rate and small effective population size. Nature Ecology and Evolution, 2022, 6, 183-194. | 3.4 | 16 |
| 2885 | Signatures of Adaptation in Mitochondrial Genomes of Palearctic Subterranean Voles (Arvicolinae,) Tj ETQq1 1 0.784314 rgBT /Overlo | 1.0 | 5 |
| 2886 | Assembling the puzzle: Complete chloroplast genome sequences of Discocactus bahiensis Britton &amp; Rose and Melocactus ernestii Vaupel (Cactaceae) and their evolutionary significance. Revista Brasileira De Botanica, 2021, 44, 877-888. | 0.5 | 3 |
| 2887 | Plastome Diversity and Phylogenomic Relationships in Asteraceae. Plants, 2021, 10, 2699. | 1.6 | 13 |
| 2888 | Mobilization of vitamin B12 transporters alters competitive dynamics in a human gut microbe. Cell Reports, 2021, 37, 110164. | 2.9 | 8 |
| 2889 | Prevalence of an Insect-Associated Genomic Region in Environmentally Acquired <i>Burkholderiaceae</i> Symbionts. Applied and Environmental Microbiology, 2022, 88, e0250221. | 1.4 | 2 |
| 2890 | Comparative Genomic Analysis Reveals Potential Pathogenicity and Slow-Growth Characteristics of Genus <i>Brevundimonas</i> and Description of <i>Brevundimonas pishanensis</i> sp. nov.. Microbiology Spectrum, 2022, 10, e0246821. | 1.2 | 5 |
| 2891 | GenomeSyn: a bioinformatics tool for visualizing genome synteny and structural variations. Journal of Genetics and Genomics, 2022, 49, 1174-1176. | 1.7 | 16 |
| 2892 | Antimicrobial resistance and genetic background of non-typhoidal Salmonella enterica strains isolated from human infections in SÃ£o Paulo, Brazil (2000â€“2019). Brazilian Journal of Microbiology, 2022, 53, 1249-1262. | 0.8 | 5 |
| 2894 | Comparative Genomic Analysis of Vibrio cincinnatiensis Provides Insights into Genetic Diversity, Evolutionary Dynamics, and Pathogenic Traits of the Species. International Journal of Molecular Sciences, 2022, 23, 4520. | 1.8 | 3 |
| 2895 | Genomic Insights into Omega-3 Polyunsaturated Fatty Acid Producing Shewanella sp. N2AIL from Fish Gut. Biology, 2022, 11, 632. | 1.3 | 4 |
| 2896 | Diversity of genomic clusters and CfiA/cfiA alleles in Bacteroides fragilis isolates from human and animals. Anaerobe, 2022, 75, 102567. | 1.0 | 5 |
| 3322 | Integrative Genomics Sheds Light on Evolutionary Forces Shaping the Acidithiobacillia Class Acidophilic Lifestyle. Frontiers in Microbiology, 2021, 12, 822229. | 1.5 | 10 |
| 3323 | Wolbachia endosymbionts in two Anopheles species indicates independent acquisitions and lack of prophage elements. Microbial Genomics, 2022, 8, . | 1.0 | 3 |
| 3324 | Construction and Analysis of the Complete Genome Sequence of Leprosy Agent Mycobacterium lepromatosis. Microbiology Spectrum, 2022, 10, e0169221. | 1.2 | 7 |
| 3325 | Whole genome sequencing and taxonomic profiling of two Pantoea sp. isolated from environmental samples in Israel. BMC Genomic Data, 2022, 23, 31. | 0.7 | 1 |
| 3326 | Gene loss, genome rearrangement, and accelerated substitution rates in plastid genome of Hypericum ascyron (Hypericaceae). BMC Plant Biology, 2022, 22, 135. | 1.6 | 16 |
| 3327 | Comparative analysis of the complete mitochondrial genomes of four cordyceps fungi. Ecology and Evolution, 2022, 12, e8818. | 0.8 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 3328 | Tracking the Origins of Pseudomonas aeruginosa Phylogroups by Diversity and Evolutionary Analysis of Important Pathogenic Marker Genes. Diversity, 2022, 14, 345. | 0.7 | 3 |
| 3329 | Genome Resource of <i>Colletotrichum spaethianum</i>, the Causal Agent of Leaf Anthracnose in <i>Polygonatum falcatum</i>. PhytoFrontiers, 2022, 2, 152-155. | 0.8 | 6 |
| 3330 | Genomic Analysis of Two Representative Strains of Shewanella putrefaciens Isolated from Bigeye Tuna: Biofilm and Spoilage-Associated Behavior. Foods, 2022, 11, 1261. | 1.9 | 8 |
| 3332 | Complete Genome Sequences of Four Strains ofÂ<i>ErwiniaÂtracheiphila</i>: A Resource for Studying aÂBacterial Plant Pathogen with a Highly Complex Genome. Molecular Plant-Microbe Interactions, 2022, 35, 500-504. | 1.4 | 4 |
| 3333 | Genomic Comparison of Eight Closed Genomes of Multidrug-Resistant Salmonella enterica Strains Isolated From Broiler Farms and Processing Plants in Trinidad and Tobago. Frontiers in Microbiology, 2022, 13, . | 1.5 | 2 |
| 3334 | Genomic analysis of two Chinese isolates of hyphantria cunea nucleopolyhedrovirus reveals a novel species of alphabaculovirus that infects hyphantria cunea drury (lepidoptera: arctiidae). BMC Genomics, 2022, 23, 367. | 1.2 | 2 |
| 3335 | Sequence Analysis of the Complete Mitochondrial Genome of a Medicinal Plant, Vitex rotundifolia Linnaeus f. (Lamiales: Lamiaceae). Genes, 2022, 13, 839. | 1.0 | 11 |
| 3336 | Comparative Genomics of Synechococcus elongatus Explains the Phenotypic Diversity of the Strains. MBio, 2022, 13, e0086222. | 1.8 | 13 |
| 3337 | Genomic and Phenotypic Characterization of Clostridium botulinum Isolates from an Infant Botulism Case Suggests Adaptation Signatures to the Gut. MBio, 2022, 13, e0238421. | 1.8 | 5 |
| 3338 | Description of a novel IncP plasmid harboring blaKPC-2 recovered from a SPM-1-producing Pseudomonas aeruginosa from ST277. Infection, Genetics and Evolution, 2022, , 105302. | 1.0 | 4 |
| 3339 | The genetic basis of natural variation in the timing of vegetative phase change in<i>Arabidopsis thaliana</i>. Development (Cambridge), 2022, 149, . | 1.2 | 8 |
| 3340 | B-assembler: a circular bacterial genome assembler. BMC Genomics, 2022, 23, 361. | 1.2 | 3 |
| 3341 | Genomic insights into the diversity of non-coding RNAs in Bacillus cereus sensu lato. Current Genetics, 2022, , . | 0.8 | 0 |
| 3342 | Structural Variation of Plastomes Provides Key Insight Into the Deep Phylogeny of Ferns. Frontiers in Plant Science, 2022, 13, . | 1.7 | 11 |
| 3343 | Distribution of pBS72-like conjugative plasmids among natural bacteria of the genus &lt;i&gt;Bacillus&lt;/i&gt;. Vestsi Natsyianal'nai Akademii Navuk Belarusi Seryia Biialahichnykh Navuk, 2022, 67, 219-228. | 0.2 | 0 |
| 3344 | Biochemical and molecular characterization of three serologically different Vibrio harveyi strains isolated from farmed Dicentrarchus labrax from the Adriatic Sea. Scientific Reports, 2022, 12, 7309. | 1.6 | 4 |
| 3345 | Dressing like a pathogen: Comparative analysis of different Pseudomonas genomospecies wearing different features to infect Corylus avellana. Journal of Phytopathology, 2022, 170, 504-516. | 0.5 | 4 |
| 3346 | Whole Genome Sequencing and Biological Characteristics of Two Strains of Porcine Escherichia coli Isolated from Saba Pigs. Current Microbiology, 2022, 79, 182. | 1.0 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 3347 | Genomic characterization of lytic bacteriophages targeting genetically diverse Pseudomonas aeruginosa clinical isolates. IScience, 2022, 25, 104372. | 1.9 | 16 |
| 3348 | Comparative genomics among cyst nematodes reveals distinct evolutionary histories among effector families and an irregular distribution of effectorâ€associated promoter motifs. Molecular Ecology, 2023, 32, 1515-1529. | 2.0 | 7 |
| 3349 | Draft genome sequence of Bacillus sp. strain FSQ1, a biological control agent against white mold in common bean (Phaseolus vulgaris L.). Current Research in Microbial Sciences, 2022, 3, 100138. | 1.4 | 3 |
| 3350 | Sequence-based pangenomic core detection. IScience, 2022, 25, 104413. | 1.9 | 5 |
| 3351 | High Prevalence of blaCTXMâ€“1/IncI1-Iî³/ST3 Plasmids in Extended-Spectrum Î²-Lactamase-Producing Escherichia coli Isolates Collected From Domestic Animals in Guadeloupe (French West Indies). Frontiers in Microbiology, 2022, 13, . | 1.5 | 3 |
| 3352 | Streptomyces benahoarensis sp. nov. Isolated From a Lava Tube of La Palma, Canary Islands, Spain. Frontiers in Microbiology, 2022, 13, . | 1.5 | 3 |
| 3353 | Genome mining of Burkholderia ambifaria strain T16, a rhizobacterium able to produce antimicrobial compounds and degrade the mycotoxin fusaric acid. World Journal of Microbiology and Biotechnology, 2022, 38, 114. | 1.7 | 8 |
| 3356 | Chromosome organization affects genome evolution in Sulfolobus archaea. Nature Microbiology, 2022, 7, 820-830. | 5.9 | 12 |
| 3357 | Widespread stop-codon recoding in bacteriophages may regulate translation of lytic genes. Nature Microbiology, 2022, 7, 918-927. | 5.9 | 25 |
| 3358 | Multi-omics analysis reveals the mechanism of seed coat color formation in Brassica rapa L.. Theoretical and Applied Genetics, 2022, 135, 2083-2099. | 1.8 | 7 |
| 3359 | Evolutionary Dynamics and Lateral Gene Transfer in Raphidophyceae Plastid Genomes. Frontiers in Plant Science, 2022, 13, . | 1.7 | 3 |
| 3360 | Genomic structural plasticity of rodentâ€associated <i>Bartonella</i> in nature. Molecular Ecology, 0, , . | 2.0 | 1 |
| 3363 | Complete Genome Sequence of Streptomyces albus Strain G153. Microbiology Resource Announcements, 0, , . | 0.3 | 1 |
| 3364 | Genome of Malassezia arunalokei and Its Distribution on Facial Skin. Microbiology Spectrum, 2022, 10, . | 1.2 | 7 |
| 3365 | Natural Products Produced in Culture by Biosynthetically Talented Salinispora arenicola Strains Isolated from Northeastern and South Pacific Marine Sediments. Molecules, 2022, 27, 3569. | 1.7 | 1 |
| 3366 | The Maternal Donor of Chrysanthemum Cultivars Revealed by Comparative Analysis of the Chloroplast Genome. Frontiers in Plant Science, 2022, 13, . | 1.7 | 8 |
| 3367 | Phenotypic characterization and analysis of complete genomes of two distinct strains of the proposed species â€œL. swaminathaniiâ€• Scientific Reports, 2022, 12, . | 1.6 | 6 |
| 3368 | Physiological and biochemical characterization and genome analysis of Rhodococcus qingshengii strain 7B capable of crude oil degradation and plant stimulation. Biotechnology Reports (Amsterdam,) Tj ETQq1 1 0.784314 rgBT /Over | 2.7 | 6 |

| # | Article | IF | Citations |
|---|---|---|---|
| 3373 | Experimental Pathogenicity and Comparative Genome Analysis of High- and Low-Virulence Strains of Rabbit-Origin Pasteurella Multocida. SSRN Electronic Journal, 0, , . | 0.4 | 0 |
| 3374 | Rediscovering â€œBaculovirus-Aâ€•(Johnson, 1976): The Complete Genome of â€˜Callinectes Sapidus Nudivirusâ€™ (Nudiviridae: Gammanudivirus). SSRN Electronic Journal, 0, , . | 0.4 | 0 |
| 3375 | Whole-genome analysis of Bacillus subtilis G8 isolated from natto. Biodiversitas, 2022, 23, . | 0.2 | 0 |
| 3376 | Characterization of the Complete Chloroplast Genome Sequence of the Socotra Dragon`s Blood Tree (Dracaena cinnabari Balf.). Forests, 2022, 13, 932. | 0.9 | 3 |
| 3377 | Suggestion for a new bacteriophage genus for the Klebsiella pneumoniae phageÂvB_KpnS-Carvaje. Current Genetics, 2022, 68, 393-406. | 0.8 | 3 |
| 3378 | Plastome characteristics and species identification of Chinese medicinal wintergreens (Gaultheria,) Tj ETQq1 1 0.784314 rgBT /Overlo | 1.8 | 4 |
| 3379 | Complete genome sequences and genomic characterization of five plasmids harbored by environmentally persistent Cronobacter sakazakii strains ST83 H322 and ST64 GK1025B obtained from powdered infant formula manufacturing facilities. Gut Pathogens, 2022, 14, . | 1.6 | 4 |
| 3380 | The compact mitogenome of <i>Ceratocystiopsis pallidobrunnea</i>. Canadian Journal of Microbiology, 2022, 68, 569-575. | 0.8 | 1 |
| 3381 | Characterization and Complete Genomic Analysis of Vibrio Parahaemolyticus-Infecting Phage KIT05. Current Microbiology, 2022, 79, . | 1.0 | 3 |
| 3382 | Complete Genome Sequences of Rhizobium gallicum M101 and Two Potential New <i>Rhizobium</i> Species Isolated from Soils in Central Canada. Microbiology Resource Announcements, 2022, 11, . | 0.3 | 1 |
| 3383 | New insights into intergeneric relationships of Hickeliinae (Poaceae: Bambusoideae) revealed by complete plastid genomes. Plant Diversity, 2023, 45, 125-132. | 1.8 | 1 |
| 3385 | Discovery of the First Lytic <i>Staphylococcus pseudintermedius</i>/<i>Staphylococcus aureus</i> Polyvalent Bacteriophages. Phage, 2022, 3, 116-124. | 0.8 | 1 |
| 3386 | Accumulation of endosymbiont genomes in an insect autosome followed by endosymbiont replacement. Current Biology, 2022, 32, 2786-2795.e5. | 1.8 | 8 |
| 3387 | Simplexviruses Successfully Adapt to Their Host by Fine-Tuning Immune Responses. Molecular Biology and Evolution, 2022, 39, . | 3.5 | 3 |
| 3388 | Taxonomic Re-Evaluation and Genomic Comparison of Novel Extracellular Electron Uptake-Capable RhodovulumÂvisakhapatnamense and Rhodovulum sulfidophilum Isolates. Microorganisms, 2022, 10, 1235. | 1.6 | 0 |
| 3389 | Annotation-free delineation of prokaryotic homology groups. PLoS Computational Biology, 2022, 18, e1010216. | 1.5 | 0 |
| 3390 | The organellar genomes of Silvetia siliquosa (Fucales, Phaeophyceae) and comparative analyses of the brown algae. PLoS ONE, 2022, 17, e0269631. | 1.1 | 0 |
| 3391 | Genome Sequences of Two New Pandoravirus Strains Isolated from Brazil and France. Microbiology Resource Announcements, 2022, 11, . | 0.3 | 1 |

| # | Article | IF | Citations |
|---|---|---|---|
| 3392 | Chromosome-scale assembly with a phased sex-determining region resolves features of early Z and W chromosome differentiation in a wild octoploid strawberry. G3: Genes, Genomes, Genetics, 2022, 12, . | 0.8 | 11 |
| 3393 | Draft genome sequence and functional analysis of Lysinibacillus xylanilyticus t26, a plant growth-promoting bacterium isolated from Capsicum chinense rhizosphere. Journal of Biosciences, 2022, 47, . | 0.5 | 2 |
| 3394 | Phylogenomic and functional characterization of an evolutionary conserved cytochrome P450-based insecticide detoxification mechanism in bees. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 3.3 | 31 |
| 3395 | Reclassification of Streptococcus ilei as a later heterotypic synonym of Streptococcus koreensis based on whole-genome sequence analysis. Archives of Microbiology, 2022, 204, . | 1.0 | 1 |
| 3396 | Widespread phages of endosymbionts: Phage WO genomics and the proposed taxonomic classification of Symbioviridae. PLoS Genetics, 2022, 18, e1010227. | 1.5 | 22 |
| 3397 | PRODUCTION OF MANNOSYLERYTHRITOL LIPIDS: BIOSYNTHESIS, MULTI-OMICS APPROACHES AND COMMERCIAL EXPLOITATION. Molecular Omics, 0, , . | 1.4 | 0 |
| 3398 | Chromosome-level assembly and annotation of the blue catfish<i>Ictalurus furcatus</i>, an aquaculture species for hybrid catfish reproduction, epigenetics, and heterosis studies. GigaScience, 2022, 11, . | 3.3 | 8 |
| 3399 | Virulence plasmid pINV as a genetic signature for Shigella flexneri phylogeny. Microbial Genomics, 2022, 8, . | 1.0 | 3 |
| 3400 | Plastid Phylogenomics and Plastome Evolution of Nandinoideae (Berberidaceae). Frontiers in Plant Science, 0, 13, . | 1.7 | 2 |
| 3401 | The complete chloroplast genome of the Egyptian henbane (<i>Hyoscyamus muticus</i> L., Solanaceae). Mitochondrial DNA Part B: Resources, 2022, 7, 1109-1111. | 0.2 | 1 |
| 3402 | Comparative Genome Analysis of Two Heterotrophic Nitrifying Pseudomonas putida Strains Isolated from Freshwater Shrimp Ponds in Soc Trang Province. Fermentation, 2022, 8, 336. | 1.4 | 1 |
| 3403 | Revised Species Delimitation in the Giant Water Lily Genus Victoria (Nymphaeaceae) Confirms a New Species and Has Implications for Its Conservation. Frontiers in Plant Science, 0, 13, . | 1.7 | 9 |
| 3404 | Identification of Peptoniphilus vaginalis-Like Bacteria, Peptoniphilus septimus sp. nov., From Blood Cultures in a Cervical Cancer Patient Receiving Chemotherapy: Case and Implications. Frontiers in Cellular and Infection Microbiology, 0, 12, . | 1.8 | 3 |
| 3405 | Characterization of Bordetella pertussis Strains Isolated from India. Pathogens, 2022, 11, 794. | 1.2 | 1 |
| 3406 | Comparative genomics of Nocardia seriolae reveals recent importation and subsequent widespread dissemination in mariculture farms in the South Central Coast region, Vietnam. Microbial Genomics, 2022, 8, . | 1.0 | 1 |
| 3407 | Within-host evolution of a gut pathobiont facilitates liver translocation. Nature, 2022, 607, 563-570. | 13.7 | 65 |
| 3408 | Characterization and phylogenetic analysis of the complete mitochondrial genome sequence of Diospyros oleifera, the first representative from the family Ebenaceae. Heliyon, 2022, 8, e09870. | 1.4 | 5 |
| 3409 | Structural Characterization of the Acer ukurunduense Chloroplast Genome Relative to Related Species in the Acer Genus. Frontiers in Genetics, 0, 13, . | 1.1 | 0 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 3410 | The C-Terminal Repeat Units of SpaA Mediate Adhesion of Erysipelothrix rhusiopathiae to Host Cells and Regulate Its Virulence. Biology, 2022, 11, 1010. | 1.3 | 1 |
| 3412 | A Chromosome Level Genome Assembly of a Winter Turnip Rape (Brassica rapa L.) to Explore the Genetic Basis of Cold Tolerance. Frontiers in Plant Science, 0, 13, . | 1.7 | 4 |
| 3413 | Genetic Characteristics and Enzymatic Activities of Bacillus velezensis KS04AU as a Stable Biocontrol Agent against Phytopathogens. International Journal of Plant Biology, 2022, 13, 201-222. | 1.1 | 10 |
| 3414 | Sympatric Recombination in Zoonotic Cryptosporidium Leads to Emergence of Populations with Modified Host Preference. Molecular Biology and Evolution, 2022, 39, . | 3.5 | 10 |
| 3416 | Analysis of 90 Listeria monocytogenes contaminated in poultry and livestock meat through whole-genome sequencing. Food Research International, 2022, 159, 111641. | 2.9 | 8 |
| 3417 | Identification of sex-specific markers and ZW-chromosome DNA clones from the genomic BAC library of the Chinese mitten crab Eriocheir sinensis. Aquaculture, 2022, 560, 738576. | 1.7 | 2 |
| 3418 | Comparative Analysis of the Complete Chloroplast Genomes in Allium Section Bromatorrhiza Species (Amaryllidaceae): Phylogenetic Relationship and Adaptive Evolution. Genes, 2022, 13, 1279. | 1.0 | 5 |
| 3419 | Time Series Genomics of Pseudomonas aeruginosa Reveals the Emergence of a Hypermutator Phenotype and Within-Host Evolution in Clinical Inpatients. Microbiology Spectrum, 2022, 10, . | 1.2 | 2 |
| 3420 | Characterization and Fitness Cost of Tn7100, a Novel Integrative and Conjugative Element Conferring Multidrug Resistance in Haemophilus influenzae. Frontiers in Microbiology, 0, 13, . | 1.5 | 3 |
| 3421 | Molecular Characterization of pBOq-IncQ and pBOq-95LK Plasmids of Escherichia coli BOq 01, a New Isolated Strain from Poultry Farming, Involved in Antibiotic Resistance. Microorganisms, 2022, 10, 1509. | 1.6 | 2 |
| 3422 | Phylogenomic analysis of <i>Salmonella</i> Indiana ST17, an emerging MDR clonal group in China. Journal of Antimicrobial Chemotherapy, 2022, 77, 2937-2945. | 1.3 | 7 |
| 3424 | Genomic evaluation of novel Kenyan virulent phage isolates infecting carbapenemase-producing Klebsiella pneumoniae and safety determination of their lysates in Balb/c mice. Archives of Microbiology, 2022, 204, . | 1.0 | 4 |
| 3425 | Comparative Genome Analyses of Plant Rust Pathogen Genomes Reveal a Confluence of Pathogenicity Factors to Quell Host Plant Defense Responses. Plants, 2022, 11, 1962. | 1.6 | 3 |
| 3426 | Complete chloroplast genomes and phylogeny in three Euterpe palms (E. edulis, E. oleracea and E.) Tj ETQq1 1 0.784314 rgBT /Overlock | 1.1 | 2 |
| 3427 | New <i>Microviridae</i> isolated from <i>Sulfitobacter</i> reveals two cosmopolitan subfamilies of single-stranded DNA phages infecting marine and terrestrial Alphaproteobacteria. Virus Evolution, 2022, 8, . | 2.2 | 5 |
| 3428 | Genomic and Functional Characterization of Vancomycin-Resistant Enterococci-Specific Bacteriophages in the Galleria mellonella Wax Moth Larvae Model. Pharmaceutics, 2022, 14, 1591. | 2.0 | 7 |
| 3430 | Comparative Genomics of Escherichia coli Serotype O55:H7 Using Complete Closed Genomes. Microorganisms, 2022, 10, 1545. | 1.6 | 0 |
| 3431 | Hidden dissemination of carbapenem-susceptible OXA-48-producing <i>Proteus mirabilis</i>. Journal of Antimicrobial Chemotherapy, 2022, 77, 3009-3015. | 1.3 | 4 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 3432 | Phylogenetic and Multiple-Locus Variable number tandem repeat analysis of Mycobacterium avium subsp. paratuberculosis isolates from Argentina. Veterinary Research Communications, 2022, 46, 1121-1129. | 0.6 | 2 |
| 3433 | Two New <i>Rhizobiales</i> Species Isolated from Root Nodules of Common Sainfoin (Onobrychis) Tj ETQq1 1 0.784314 rgBT /Overlo | 1.2 | 6 |
| 3434 | Intrinsic tet(L) sub-class in Bacillus velezensis and Bacillus amyloliquefaciens is associated with a reduced susceptibility toward tetracycline. Frontiers in Microbiology, 0, 13, . | 1.5 | 1 |
| 3436 | <i>FLOWERING LOCUS T</i> indel variants confer vernalization-independent and photoperiod-insensitive flowering of yellow lupin (<i>Lupinus luteus</i> L.). Horticulture Research, 0, , . | 2.9 | 0 |
| 3437 | Genomic insights into symbiosis and host adaptation of an ascidian-associated bacterium Bacillus aryabhattai MCCB 387. Symbiosis, 0, , . | 1.2 | 0 |
| 3438 | PanExplorer: a web-based tool for exploratory analysis and visualization of bacterial pan-genomes. Bioinformatics, 2022, 38, 4412-4414. | 1.8 | 3 |
| 3439 | Genomic features of Mycoplasma bovis subtypes currently circulating in France. BMC Genomics, 2022, 23, . | 1.2 | 2 |
| 3440 | The transcriptional regulator CtrA controls gene expression in Alphaproteobacteria phages: Evidence for a lytic deferment pathway. Frontiers in Microbiology, 0, 13, . | 1.5 | 4 |
| 3441 | Comparative genomic analysis of five freshwater cyanophages and reference-guided metagenomic data mining. Microbiome, 2022, 10, . | 4.9 | 8 |
| 3442 | Bioinformatics and its role in the study of the evolution and probiotic potential of lactic acid bacteria. Food Science and Biotechnology, 2023, 32, 389-412. | 1.2 | 4 |
| 3443 | Genomic analysis reveals the role of integrative and conjugative elements in plant pathogenic bacteria. Mobile DNA, 2022, 13, . | 1.3 | 6 |
| 3444 | Isolation and Characterization of the Lytic Pseudoxanthomonas kaohsiungensi Phage PW916. Viruses, 2022, 14, 1709. | 1.5 | 4 |
| 3446 | Insights into Evolutionary, Genomic, and Biogeographic Characterizations of Chryseobacterium nepalense Represented by a Polyvinyl Alcohol-Degrading Bacterium, AC3. Microbiology Spectrum, 2022, 10, . | 1.2 | 1 |
| 3447 | Genomic comparison of Planktothrix agardhii isolates from a Lake Erie embayment. PLoS ONE, 2022, 17, e0273454. | 1.1 | 6 |
| 3448 | A large chromosomal inversion affects antimicrobial sensitivity of Escherichia coli to sodium deoxycholate. Microbiology (United Kingdom), 2022, 168, . | 0.7 | 2 |
| 3450 | Complete genome sequence of a multiple-stress-tolerant bacterium Halomonas piezotolerans NBT06E8T isolated from a deep-sea sediment sample of the New Britain Trench. 3 Biotech, 2022, 12, . | 1.1 | 1 |
| 3451 | In silico analysis reveals the co-existence of CRISPR-Cas type I-F1 and type I-F2 systems and its association with restricted phage invasion in Acinetobacter baumannii. Frontiers in Microbiology, 0, 13, . | 1.5 | 5 |
| 3452 | Genome Sequence of a Potent Biosurfactant-Producing Bacterium, <i>Franconibacter</i> sp. Strain IITDAS19. Microbiology Resource Announcements, 2022, 11, . | 0.3 | 0 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 3453 | Microbiota of the Pregnant Mouse: Characterization of the Bacterial Communities in the Oral Cavity, Lung, Intestine, and Vagina through Culture and DNA Sequencing. Microbiology Spectrum, 2022, 10, . | 1.2 | 6 |
| 3454 | Genomic and Phenotypic Characterization of Cutibacterium acnes Bacteriophages Isolated from Acne Patients. Antibiotics, 2022, 11, 1041. | 1.5 | 5 |
| 3455 | First report and whole-genome sequencing of Pseudochrobactrum saccharolyticum in Latin America. Microbes and Infection, 2023, 25, 105018. | 1.0 | 0 |
| 3456 | The Sixth Element: a 102-kb RepABC Plasmid of Xenologous Origin Modulates Chromosomal Gene Expression in Dinoroseobacter shibae. MSystems, 0, , . | 1.7 | 0 |
| 3457 | Sequencing and comparative analysis of chloroplast genomes of three medicinal plants: Gentiana manshurica, G. scabra and G. triflora. Physiology and Molecular Biology of Plants, 0, , . | 1.4 | 3 |
| 3458 | The microbiome of a bacterivorous marine choanoflagellate contains a resource-demanding obligate bacterial associate. Nature Microbiology, 2022, 7, 1466-1479. | 5.9 | 5 |
| 3459 | New Insights Into the Backbone Phylogeny and Character Evolution of Corydalis (Papaveraceae) Based on Plastome Data. Frontiers in Plant Science, 0, 13, . | 1.7 | 4 |
| 3460 | Comprehensive investigation of antibiotic resistance gene content in cfiA-harboring Bacteroides fragilis isolates of human and animal origins by whole genome sequencing. International Journal of Medical Microbiology, 2022, 312, 151559. | 1.5 | 8 |
| 3461 | Histological characterization of anther structure in Tetep-cytoplasmic male sterility and fine mapping of restorer-of-fertility gene in rice. PLoS ONE, 2022, 17, e0268174. | 1.1 | 0 |
| 3462 | Development and evaluation of temperature-sensitive <i>Mycoplasma anserisalpingitidis</i> clones as vaccine candidates. Avian Pathology, 2022, 51, 535-549. | 0.8 | 2 |
| 3463 | CulebrONT: a streamlined long reads multi-assembler pipeline for prokaryotic and eukaryotic genomes. , 0, 2, . |  | 5 |
| 3464 | Structural mutations of small single copy (SSC) region in the plastid genomes of five Cistanche species and inter-species identification. BMC Plant Biology, 2022, 22, . | 1.6 | 5 |
| 3465 | Phylogenetic analysis based on single-copy orthologous proteins in highly variable chloroplast genomes of Corydalis. Scientific Reports, 2022, 12, . | 1.6 | 1 |
| 3467 | The chloroplast genome of Salix floderusii and characterization of chloroplast regulatory elements. Frontiers in Plant Science, 0, 13, . | 1.7 | 2 |
| 3469 | Genomic characteristics of two most widely used BCG vaccine strains: Danish 1331 and Pasteur 1173P2. BMC Genomics, 2022, 23, . | 1.2 | 1 |
| 3470 | Phage Resistance Accompanies Reduced Fitness of Uropathogenic Escherichia coli in the Urinary Environment. MSphere, 2022, 7, . | 1.3 | 12 |
| 3471 | Molecular Factors and Mechanisms Driving Multidrug Resistance in Uropathogenic Escherichia coliâ€"An Update. Genes, 2022, 13, 1397. | 1.0 | 19 |
| 3472 | Tracking the Transmission of Antimicrobial-Resistant Non-O157 <i>Escherichia coli</i> and <i>Salmonella</i> Isolates at the Interface of Food Animals and Fresh Produce from Agriculture Operations Using Whole-Genome Sequencing. Foodborne Pathogens and Disease, 0, , . | 0.8 | 0 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 3473 | Rediscovering â€œBaculovirus-Aâ€•(Johnson, 1976): The complete genome of â€˜Callinectes sapidus nudivirusâ€™ Journal of Invertebrate Pathology, 2022, 194, 107822. | 1.5 | 3 |
| 3474 | Plastome structure, phylogenomics, and divergence times of tribe Cinnamomeae (Lauraceae). BMC Genomics, 2022, 23, . | 1.2 | 7 |
| 3475 | Clonal Dissemination of Extended-Spectrum Cephalosporin-Resistant Enterobacterales between Dogs and Humans in Households and Animal Shelters of Romania. Antibiotics, 2022, 11, 1242. | 1.5 | 8 |
| 3476 | Analysis of complete chloroplast genome sequences and insight into the phylogenetic relationships of Ferula L.. BMC Genomics, 2022, 23, . | 1.2 | 11 |
| 3477 | Characterization, comparative phylogenetic, and gene transfer analyses of organelle genomes of Rhododendron Ã— pulchrum. Frontiers in Plant Science, 0, 13, . | 1.7 | 2 |
| 3478 | Pseudomonas putida mediates bacterial killing, biofilm invasion and biocontrol with a type IVB secretion system. Nature Microbiology, 2022, 7, 1547-1557. | 5.9 | 23 |
| 3479 | Effects of a Carnobacterium maltaromaticum strain at natural contamination levels on the microbiota of vacuum-packaged beef steaks during chilled storage. LWT - Food Science and Technology, 2022, 168, 113944. | 2.5 | 2 |
| 3480 | Genome-scale prediction of bacterial promoters. BioSystems, 2022, 221, 104771. | 0.9 | 3 |
| 3481 | The complete plastome of Blidingia marginata and comparative analysis with the relative species in Ulvales. Aquatic Botany, 2022, 183, 103568. | 0.8 | 1 |
| 3482 | The entire chloroplast genome sequence of <i>Asparagus cochinchinensis</i> and genetic comparison to <i>Asparagus</i> species. Open Life Sciences, 2022, 17, 893-906. | 0.6 | 3 |
| 3483 | Multiple genome alignment in the telomere-to-telomere assembly era. Genome Biology, 2022, 23, . | 3.8 | 17 |
| 3484 | Comparative chloroplast genome analyses of 23 species in Swertia L. (Gentianaceae) with implications for its phylogeny. Frontiers in Genetics, 0, 13, . | 1.1 | 10 |
| 3485 | Complete Chloroplast Genomes of 14 Subspecies of D. glomerata: Phylogenetic and Comparative Genomic Analyses. Genes, 2022, 13, 1621. | 1.0 | 6 |
| 3486 | Telomere-to-telomere genome sequence of the model mould pathogen Aspergillus fumigatus. Nature Communications, 2022, 13, . | 5.8 | 8 |
| 3487 | Plastome structure, phylogenomic analyses and molecular dating of Arecaceae. Frontiers in Plant Science, 0, 13, . | 1.7 | 2 |
| 3488 | Convergent structure with divergent adaptations in combinatorial microbiome communities. FEMS Microbiology Ecology, 2022, 98, . | 1.3 | 0 |
| 3489 | A functional selection reveals previously undetected anti-phage defence systems in the E. coli pangenome. Nature Microbiology, 2022, 7, 1568-1579. | 5.9 | 108 |
| 3490 | Genomic Profiling of Non-O157 Shiga Toxigenic<i>Escherichia coli</i>-Infecting Bacteriophages from South Africa. Phage, 2022, 3, 221-230. | 0.8 | 1 |

| # | Article | IF | Citations |
|---|---|---|---|
| 3491 | Genome-guided prediction of acid resistance mechanisms in acidophilic methanotrophs of phylogenetically deep-rooted Verrucomicrobia isolated from geothermal environments. Frontiers in Microbiology, 0, 13, . | 1.5 | 1 |
| 3492 | Weizmannia faecalis sp. nov., isolated from a human stool sample. Archives of Microbiology, 2022, 204, . | 1.0 | 4 |
| 3493 | A turn in species conservation for hairpin banksias: demonstration of oversplitting leads to better management of diversity. American Journal of Botany, 2022, 109, 1652-1671. | 0.8 | 5 |
| 3494 | Intraspecific comparison of mitochondrial genomes reveals the evolution in medicinal fungus Ganoderma lingzhi. Journal of Bioscience and Bioengineering, 2022, 134, 374-383. | 1.1 | 1 |
| 3495 | Pangenomes-identified singletons for designing specific primers to identify bacterial strains in a plant growth-promoting consortium. Molecular Biology Reports, 2022, 49, 10489-10498. | 1.0 | 3 |
| 3496 | The complete mitochondrial genome of Isochrysis galbana harbors a unique repeat structure and a specific trans-spliced cox1 gene. Frontiers in Microbiology, 0, 13, . | 1.5 | 1 |
| 3497 | Comparative chloroplast genome and phylogenetic analyses of Chinese Polyspora. Scientific Reports, 2022, 12, . | 1.6 | 5 |
| 3498 | Complete Chloroplast Genome of Gladiolus gandavensis (Gladiolus) and Genetic Evolutionary Analysis. Genes, 2022, 13, 1599. | 1.0 | 2 |
| 3499 | A Plasmid Carrying blaIMP-56 in Pseudomonas aeruginosa Belonging to a Novel Resistance Plasmid Family. Microorganisms, 2022, 10, 1863. | 1.6 | 3 |
| 3501 | Breaking the ICE: an easy workflow for identifying and analyzing integrative and conjugative elements in bacterial genomes. Functional and Integrative Genomics, 0, , . | 1.4 | 5 |
| 3502 | Complete chloroplast genome sequence of Lens ervoides and comparison to Lens culinaris. Scientific Reports, 2022, 12, . | 1.6 | 5 |
| 3503 | Isolation and characterization of a Vibrio owensii phage phi50-12. Scientific Reports, 2022, 12, . | 1.6 | 2 |
| 3504 | The complete chloroplast genome of Campsis grandiflora (Bignoniaceae). Korean Journal of Plant Taxonomy, 2022, 52, 156-172. | 0.3 | 2 |
| 3506 | Characterization of Phage Resistance and Their Impacts on Bacterial Fitness in Pseudomonas aeruginosa. Microbiology Spectrum, 2022, 10, . | 1.2 | 6 |
| 3507 | Integrating diverse layers of omic data to identify novel drug targets in Listeria monocytogenes. Frontiers in Drug Discovery, 0, 2, . | 1.1 | 4 |
| 3508 | Comparative mitogenome analysis reveals mitochondrial genome characteristics in eight strains of <i>Beauveria</i>. PeerJ, 0, 10, e14067. | 0.9 | 2 |
| 3509 | Evolutionary Comparison of the Complete Chloroplast Genomes in Convallaria Species and Phylogenetic Study of Asparagaceae. Genes, 2022, 13, 1724. | 1.0 | 5 |
| 3511 | Prevalence and mobility of integrative and conjugative elements within a Streptomyces natural population. Frontiers in Microbiology, 0, 13, . | 1.5 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 3512 | Comparative genomic and functional analyses of Paenibacillus peoriae ZBSF16 with biocontrol potential against grapevine diseases, provide insights into its genes related to plant growth-promoting and biocontrol mechanisms. Frontiers in Microbiology, 0, 13, . | 1.5 | 1 |
| 3513 | Identification of Male-Specific Molecular Marker and Development of PCR-Based Genetic Sex Identification Technique in Spotted Knifejaw (Oplegnathus punctatus). Marine Biotechnology, 0, , . | 1.1 | 0 |
| 3515 | Whole genome sequence analysis of two subspecies of Companilactobacillus Futsaii and experimental verification of drug resistance and effect on the exploratory behavior of mice based on unique gene. PLoS ONE, 2022, 17, e0274244. | 1.1 | 1 |
| 3516 | Role of Bifidobacterium pseudocatenulatum in Degradation and Consumption of Xylan-Derived Carbohydrates. Applied and Environmental Microbiology, 2022, 88, . | 1.4 | 6 |
| 3517 | Spontaneous Prophage Induction Contributes to the Production of Membrane Vesicles by the Gram-Positive Bacterium <i>Lacticaseibacillus casei</i> BL23. MBio, 2022, 13, . | 1.8 | 9 |
| 3518 | Whole genome population structure of North Atlantic kelp confirms highâ€latitude glacial refugia. Molecular Ecology, 2022, 31, 6473-6488. | 2.0 | 5 |
| 3519 | Monkeypox virus: The changing facets of a zoonotic pathogen. Infection, Genetics and Evolution, 2022, 105, 105372. | 1.0 | 16 |
| 3520 | Designing Tobacco Genomes for Resistance to Biotic Stresses. , 2022, , 441-581. |  | 1 |
| 3521 | Abiotic Stress Resistance in Tobacco: Advances and Strategies. , 2022, , 329-427. |  | 0 |
| 3522 | The Effect of Mutation in Lipopolysaccharide Biosynthesis on Bacterial Fitness. Cells, 2022, 11, 3249. | 1.8 | 1 |
| 3523 | Whole genome sequence data of Stenotrophomonas maltophilia SCAID WND1-2022 (370). Data in Brief, 2022, , 108694. | 0.5 | 0 |
| 3524 | Borgs are giant genetic elements with potential to expand metabolic capacity. Nature, 2022, 610, 731-736. | 13.7 | 29 |
| 3525 | Folding Features and Dynamics of 3D Genome Architecture in Plant Fungal Pathogens. Microbiology Spectrum, 2022, 10, . | 1.2 | 5 |
| 3526 | The acquisition of transferable extrachromosomal <i>fec</i> operon is associated with a cefiderocol MIC increase in Enterobacterales. Journal of Antimicrobial Chemotherapy, 0, , . | 1.3 | 3 |
| 3528 | Emergence of a Novel Lineage and Wide Spread of a blaCTX-M-15/IncHI2/ST1 Plasmid among Nosocomial Enterobacter in Guadeloupe. Antibiotics, 2022, 11, 1443. | 1.5 | 1 |
| 3529 | Comparison of clinical severity, genotype and toxin gene expression of binary toxin-producing Clostridioides difficile clinical isolates in Japan. Access Microbiology, 2022, 4, . | 0.2 | 1 |
| 3530 | Ancient homomorphy of molluscan sex chromosomes sustained by reversible sex-biased genes and sex determiner translocation. Nature Ecology and Evolution, 2022, 6, 1891-1906. | 3.4 | 23 |
| 3531 | Complete Genome Sequences of Two <i>Rhizobium</i> Strains Producing Azol(in)e-Modified Antibiotics. Microbiology Resource Announcements, 2022, 11, . | 0.3 | 1 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 3532 | Comparative Genomic Analysis of Phytopathogenic Xanthomonas Species Suggests High Level of Genome Plasticity Related to Virulence and Host Adaptation. , 2022, 1, 218-241. | | 4 |
| 3534 | Development of Genome-Driven, Lifestyle-Informed Markers for Identification of the Cereal-Infecting Pathogens <i>Xanthomonas translucens</i> Pathovars <i>undulosa</i> and <i>translucens</i>. Phytopathology, 2023, 113, 2110-2118. | 1.1 | 6 |
| 3535 | Detection of an IMI-2 carbapenemase-producing Enterobacter asburiae at a Swedish feed mill. Frontiers in Microbiology, 0, 13, . | 1.5 | 5 |
| 3536 | Characterization and Comparative Analysis of Chloroplast Genomes in Five Uncaria Species Endemic to China. International Journal of Molecular Sciences, 2022, 23, 11617. | 1.8 | 10 |
| 3537 | Endogenous giant viruses contribute to intraspecies genomic variability in the model green alga <i>Chlamydomonas reinhardtii</i>. Virus Evolution, 2022, 8, . | 2.2 | 12 |
| 3538 | An update to the database for Acinetobacter baumannii capsular polysaccharide locus typing extends the extensive and diverse repertoire of genes found at and outside the K locus. Microbial Genomics, 2022, 8, . | 1.0 | 13 |
| 3539 | Genomic Features of Pseudomonas putida PCL1760: A Biocontrol Agent Acting via Competition for Nutrient and Niche. Applied Microbiology, 2022, 2, 749-765. | 0.7 | 1 |
| 3540 | Draft Genome Sequences of Bacillus pumilus 36R ATNSAL and B. safensis 13L LOBSAL, Two Potential Candidate Probiotic Strains for Shrimp Aquaculture. Journal of Global Antimicrobial Resistance, 2022, , . | 0.9 | 1 |
| 3541 | Genome sequence of the entomopathogenic Serratia entomophila isolate 626 and characterisation of the species specific itaconate degradation pathway. BMC Genomics, 2022, 23, . | 1.2 | 4 |
| 3542 | Sequencing and de novo assembly of the Koshihikari genome and identification of the genomic region related to the eating quality of cooked rice. Molecular Breeding, 2022, 42, . | 1.0 | 1 |
| 3543 | Comparative analysis of the complete chloroplast genomes of six threatened subgenus Gynopodium (Magnolia) species. BMC Genomics, 2022, 23, . | 1.2 | 1 |
| 3544 | New Saccharomyces cerevisiae-Kluyveromyces marxianus fusant shows enhanced alcoholic fermentation performance. World Journal of Microbiology and Biotechnology, 2022, 38, . | 1.7 | 1 |
| 3545 | A High-Quality Genome Assembly of the Mitochondrial Genome of the Oil-Tea Tree Camellia gigantocarpa (Theaceae). Diversity, 2022, 14, 850. | 0.7 | 6 |
| 3546 | Draft Genome Sequence of â€œ <i>Candidatus</i> Nardonella dryophthoridicolaâ€•Strain NARMHE1, Endosymbiont of Metamasius hemipterus (Coleoptera, Curculionidae, Dryophthorinae). Microbiology Resource Announcements, 2022, 11, . | 0.3 | 1 |
| 3547 | Phylogenomics and plastome evolution of a Brazilian mycoheterotrophic orchid, <i>Pogoniopsis schenckii</i>. American Journal of Botany, 2022, 109, 2030-2050. | 0.8 | 8 |
| 3549 | In silico genomic analysis of the potential probiotic Lactiplantibacillus pentosus CF2-10N reveals promising beneficial effects with health promoting properties. Frontiers in Microbiology, 0, 13, . | 1.5 | 6 |
| 3550 | Hybrid assembly using long reads resolves repeats and completes the genome sequence of a laboratory strain of Staphylococcus aureus subsp. Aureus RN4220. Heliyon, 2022, , e11376. | 1.4 | 0 |
| 3551 | Deciphering the potential of a plant growth promoting endophyte Rhizobium sp. WYJ-E13, and functional annotation of the genes involved in the metabolic pathway. Frontiers in Microbiology, 0, 13, . | 1.5 | 1 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 3552 | Experimental pathogenicity and comparative genome analysis of high- and low-virulence strains of rabbit-origin Pasteurella multocida. Comparative Immunology, Microbiology and Infectious Diseases, 2022, 90-91, 101889. | 0.7 | 0 |
| 3553 | A specific reverse complement sequence for distinguishing Brucella canis from other Brucella species. Frontiers in Veterinary Science, 0, 9, . | 0.9 | 0 |
| 3554 | In silico genomic analysis of Rhodopseudomonas palustris strains revealed potential biocontrol agents and crop yield enhancers. Biological Control, 2022, 176, 105085. | 1.4 | 9 |
| 3555 | Evolution of the orthopoxvirus core genome. Virus Research, 2023, 323, 198975. | 1.1 | 3 |
| 3556 | Comparative genomic analyses of Lutimaribacter degradans sp. nov. With the ability to PAHs-biodegradation and transformation. International Biodeterioration and Biodegradation, 2023, 176, 105505. | 1.9 | 8 |
| 3557 | The complete plastid genome of Bactris riparia (Arecaceae) and a comparative analysis in Bactridinae (Cocoseae, Arecaceae). Genetics and Molecular Biology, 2022, 45, . | 0.6 | 0 |
| 3558 | Full-length whole-genome sequencing analysis of emerged meropenem-resistant mutants during long-term <i>in vitro</i> exposure to meropenem for borderline meropenem-susceptible carbapenemase-producing and non-carbapenemase-producing <i>Enterobacterales</i>. Journal of Antimicrobial Chemotherapy, 2023, 78, 209-215. | 1.3 | 2 |
| 3559 | Comparative Analyses of Plastomes of Four Anubias (Araceae) Taxa, Tropical Aquatic Plants Endemic to Africa. Genes, 2022, 13, 2043. | 1.0 | 1 |
| 3560 | <scp>NGSEP</scp> 4: Efficient and accurate identification of orthogroups and wholeâ€genome alignment. Molecular Ecology Resources, 2023, 23, 712-724. | 2.2 | 7 |
| 3561 | Evaluation of tangential flow filtration coupled to long-read sequencing for ostreid herpesvirus type 1 genome assembly. Microbial Genomics, 2022, 8, . | 1.0 | 2 |
| 3562 | Shared properties of gene transfer agent and core genes revealed by comparative genomics of Alphaproteobacteria. Microbial Genomics, 2022, 8, . | 1.0 | 0 |
| 3563 | Comparative genomics of Lactobacillaceae from the gut of honey bees, <i>Apis mellifera</i>, from the Eastern United States. G3: Genes, Genomes, Genetics, 2022, 12, . | 0.8 | 3 |
| 3564 | Complete Genome and Partial Megaplasmid Sequences of Mycobacterium pseudoshottsii Strain NJB1907-Z4, Isolated from an Aquarium-Reared Japanese Sardine (Sardinops melanostictus) in Japan. Microbiology Resource Announcements, 2022, 11, . | 0.3 | 1 |
| 3565 | The complete chloroplast genome sequences of eight Orostachys species: Comparative analysis and assessment of phylogenetic relationships. PLoS ONE, 2022, 17, e0277486. | 1.1 | 5 |
| 3566 | Comparative genomic analyses reveal genetic characteristics and pathogenic factors of Bacillus pumilus HM-7. Frontiers in Microbiology, 0, 13, . | 1.5 | 0 |
| 3567 | Molecular Structure and Phylogenetic Analyses of the Plastomes of Eight Sorbus Sensu Stricto Species. Biomolecules, 2022, 12, 1648. | 1.8 | 2 |
| 3568 | Whole-genome sequence of the filamentous diazotrophic cyanobacterium Tolypothrix sp. PCC 7712 and its comparison with non-diazotrophic Tolypothrix sp. PCC 7601. Frontiers in Microbiology, 0, 13, . | 1.5 | 2 |
| 3569 | Next-generation sequencing data show rapid radiation and several long-distance dispersal events in early Costaceae. Molecular Phylogenetics and Evolution, 2023, 179, 107664. | 1.2 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 3570 | The phylogeny of Seseli (Apiaceae, Apioideae): insights from molecular and morphological data. BMC Plant Biology, 2022, 22, . | 1.6 | 4 |
| 3571 | Phage Cocktail in Combination with Kasugamycin as a Potential Treatment for Fire Blight Caused by Erwinia amylovora. Antibiotics, 2022, 11, 1566. | 1.5 | 6 |
| 3572 | Comparative genomics to examine the endophytic potential of Pantoea agglomerans DAPP-PG 734. BMC Genomics, 2022, 23, . | 1.2 | 6 |
| 3573 | Characterization of the Evolutionary Pressure on Anisodus tanguticus Maxim. with Complete Chloroplast Genome Sequence. Genes, 2022, 13, 2125. | 1.0 | 3 |
| 3574 | Genomic analysis of Paenibacillus sp. MDMC362 from the Merzouga desert leads to the identification of a potentially thermostable catalase. Antonie Van Leeuwenhoek, 2023, 116, 21-38. | 0.7 | 1 |
| 3575 | Metagenome-assembled genome extraction and analysis from microbiomes using KBase. Nature Protocols, 2023, 18, 208-238. | 5.5 | 7 |
| 3576 | Type IV Pili Are a Critical Virulence Factor in Clinical Isolates of Paenibacillus thiaminolyticus. MBio, 2022, 13, . | 1.8 | 2 |
| 3577 | Whole genome analysis for plant growth promotion profiling of Pantoea agglomerans CPHN2, a non-rhizobial nodule endophyte. Frontiers in Microbiology, 0, 13, . | 1.5 | 3 |
| 3578 | Introducing the Bacterial and Viral Bioinformatics Resource Center (BV-BRC): a resource combining PATRIC, IRDÂand ViPR. Nucleic Acids Research, 2023, 51, D678-D689. | 6.5 | 229 |
| 3580 | The first complete genome of the simian malaria parasite Plasmodium brasilianum. Scientific Reports, 2022, 12, . | 1.6 | 5 |
| 3581 | Genomic Analysis to Elucidate the Lignocellulose Degrading Capability of a New Halophile Robertkochia solimangrovi. Genes, 2022, 13, 2135. | 1.0 | 0 |
| 3582 | Twisting development, the birth of a potential new gene. IScience, 2022, 25, 105627. | 1.9 | 4 |
| 3583 | Analysis of the Features of the Genomic Organization of Plague Microbe Strains Suitable for the Creation of a New Attenuated Vaccine. Epidemiologiya I Vaktsinoprofilaktika, 2022, 21, 49-57. | 0.2 | 0 |
| 3585 | Genomic Analysis of 13 Putative Active Prophages Located in the Genomes of Walnut Blight Pathogen <i>Xanthomonas arboricola</i> pv. <i>juglandis</i>. Microbiology and Biotechnology Letters, 2022, 50, 563-573. | 0.2 | 0 |
| 3586 | HELIOS: High-speed sequence alignment in optics. PLoS Computational Biology, 2022, 18, e1010665. | 1.5 | 1 |
| 3587 | Proteiniphilum propionicum sp. nov., a novel member of the phylum Bacteroidota isolated from pit clay used to produce Chinese liquor. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, . | 0.8 | 1 |
| 3588 | Throughput screening of Bacillus subtilis strains that abundantly secrete surfactin in vitro identifies effective probiotic candidates. PLoS ONE, 2022, 17, e0277412. | 1.1 | 5 |
| 3589 | Evidence from Phylogenomics and Morphology Provide Insights into the Phylogeny, Plastome Evolution, and Taxonomy of Kitagawia. Plants, 2022, 11, 3275. | 1.6 | 4 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 3590 | Recombination Events in Putative Tail Fibre Gene in Litunavirus Phages Infecting Pseudomonas aeruginosa and Their Phylogenetic Consequences. Viruses, 2022, 14, 2669. | 1.5 | 1 |
| 3592 | Complete Chloroplast Genome Sequence of a New Variety of Brasenia schreberi: Genome Characteristics, Comparative Analysis, and Phylogenetic Relationships. Agronomy, 2022, 12, 2972. | 1.3 | 1 |
| 3594 | Untargeted metabolomics screening reveals unique secondary metabolite production from Alternaria section Alternaria. Frontiers in Molecular Biosciences, 0, 9, . | 1.6 | 0 |
| 3595 | Genome Analysis and Antibiofilm Activity of Phage 590B against Multidrug-Resistant and Extensively Drug-Resistant Uropathogenic Escherichia coli Isolates, India. Pathogens, 2022, 11, 1448. | 1.2 | 4 |
| 3596 | Species-Specific Duplication of Surface Antigen Genes in Paramecium. Microorganisms, 2022, 10, 2378. | 1.6 | 1 |
| 3597 | Untying the Gordian knot of plastid phylogenomic conflict: A case from ferns. Frontiers in Plant Science, 0, 13, . | 1.7 | 0 |
| 3598 | Complete genome sequencing and comparative genomic analyses of a new spotted-fever <i>Rickettsia heilongjiangensis</i> strain B8. Emerging Microbes and Infections, 2023, 12, . | 3.0 | 4 |
| 3599 | Identifying magnetosome-associated genes in the extended CtrA regulon in <i>Magnetospirillum magneticum</i> AMB-1 using a combinational approach. Briefings in Functional Genomics, 0, , . | 1.3 | 0 |
| 3600 | Biocomputational Identification of sRNAs in Leptospira interrogans Serovar Lai. Indian Journal of Microbiology, 0, , . | 1.5 | 0 |
| 3601 | Comparative chloroplast genomics provides insights into the genealogical relationships of endangered Tetraena mongolica and the chloroplast genome evolution of related Zygophyllaceae species. Frontiers in Genetics, 0, 13, . | 1.1 | 3 |
| 3604 | Genetic Features of Mycobacterium avium subsp. <i>paratuberculosis</i> Strains Circulating in the West of France Deciphered by Whole-Genome Sequencing. Microbiology Spectrum, 2022, 10, . | 1.2 | 6 |
| 3605 | Genomic diversity and comprehensive taxonomical classification of 61 Bacillus subtilis group member infecting bacteriophages, and the identification of ortholog taxonomic signature genes. BMC Genomics, 2022, 23, . | 1.2 | 0 |
| 3606 | Genomics, Transcriptomics, and Metabolomics Reveal That Minimal Modifications in the Host Are Crucial for the Compensatory Evolution of ColE1-Like Plasmids. MSphere, 2022, 7, . | 1.3 | 5 |
| 3607 | Horizontal Transfer of Bacteriocin Biosynthesis Genes Requires Metabolic Adaptation To Improve Compound Production and Cellular Fitness. Microbiology Spectrum, 2023, 11, . | 1.2 | 4 |
| 3608 | High-Quality Genome and Annotation Resource of Orange Pink Rot Pathogen Trichothecium roseum strain YXFP-22015 Isolated from Hubei, China. Plant Disease, 0, , . | 0.7 | 0 |
| 3609 | Diverse infective and lytic machineries identified in genome analysis of tailed coliphages against broad spectrum multidrug-resistant Escherichia coli. International Microbiology, 0, , . | 1.1 | 1 |
| 3610 | Characterization of the complete mitochondrial genome of the striped soldier shrimp, <i>Plesionika edwardsii</i> (Brandt, 1851) (Crustacea: Decapoda: Pandalidae), and comparison with other species of Caridea. Journal of Crustacean Biology, 2022, 42, . | 0.3 | 1 |
| 3611 | Fervidobacterium pennivorans subsp. keratinolyticus subsp. nov., a Novel Feather-Degrading Anaerobic Thermophile. Microorganisms, 2023, 11, 22. | 1.6 | 0 |

| # | Article | IF | Citations |
|---|---|---|---|
| 3613 | Genomic diversity of <i>Helicobacter pylori</i> populations from different regions of the human stomach. Gut Microbes, 2022, 14, . | 4.3 | 4 |
| 3614 | Genetic Adaptation and Acquisition of Macrolide Resistance in Haemophilus spp. during Persistent Respiratory Tract Colonization in Chronic Obstructive Pulmonary Disease (COPD) Patients Receiving Long-Term Azithromycin Treatment. Microbiology Spectrum, 2023, 11, . | 1.2 | 6 |
| 3615 | New Insights into Lymphocystis Disease Virus Genome Diversity. Viruses, 2022, 14, 2741. | 1.5 | 3 |
| 3617 | Genomic Characterization of Livestock-Associated Methicillin-Resistant Staphylococcus aureus ST7 Isolates from a Case of Human Bacteremia in China. Infection and Drug Resistance, 0, Volume 15, 7449-7457. | 1.1 | 3 |
| 3618 | Jack of all trades: Genome assembly of Wild Jack and comparative genomics of Artocarpus. Frontiers in Plant Science, 0, 13, . | 1.7 | 1 |
| 3619 | Disinfectant Susceptibility of Third-Generation-Cephalosporin/Carbapenem-Resistant Gram-Negative Bacteria Isolated from the Oral Cavity of Residents of Long-Term-Care Facilities. Applied and Environmental Microbiology, 2023, 89, . | 1.4 | 1 |
| 3620 | Morphological Characteristics and Comparative Chloroplast Genome Analyses between Red and White Flower Phenotypes of Pyracantha fortuneana (Maxim.) Li (Rosaceae), with Implications for Taxonomy and Phylogeny. Genes, 2022, 13, 2404. | 1.0 | 3 |
| 3621 | Type IV pili trigger episymbiotic association of Saccharibacteria with its bacterial host. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 3.3 | 18 |
| 3622 | Phylogenomic analyses based on the plastid genome and concatenated nrDNA sequence data reveal cytonuclear discordance in genus Atractylodes (Asteraceae: Carduoideae). Frontiers in Plant Science, 0, 13, . | 1.7 | 5 |
| 3624 | Comparative Genomic Analysis of the Hydrocarbon-Oxidizing Dibenzothiophene-Desulfurizing Gordonia Strains. Microorganisms, 2023, 11, 4. | 1.6 | 5 |
| 3625 | An Emerging Lineage of Uropathogenic Extended Spectrum Î²-Lactamase Escherichia coli ST127. Microbiology Spectrum, 2022, 10, . | 1.2 | 1 |
| 3626 | Comparative genomics of trimethoprim-sulfamethoxazole-resistant Achromobacter xylosoxidans clinical isolates from Serbia reveals shortened variant of class 1 integron integrase gene. Folia Microbiologica, 2023, 68, 431-440. | 1.1 | 2 |
| 3627 | At the threshold of symbiosis: the genome of obligately endosymbiotic â€˜Candidatus Nebulobacter yamunensisâ€™ is almost indistinguishable from that of a cultivable strain. Microbial Genomics, 2022, 8, . | 1.0 | 1 |
| 3628 | Identification of a conserved maxicircle and unique minicircles as part of the mitochondrial genome of Leishmania martiniquensis strain PCM3 in Thailand. Parasites and Vectors, 2022, 15, . | 1.0 | 0 |
| 3629 | The chloroplast genome of black pepper (Piper nigrum L.) and its comparative analysis with related Piper species. Frontiers in Plant Science, 0, 13, . | 1.7 | 3 |
| 3630 | Complete chloroplast genome and phylogenetic relationship of Nymphaea nouchali (Nymphaeaceae), a rare species of water lily in China. Gene, 2023, 858, 147139. | 1.0 | 1 |
| 3631 | Insights into chloroplast genome structure, intraspecific variation, and phylogeny of Cyclamen species (Myrsinoideae). Scientific Reports, 2023, 13, . | 1.6 | 2 |
| 3632 | Pan-genome association study of Mycobacterium tuberculosis lineage-4 revealed specific genes related to the high and low prevalence of the disease in patients from the North-Eastern area of MedellÃn, Colombia. Frontiers in Microbiology, 0, 13, . | 1.5 | 2 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 3633 | Comparative Genomics Revealed a Potential Threat of AeromonasÂrivipollensis G87 Strain and Its Antibiotic Resistance. Antibiotics, 2023, 12, 131. | 1.5 | 1 |
| 3634 | Towards the isolation of more robust next generation probiotics: The first aerotolerant Bifidobacterium bifidum strain. Food Research International, 2023, 165, 112481. | 2.9 | 2 |
| 3635 | A comparison of 25 complete chloroplast genomes between sister mangrove species Kandelia obovata and Kandelia candel geographically separated by the South China Sea. Frontiers in Plant Science, 0, 13, . | 1.7 | 2 |
| 3636 | Complete sequence and comparative analysis of the mitochondrial genome of the rare and endangered Clematis acerifolia, the first clematis mitogenome to provide new insights into the phylogenetic evolutionary status of the genus. Frontiers in Genetics, 0, 13, . | 1.1 | 6 |
| 3637 | Wholeâ€“genome sequencing, annotation, and biological characterization of a novel Siphoviridae phage against multiâ€“drug resistant Propionibacterium acne. Frontiers in Microbiology, 0, 13, . | 1.5 | 1 |
| 3638 | Phylogenetic Analysis of Wild Pomegranate (Punica granatum L.) Based on Its Complete Chloroplast Genome from Tibet, China. Agronomy, 2023, 13, 126. | 1.3 | 4 |
| 3639 | The Complete Chloroplast Genomes of Two Physalis Species, Physalis macrophysa and P. ixocarpa: Comparative Genomics, Evolutionary Dynamics and Phylogenetic Relationships. Agronomy, 2023, 13, 135. | 1.3 | 4 |
| 3640 | Phylogenomics, divergence time estimation, and adaptive evolution in the Polygonoideae (Polygonaceae). Journal of Systematics and Evolution, 2023, 61, 1004-1019. | 1.6 | 0 |
| 3641 | PRAWNS: compact pan-genomic features for whole-genome population genomics. Bioinformatics, 2023, 39, . | 1.8 | 0 |
| 3642 | Two <i>Xylella fastidiosa</i> subsp. <i>multiplex</i> strains isolated from almond in Spain differ in plasmid content and virulence traits. Phytopathology, 0, , . | 1.1 | 1 |
| 3643 | Plastid Phylogenomics Provide Evidence to Accept Two New Members of Ligusticopsis (Apiaceae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 | 1.8 | 0 |
| 3644 | Plastid Phylogenomic Analyses Reveal the Taxonomic Position of Peucedanum franchetii. Plants, 2023, 12, 97. | 1.6 | 1 |
| 3645 | Seeds of Stevia rebaudiana Bertoni as a Source of Plant Growth-Promoting Endophytic Bacteria with the Potential to Synthesize Rebaudioside A. International Journal of Molecular Sciences, 2023, 24, 2174. | 1.8 | 5 |
| 3646 | Chloroplast genomes of four Carex species: Long repetitive sequences trigger dramatic changes in chloroplast genome structure. Frontiers in Plant Science, 0, 14, . | 1.7 | 8 |
| 3647 | Using a combination of short- and long-read sequencing to investigate the diversity in plasmid- and chromosomally encoded extended-spectrum beta-lactamases (ESBLs) in clinical Shigella and Salmonella isolates in Belgium. Microbial Genomics, 2023, 9, . | 1.0 | 1 |
| 3648 | The effect of in vitro consecutive passages and culture medium on the genetic variations in BCG Pasteur 1173P2 vaccine. PLoS ONE, 2023, 18, e0280294. | 1.1 | 0 |
| 3649 | Pathological Features and Genomic Characterization of an Actinobacillus equuli subsp. equuli Bearing Unique Virulence-Associated Genes from an Adult Horse with Pleuropneumonia. Pathogens, 2023, 12, 224. | 1.2 | 0 |
| 3650 | Klebsiella pneumoniae carrying multiple alleles of antigen 43-encoding gene of Escherichia coli associated with biofilm formation. European Journal of Clinical Microbiology and Infectious Diseases, 2023, 42, 371-377. | 1.3 | 0 |

| # | Article | IF | Citations |
|---|---|---|---|
| 3651 | Genomic Diversity among Actinomyces naeslundii Strains and Closely Related Species. Microorganisms, 2023, 11, 254. | 1.6 | 1 |
| 3652 | Characterization of Escherichia coli and Other Enterobacterales Resistant to Extended-Spectrum Cephalosporins Isolated from Dairy Manure in Ontario, Canada. Applied and Environmental Microbiology, 2023, 89, . | 1.4 | 2 |
| 3653 | In Silico Genomic Characterization of Bacillus velezensis Strain AAK_S6 for Secondary Metabolite and Biocontrol Potential. Current Microbiology, 2023, 80, . | 1.0 | 3 |
| 3654 | Wolbachia in natural Drosophila simulans (Diptera: Drosophilidae) populations in Ukraine. Symbiosis, 0, , . | 1.2 | 0 |
| 3655 | Leveraging comparative genomics to uncover alien genes in bacterial genomes. Microbial Genomics, 2023, 9, . | 1.0 | 4 |
| 3656 | Description and Genomic Analysis of the First Facultatively Lithoautotrophic, Thermophilic Bacteria of the Genus Thermaerobacter Isolated from Low-temperature Sediments of Lake Baikal. Microbial Ecology, 0, , . | 1.4 | 0 |
| 3657 | Chloroplast genome sequence of triploid Toxicodendron vernicifluum and comparative analyses with other lacquer chloroplast genomes. BMC Genomics, 2023, 24, . | 1.2 | 3 |
| 3658 | Plastid phylogenomics and molecular evolution of Thismiaceae (Dioscoreales). American Journal of Botany, 2023, 110, . | 0.8 | 3 |
| 3659 | Complete chloroplast genome sequences of the medicinal plant Aconitum transsectum (Ranunculaceae): comparative analysis and phylogenetic relationships. BMC Genomics, 2023, 24, . | 1.2 | 6 |
| 3660 | Genome sequences of BCG Pasteur ATCC 35734 and its derivative, the vaccine candidate BCGÎ”BCG1419c. BMC Genomics, 2023, 24, . | 1.2 | 2 |
| 3661 | Phylogenomics and phylogeography of Menispermum (Menispermaceae). Frontiers in Plant Science, 0, 14, . | 1.7 | 0 |
| 3662 | Structural Diversity among Edwardsiellaceae Core Oligosaccharides. International Journal of Molecular Sciences, 2023, 24, 4768. | 1.8 | 0 |
| 3663 | Revised classification of the Cyanidiophyceae based on plastid genome data with descriptions of the Cavernulicolales ord. nov. and Galdieriales ord. nov. (Rhodophyta). Journal of Phycology, 2023, 59, 444-466. | 1.0 | 11 |
| 3665 | Characterization and phylogenetic analyses of ten complete plastomes of Spiraea species. BMC Genomics, 2023, 24, . | 1.2 | 2 |
| 3666 | The Evolution of Mitochondrial Genomes between Two Cymbidium Sister Species: Dozens of Circular Chromosomes and the Maintenance and Deterioration of Genome Synteny. Genes, 2023, 14, 864. | 1.0 | 7 |
| 3667 | Polluted wetlands contain multidrug-resistance plasmids encoding CTX-M-type extended-spectrum Î²-lactamases. Plasmid, 2023, 126, 102682. | 0.4 | 0 |
| 3668 | A K-17 serotype specific Klebsiella phage JKP2 with biofilm reduction potential. Virus Research, 2023, 329, 199107. | 1.1 | 1 |
| 3669 | Genomic insights into a Pseudomonas amygdali isolate from Hibiscus rosa-sinensis. Genomics, 2023, 115, 110600. | 1.3 | 2 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 3670 | Phylogenomics and taxon-rich phylogenies of new and historical specimens shed light on the systematics of Hypnea (Cystocloniaceae, Rhodophyta). Molecular Phylogenetics and Evolution, 2023, 183, 107752. | 1.2 | 1 |
| 3673 | Stutzerimonas decontaminans sp. nov. isolated from marine polluted sediments. Systematic and Applied Microbiology, 2023, 46, 126400. | 1.2 | 4 |
| 3674 | Plastome evolution and phylogenomics of Impatiens (Balsaminaceae). Planta, 2023, 257, . | 1.6 | 3 |
| 3677 | Plastid Phylogenomic Insights into the Inter-Tribal Relationships of Plantaginaceae. Biology, 2023, 12, 263. | 1.3 | 2 |
| 3678 | Interplay between transcriptional regulators and <scp>VapBC toxinâ€“antitoxin</scp> loci during thermal stress response in extremely thermoacidophilic archaea. Environmental Microbiology, 2023, 25, 1200-1215. | 1.8 | 4 |
| 3679 | Investigating the origin of subtelomeric and centromeric AT-rich elements in Aspergillus flavus. PLoS ONE, 2023, 18, e0279148. | 1.1 | 1 |
| 3680 | Comparative Genomics of Legionella pneumophila Isolates from the West Bank and Germany Support Molecular Epidemiology of Legionnairesâ€™ Disease. Microorganisms, 2023, 11, 449. | 1.6 | 2 |
| 3681 | Comparative Genomic Analysis of a Thermophilic Protease-Producing Strain Geobacillus stearothermophilus H6. Genes, 2023, 14, 466. | 1.0 | 1 |
| 3682 | Complete Chloroplast Genome Sequence of the Long Blooming Cultivar Camellia â€˜Xiari Qixinâ€™: Genome Features, Comparative and Phylogenetic Analysis. Genes, 2023, 14, 460. | 1.0 | 0 |
| 3683 | Biotechnologically potential genes in a polysaccharide-degrading epibiont of the Indonesian brown algae Hydroclathrus sp.. Journal of Genetic Engineering and Biotechnology, 2023, 21, 18. | 1.5 | 1 |
| 3684 | Kojic Acid Gene Clusters and the Transcriptional Activation Mechanism of Aspergillus flavus KojR on Expression of Clustered Genes. Journal of Fungi (Basel, Switzerland), 2023, 9, 259. | 1.5 | 4 |
| 3685 | Staying below the Radar: Unraveling a New Family of Ubiquitous â€œCrypticâ€• Non-Tailed Temperate Vibriophages and Implications for Their Bacterial Hosts. International Journal of Molecular Sciences, 2023, 24, 3937. | 1.8 | 1 |
| 3686 | Insight into the Organization of the B10v3 Cucumber Genome by Integration of Biological and Bioinformatic Data. International Journal of Molecular Sciences, 2023, 24, 4011. | 1.8 | 4 |
| 3687 | Resistance to the Bacteriocin Lcn972 Deciphered by Genome Sequencing. Microorganisms, 2023, 11, 501. | 1.6 | 2 |
| 3689 | Horizontal Gene Transfer and Fusion Spread Carotenogenesis Among Diverse Heterotrophic Protists. Genome Biology and Evolution, 2023, 15, . | 1.1 | 4 |
| 3690 | Strainâ€specific quorumâ€sensing responses determine virulence properties in <scp><i>Vibrio anguillarum</i></scp>. Environmental Microbiology, 2023, 25, 1344-1362. | 1.8 | 4 |
| 3691 | Profiling of Antimicrobial Metabolites Synthesized by the Endophytic and Genetically Amenable Biocontrol Strain Bacillus velezensis DMW1. Microbiology Spectrum, 2023, 11, . | 1.2 | 5 |
| 3692 | Genomic Epidemiological Analysis of Antimicrobial-Resistant Bacteria with Nanopore Sequencing. Methods in Molecular Biology, 2023, , 227-246. | 0.4 | 0 |

| # | Article | IF | Citations |
|---|---|---|---|
| 3693 | Characterization of a novel<i>Bacillus methylotrophicus</i>phage BM-P1. Food Quality and Safety, 2023, 7, . | 0.6 | 3 |
| 3694 | Genomic Characteristics and Molecular Epidemiology of Multidrug-Resistant Klebsiella pneumoniae Strains Carried by Wild Birds. Microbiology Spectrum, 2023, 11, . | 1.2 | 0 |
| 3697 | Genomic characterization and molecular dating of the novel bacterium Permianibacter aggregans HW001T, which originated from Permian ground water. Marine Life Science and Technology, 2023, 5, 12-27. | 1.8 | 0 |
| 3698 | Isolation, characterization, therapeutic potency, and genomic analysis of a novel bacteriophage vB_KshKPC-M against carbapenemase-producing Klebsiella pneumoniae strains (CRKP) isolated from Ventilator-associated pneumoniae (VAP) infection of COVID-19 patients. Annals of Clinical Microbiology and Antimicrobials, 2023, 22, . | 1.7 | 4 |
| 3699 | Adaptations of <i>Pseudoxylaria</i> towards a comb-associated lifestyle in fungus-farming termite colonies. ISME Journal, 2023, 17, 733-747. | 4.4 | 4 |
| 3700 | A new and accurate qPCR protocol to detect plant pathogenic bacteria of the genus â€˜Candidatus Liberibacterâ€™ in plants and insects. Scientific Reports, 2023, 13, . | 1.6 | 1 |
| 3701 | Prevalence and molecular characteristics of mcr-1-positive Escherichia coli isolated from duck farms and the surrounding environments in coastal China. Microbiological Research, 2023, 270, 127348. | 2.5 | 2 |
| 3702 | Pan-Chromosome and Comparative Analysis of <i>Agrobacterium fabrum</i> Reveal Important Traits Concerning the Genetic Diversity, Evolutionary Dynamics, and Niche Adaptation of the Species. Microbiology Spectrum, 2023, 11, . | 1.2 | 0 |
| 3703 | Emergence of Carbapenemase-Producing Hypervirulent Klebsiella pneumoniae in Switzerland. Antimicrobial Agents and Chemotherapy, 0, , . | 1.4 | 4 |
| 3704 | A caste differentiation mutant elucidates the evolution of socially parasitic ants. Current Biology, 2023, 33, 1047-1058.e4. | 1.8 | 4 |
| 3705 | Complete Genome Sequence of <i>Oceanotoga</i> sp. Strain T3B (DSM 15011). Microbiology Resource Announcements, 2023, 12, . | 0.3 | 0 |
| 3706 | The Complete Mitochondrial Genome of Dendrogale murina (Tupaiidae) and Phylogeny of Scandentia. Genes, 2023, 14, 624. | 1.0 | 1 |
| 3707 | Genomic Comparisons Reveal Selection Pressure and Functional Variation Between Nutritional Endosymbionts of Cave-Adapted and Epigean Hawaiian Planthoppers. Genome Biology and Evolution, 2023, 15, . | 1.1 | 5 |
| 3708 | Whole-Genome Sequencing-Based Resistome Analysis of Nosocomial Multidrug-Resistant Non-Fermenting Gram-Negative Pathogens from the Balkans. Microorganisms, 2023, 11, 651. | 1.6 | 4 |
| 3709 | Genomic Investigation of Salmonella Typhi in Hong Kong Revealing the Predominance of Genotype 3.2.2 and the First Case of an Extensively Drug-Resistant H58 Genotype. Microorganisms, 2023, 11, 667. | 1.6 | 1 |
| 3710 | The terrestrial isopod symbiont â€˜<i>Candidatus</i> Hepatincola porcellionumâ€™ is a potential nutrient scavenger related to <i>Holosporales</i> symbionts of protists. ISME Communications, 2023, 3, . | 1.7 | 2 |
| 3711 | Complete chloroplast genome sequence and phylogenetic analysis of Rhododendron molle G. Don, an endangered Ericaceae species located on Dabie Mountains (central China). Plant Biotechnology Reports, 0, , . | 0.9 | 0 |
| 3712 | Investigation of monacolin K, yellow pigments, and citrinin production capabilities of Monascus purpureus and Monascus ruber (Monascus pilosus). Journal of Food and Drug Analysis, 2023, 31, 85-94. | 0.9 | 2 |

| # | Article | IF | Citations |
|---|---|---|---|
| 3713 | The complete mitochondrial genome of a wild-collected <i>Kappaphycus malesianus</i> (Solieriaceae,) Tj ETQq0 0 0 rgBT /Overlock 10 T | 0.2 | 1 |
| 3715 | Mitogenomic and Phylogenetic Analysis of the Entomopathogenic Fungus Ophiocordyceps lanpingensis and Comparative Analysis with Other Ophiocordyceps Species. Genes, 2023, 14, 710. | 1.0 | 3 |
| 3716 | Characterization of Shigella flexneri Serotype 6 Strains Isolated from Bangladesh and Identification of a New Phylogenetic Cluster. Journal of Bacteriology, 2023, 205, . | 1.0 | 1 |
| 3717 | Adaptation Strategies to High Hydrostatic Pressures in Pseudothermotoga species Revealed by Transcriptional Analyses. Microorganisms, 2023, 11, 773. | 1.6 | 1 |
| 3718 | Complete sequences of six major histocompatibility complex haplotypes, including all the major <scp>MHC</scp> class <scp>II</scp> structures. Hla, 2023, 102, 28-43. | 0.4 | 5 |
| 3719 | Integrative omics identifies conserved and pathogen-specific responses of sepsis-causing bacteria. Nature Communications, 2023, 14, . | 5.8 | 10 |
| 3720 | Plastid Genome Assembly Using Longâ€read data. Molecular Ecology Resources, 2023, 23, 1442-1457. | 2.2 | 4 |
| 3721 | Examination of Large Chromosomal Inversions in the Genome of <i>Erwinia amylovora</i> Strains Reveals Worldwide Distribution and North America-Specific Types. Phytopathology, 2023, 113, 2174-2186. | 1.1 | 3 |
| 3723 | A Complete Genome of the Alphaproteobacterial Methanotroph Methylocystis parvus OBBP. Microbiology Resource Announcements, 2023, 12, . | 0.3 | 0 |
| 3724 | The evolution of white-tailed jackrabbit camouflage in response to past and future seasonal climates. Science, 2023, 379, 1238-1242. | 6.0 | 5 |
| 3725 | Global scenario of the RmtE pan-aminoglycoside-resistance mechanism: emergence of the rmtE4 gene in South America associated with a hospital-related IncL plasmid. Microbial Genomics, 2023, 9, . | 1.0 | 0 |
| 3726 | Comparative analysis of complete Artemisia subgenus Seriphidium (Asteraceae: Anthemideae) chloroplast genomes: insights into structural divergence and phylogenetic relationships. BMC Plant Biology, 2023, 23, . | 1.6 | 5 |
| 3727 | Comparative genome and phylogenetic analysis revealed the complex mitochondrial genome and phylogenetic position of Conopomorpha sinensis Bradley. Scientific Reports, 2023, 13, . | 1.6 | 0 |
| 3728 | Assembling highly repetitive Xanthomonas TALomes using Oxford Nanopore sequencing. BMC Genomics, 2023, 24, . | 1.2 | 3 |
| 3729 | Highly contiguous genomes of human clinical isolates of Giardia duodenalis reveal assemblage- and sub-assemblage-specific presenceâ€“absence variation in protein-coding genes. Microbial Genomics, 2023, 9, . | 1.0 | 1 |
| 3730 | NGS Reads Dataset of Sunflower Interspecific Hybrids. Data, 2023, 8, 67. | 1.2 | 1 |
| 3731 | Genome Alignments. , 2023, , . |  | 0 |
| 3732 | Vibrio type III secretion system 2 is not restricted to the Vibrionaceae and encodes differentially distributed repertoires of effector proteins. Microbial Genomics, 2023, 9, . | 1.0 | 0 |

| # | ARTICLE | IF | CITATIONS |
|---|---|---|---|
| 3733 | Genomic Islands in Helicobacter Species. , 2023, , 197-206. | | 0 |
| 3734 | Computation Tools for Prediction and Analysis of Genomic Islands. , 2023, , 17-31. | | 0 |
| 3735 | Parapatric speciation of Meiothermus in serpentinite-hosted aquifers in Oman. Frontiers in Microbiology, 0, 14, . | 1.5 | 1 |
| 3736 | A conserved hymenopteran-specific family of cytochrome P450s protects bee pollinators from toxic nectar alkaloids. Science Advances, 2023, 9, . | 4.7 | 4 |
| 3737 | Genome Organization of Four Brazilian Xanthomonas albilineans Strains Does Not Correlate with Aggressiveness. Microbiology Spectrum, 0, , . | 1.2 | 1 |
| 3738 | Exploration of the diversity of multi-drug resistant Mycobacterium tuberculosis complex in Lagos, Nigeria using WGS: Distribution of lineages, drug resistance patterns and genetic mutations. Tuberculosis, 2023, 140, 102343. | 0.8 | 0 |
| 3739 | Draft Genome Sequences and Genome Characterization of Three Toxigenic and Two Nontoxigenic Clostridioides difficile Clinical Isolates from Florida, USA. Microbiology Resource Announcements, 0, , . | 0.3 | 0 |
| 3741 | Genomic determination of breeding systems and trans-specific evolution of <i>HD MAT</i> genes in suilloid fungi. Genetics, 2023, 224, . | 1.2 | 1 |
| 3742 | Plastid Phylogenomic Analyses Reveal a Cryptic Species of Ligusticopsis (Apiaceae, Angiosperms). International Journal of Molecular Sciences, 2023, 24, 7419. | 1.8 | 1 |
| 3743 | A pathogenicity locus of Streptococcus gallolyticus subspecies gallolyticus. Scientific Reports, 2023, 13, . | 1.6 | 4 |
| 3744 | Comparative genomic insights into habitat adaptation of coral-associated Prosthecochloris. Frontiers in Microbiology, 0, 14, . | 1.5 | 1 |
| 3745 | Integrated computational approaches to aid precision medicine for cancer therapy: Present scenario and future prospects. , 2023, , 403-424. | | 0 |
| 3746 | Asfarviruses and Closely Related Giant Viruses. Viruses, 2023, 15, 1015. | 1.5 | 1 |
| 4042 | Generation of host-pathogen interaction data: an overview of recent technological advancements. , 2024, , 53-79. | | 0 |