

Johan Bengtsson-Palme

List of Publications by Year in descending order

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Version: 2024-02-01

74
papers

14,351
citations

117453

34
h-index

98622

67
g-index

84
all docs

84
docs citations

84
times ranked

17546
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | CAFE: a software suite for analysis of paired-sample transposon insertion sequencing data. <i>Bioinformatics</i> , 2021, 37, 121-122. | 1.8 | 4 |
| 2 | Microbial retention and resistances in stormwater quality improvement devices treating road runoff. <i>FEMS Microbes</i> , 2021, 2, . | 0.8 | 1 |
| 3 | Microbial Community Interactions Are Sensitive to Small Changes in Temperature. <i>Frontiers in Microbiology</i> , 2021, 12, 672910. | 1.5 | 15 |
| 4 | Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 8: Pleuromutilins: tiamulin and valnemulin. <i>EFSA Journal</i> , 2021, 19, e06860. | 0.9 | 8 |
| 5 | Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 10: Quinolones: flumequine and oxolinic acid. <i>EFSA Journal</i> , 2021, 19, e06862. | 0.9 | 8 |
| 6 | Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 1: Methodology, general data gaps and uncertainties. <i>EFSA Journal</i> , 2021, 19, e06852. | 0.9 | 11 |
| 7 | Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 13: Diaminopyrimidines: trimethoprim. <i>EFSA Journal</i> , 2021, 19, e06865. | 0.9 | 12 |
| 8 | Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 9: Polymyxins: colistin. <i>EFSA Journal</i> , 2021, 19, e06861. | 0.9 | 10 |
| 9 | Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 7: Amphenicols: florfenicol and thiamphenicol. <i>EFSA Journal</i> , 2021, 19, e06859. | 0.9 | 4 |
| 10 | Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 11: Sulfonamides. <i>EFSA Journal</i> , 2021, 19, e06863. | 0.9 | 13 |
| 11 | Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 12: Tetracyclines: tetracycline, chlortetracycline, oxytetracycline, and doxycycline. <i>EFSA Journal</i> , 2021, 19, e06864. | 0.9 | 5 |
| 12 | Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 6: Macrolides: tilmicosin, tylosin and tylvalosin. <i>EFSA Journal</i> , 2021, 19, e06858. | 0.9 | 8 |
| 13 | Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 2: Aminoglycosides/aminocyclitols: apramycin, paromomycin, neomycin and spectinomycin. <i>EFSA Journal</i> , 2021, 19, e06853. | 0.9 | 9 |
| 14 | Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 4: β -Lactams: amoxicillin and penicillin V. <i>EFSA Journal</i> , 2021, 19, e06855. | 0.9 | 3 |
| 15 | Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 5: Lincosamides: lincomycin. <i>EFSA Journal</i> , 2021, 19, e06856. | 0.9 | 14 |
| 16 | What Is the Role of the Environment in the Emergence of Novel Antibiotic Resistance Genes? A Modeling Approach. <i>Environmental Science & Technology</i> , 2021, 55, 15734-15743. | 4.6 | 28 |
| 17 | Microbial model communities: To understand complexity, harness the power of simplicity. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3987-4001. | 1.9 | 27 |
| 18 | Industrial wastewater treatment plant enriches antibiotic resistance genes and alters the structure of microbial communities. <i>Water Research</i> , 2019, 162, 437-445. | 5.3 | 95 |

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|----|--|------|-----------|
| 19 | Diarrheal bacterial pathogens and multi-resistant enterobacteria in the Choqueyapu River in La Paz, Bolivia. PLoS ONE, 2019, 14, e0210735. | 1.1 | 33 |
| 20 | Assessment and Management of Risks Associated With Antibiotic Resistance in the Environment. , 2019, , 243-263. | | 6 |
| 21 | The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. Nucleic Acids Research, 2019, 47, D259-D264. | 6.5 | 2,072 |
| 22 | Introducing ribosomal tandem repeat barcoding for fungi. Molecular Ecology Resources, 2019, 19, 118-127. | 2.2 | 78 |
| 23 | Selective concentration for ciprofloxacin resistance in Escherichia coli grown in complex aquatic bacterial biofilms. Environment International, 2018, 116, 255-268. | 4.8 | 71 |
| 24 | Protection goals must guide risk assessment for antibiotics. Environment International, 2018, 111, 352-353. | 4.8 | 12 |
| 25 | Environmental factors influencing the development and spread of antibiotic resistance. FEMS Microbiology Reviews, 2018, 42, . | 3.9 | 612 |
| 26 | Can branding and price of pharmaceuticals guide informed choices towards improved pollution control during manufacturing?. Journal of Cleaner Production, 2018, 171, 137-146. | 4.6 | 25 |
| 27 | The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of antimicrobial resistance determinants using next generation sequencing technologies. F1000Research, 2018, 7, 459. | 0.8 | 31 |
| 28 | Maternal gut and breast milk microbiota affect infant gut antibiotic resistome and mobile genetic elements. Nature Communications, 2018, 9, 3891. | 5.8 | 313 |
| 29 | Metaxa2 Database Builder: enabling taxonomic identification from metagenomic or metabarcoding data using any genetic marker. Bioinformatics, 2018, 34, 4027-4033. | 1.8 | 36 |
| 30 | Structure and function of the global topsoil microbiome. Nature, 2018, 560, 233-237. | 13.7 | 1,370 |
| 31 | The diversity of uncharacterized antibiotic resistance genes can be predicted from known gene variantsâ€”but not always. Microbiome, 2018, 6, 125. | 4.9 | 39 |
| 32 | Taxonomic annotation of public fungal ITS sequences from the built environment â€” a report from an April 10â€”11, 2017 workshop (Aberdeen, UK). MycoKeys, 2018, 28, 65-82. | 0.8 | 33 |
| 33 | Substrate-bound outward-open structure of a Na ⁺ -coupled sialic acid symporter reveals a new Na ⁺ site. Nature Communications, 2018, 9, 1753. | 5.8 | 62 |
| 34 | Strategies for Taxonomic and Functional Annotation of Metagenomes. , 2018, , 55-79. | | 11 |
| 35 | Critical knowledge gaps and research needs related to the environmental dimensions of antibiotic resistance. Environment International, 2018, 117, 132-138. | 4.8 | 281 |
| 36 | The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of antimicrobial resistance determinants using next generation sequencing technologies. F1000Research, 2018, 7, 459. | 0.8 | 24 |

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|----|--|-----|-----------|
| 37 | A reference cytochrome c oxidase subunit I database curated for hierarchical classification of arthropod metabarcoding data. PeerJ, 2018, 6, e5126. | 0.9 | 14 |
| 38 | Antibiotic resistance in the food supply chain: where can sequencing and metagenomics aid risk assessment?. Current Opinion in Food Science, 2017, 14, 66-71. | 4.1 | 76 |
| 39 | Does antifouling paint select for antibiotic resistance?. Science of the Total Environment, 2017, 590-591, 461-468. | 3.9 | 70 |
| 40 | The complete mitochondrial genome of the copepod Calanus glacialis. Mitochondrial DNA Part B: Resources, 2017, 2, 506-507. | 0.2 | 2 |
| 41 | <i>In Vivo</i> Analysis of the Viable Microbiota and Helicobacter pylori Transcriptome in Gastric Infection and Early Stages of Carcinogenesis. Infection and Immunity, 2017, 85, . | 1.0 | 55 |
| 42 | Using metagenomics to investigate human and environmental resistomes. Journal of Antimicrobial Chemotherapy, 2017, 72, 2690-2703. | 1.3 | 87 |
| 43 | Evaluating and optimizing the performance of software commonly used for the taxonomic classification of <i>scp</i> DNA <i>scp</i> metabarcoding sequence data. Molecular Ecology Resources, 2017, 17, 760-769. | 2.2 | 38 |
| 44 | Computational discovery and functional validation of novel fluoroquinolone resistance genes in public metagenomic data sets. BMC Genomics, 2017, 18, 682. | 1.2 | 24 |
| 45 | The relation between Blastocystis and the intestinal microbiota in Swedish travellers. BMC Microbiology, 2017, 17, 231. | 1.3 | 56 |
| 46 | Identification of 76 novel B1 metallo- β -lactamases through large-scale screening of genomic and metagenomic data. Microbiome, 2017, 5, 134. | 4.9 | 75 |
| 47 | Metaxa2 Diversity Tools: Easing microbial community analysis with Metaxa2. Ecological Informatics, 2016, 33, 45-50. | 2.3 | 30 |
| 48 | The structure and diversity of human, animal and environmental resistomes. Microbiome, 2016, 4, 54. | 4.9 | 355 |
| 49 | FARAO: the flexible all-round annotation organizer. Bioinformatics, 2016, 32, 3664-3666. | 1.8 | 6 |
| 50 | Elucidating selection processes for antibiotic resistance in sewage treatment plants using metagenomics. Science of the Total Environment, 2016, 572, 697-712. | 3.9 | 213 |
| 51 | Strategies to improve usability and preserve accuracy in biological sequence databases. Proteomics, 2016, 16, 2454-2460. | 1.3 | 27 |
| 52 | Minimal selective concentrations of tetracycline in complex aquatic bacterial biofilms. Science of the Total Environment, 2016, 553, 587-595. | 3.9 | 166 |
| 53 | Concentrations of antibiotics predicted to select for resistant bacteria: Proposed limits for environmental regulation. Environment International, 2016, 86, 140-149. | 4.8 | 612 |
| 54 | A Comprehensive, Automatically Updated Fungal ITS Sequence Dataset for Reference-Based Chimera Control in Environmental Sequencing Efforts. Microbes and Environments, 2015, 30, 145-150. | 0.7 | 231 |

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|----|--|------|-----------|
| 55 | Co-occurrence of resistance genes to antibiotics, biocides and metals reveals novel insights into their co-selection potential. <i>BMC Genomics</i> , 2015, 16, 964. | 1.2 | 587 |
| 56 | <scp>metaxa</scp>2: improved identification and taxonomic classification of small and large subunit rRNA in metagenomic data. <i>Molecular Ecology Resources</i> , 2015, 15, 1403-1414. | 2.2 | 426 |
| 57 | Metagenomic sequencing of marine periphyton: taxonomic and functional insights into biofilm communities. <i>Frontiers in Microbiology</i> , 2015, 6, 1192. | 1.5 | 49 |
| 58 | Antibiotic resistance genes in the environment: prioritizing risks. <i>Nature Reviews Microbiology</i> , 2015, 13, 396-396. | 13.6 | 194 |
| 59 | The European technical report on aquatic effect-based monitoring tools under the water framework directive. <i>Environmental Sciences Europe</i> , 2015, 27, . | 11.0 | 196 |
| 60 | The Human Gut Microbiome as a Transporter of Antibiotic Resistance Genes between Continents. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 6551-6560. | 1.4 | 155 |
| 61 | <scp>ITS</scp>1: a <scp>DNA</scp> barcode better than <scp>ITS</scp>2 in eukaryotes?. <i>Molecular Ecology Resources</i> , 2015, 15, 573-586. | 2.2 | 152 |
| 62 | Metaxa, Overview. , 2015, , 467-471. | | 0 |
| 63 | Metagenomics reveals that detoxification systems are underrepresented in marine bacterial communities. <i>BMC Genomics</i> , 2014, 15, 749. | 1.2 | 35 |
| 64 | Shotgun metagenomics reveals a wide array of antibiotic resistance genes and mobile elements in a polluted lake in India. <i>Frontiers in Microbiology</i> , 2014, 5, 648. | 1.5 | 193 |
| 65 | BacMet: antibacterial biocide and metal resistance genes database. <i>Nucleic Acids Research</i> , 2014, 42, D737-D743. | 6.5 | 564 |
| 66 | Improving ITS sequence data for identification of plant pathogenic fungi. <i>Fungal Diversity</i> , 2014, 67, 11-19. | 4.7 | 123 |
| 67 | Metaxa, Overview. , 2014, , 1-5. | | 1 |
| 68 | Improved software detection and extraction of ITS1 and <scp>ITS</scp>2 from ribosomal <scp>ITS</scp> sequences of fungi and other eukaryotes for analysis of environmental sequencing data. <i>Methods in Ecology and Evolution</i> , 2013, 4, 914-919. | 2.2 | 868 |
| 69 | Towards a unified paradigm for sequence-based identification of fungi. <i>Molecular Ecology</i> , 2013, 22, 5271-5277. | 2.0 | 2,997 |
| 70 | Megraft: a software package to graft ribosomal small subunit (16S/18S) fragments onto full-length sequences for accurate species richness and sequencing depth analysis in pyrosequencing-length metagenomes and similar environmental datasets. <i>Research in Microbiology</i> , 2012, 163, 407-412. | 1.0 | 12 |
| 71 | Metaxa: a software tool for automated detection and discrimination among ribosomal small subunit (12S/16S/18S) sequences of archaea, bacteria, eukaryotes, mitochondria, and chloroplasts in metagenomes and environmental sequencing datasets. <i>Antonie Van Leeuwenhoek</i> , 2011, 100, 471-475. | 0.7 | 88 |
| 72 | Five simple guidelines for establishing basic authenticity and reliability of newly generated fungal ITS sequences. <i>MycoKeys</i> , 0, 4, 37-63. | 0.8 | 157 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 73 | Mumame: a software tool for quantifying gene-specific point-mutations in shotgun metagenomic data. Metabarcoding and Metagenomics, 0, 3, . | 0.0 | 2 |
| 74 | Annotating public fungal ITS sequences from the built environment according to the MlxS-Built Environment standard "a report from a May 23-24, 2016 workshop (Gothenburg, Sweden). MycoKeys, 0, 16, 1-15. | 0.8 | 16 |