

Johan Bengtsson-Palme

List of Publications by Citations

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Version: 2024-04-19

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

72
papers

8,354
citations

33
h-index

84
g-index

84
ext. papers

11,742
ext. citations

7.8
avg. IF

6.36
L-index

#	Paper	IF	Citations
72	Towards a unified paradigm for sequence-based identification of fungi. <i>Molecular Ecology</i> , 2013 , 22, 5271-7	3.7	2019
71	The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. <i>Nucleic Acids Research</i> , 2019 , 47, D259-D264	20.1	864
70	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018 , 560, 233-237	50.4	654
69	Concentrations of antibiotics predicted to select for resistant bacteria: Proposed limits for environmental regulation. <i>Environment International</i> , 2016 , 86, 140-9	12.9	386
68	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	4.5	370
67	Environmental factors influencing the development and spread of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , 2018 , 42,	15.1	361
66	Improved software detection and extraction of ITS1 and ITS2 from ribosomal ITS sequences of fungi and other eukaryotes for analysis of environmental sequencing data. <i>Methods in Ecology and Evolution</i> , 2013 , 4, n/a-n/a	7.7	312
65	BacMet: antibacterial biocide and metal resistance genes database. <i>Nucleic Acids Research</i> , 2014 , 42, D737-43	20.1	310
64	METAXA2: improved identification and taxonomic classification of small and large subunit rRNA in metagenomic data. <i>Molecular Ecology Resources</i> , 2015 , 15, 1403-14	8.4	252
63	The structure and diversity of human, animal and environmental resistomes. <i>Microbiome</i> , 2016 , 4, 54	16.6	239
62	Critical knowledge gaps and research needs related to the environmental dimensions of antibiotic resistance. <i>Environment International</i> , 2018 , 117, 132-138	12.9	183
61	Elucidating selection processes for antibiotic resistance in sewage treatment plants using metagenomics. <i>Science of the Total Environment</i> , 2016 , 572, 697-712	10.2	152
60	The European technical report on aquatic effect-based monitoring tools under the water framework directive. <i>Environmental Sciences Europe</i> , 2015 , 27,		151
59	Maternal gut and breast milk microbiota affect infant gut antibiotic resistome and mobile genetic elements. <i>Nature Communications</i> , 2018 , 9, 3891	17.4	145
58	A Comprehensive, Automatically Updated Fungal ITS Sequence Dataset for Reference-Based Chimera Control in Environmental Sequencing Efforts. <i>Microbes and Environments</i> , 2015 , 30, 145-50	2.6	144
57	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	5.7	144
56	Antibiotic resistance genes in the environment: prioritizing risks. <i>Nature Reviews Microbiology</i> , 2015 , 13, 396	22.2	134

55	Five simple guidelines for establishing basic authenticity and reliability of newly generated fungal ITS sequences. <i>MycoKeys</i> , 2012 , 4, 37-63	2.4	126
54	The Human Gut Microbiome as a Transporter of Antibiotic Resistance Genes between Continents. <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 6551-60	5.9	120
53	Minimal selective concentrations of tetracycline in complex aquatic bacterial biofilms. <i>Science of the Total Environment</i> , 2016 , 553, 587-595	10.2	116
52	Improving ITS sequence data for identification of plant pathogenic fungi. <i>Fungal Diversity</i> , 2014 , 67, 11-19	7.6	101
51	ITS1: a DNA barcode better than ITS2 in eukaryotes?. <i>Molecular Ecology Resources</i> , 2015 , 15, 573-86	8.4	97
50	Using metagenomics to investigate human and environmental resistomes. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 2690-2703	5.1	63
49	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, 471-5	2.1	61
48	Antibiotic resistance in the food supply chain: where can sequencing and metagenomics aid risk assessment?. <i>Current Opinion in Food Science</i> , 2017 , 14, 66-71	9.8	58
47	Selective concentration for ciprofloxacin resistance in <i>Escherichia coli</i> grown in complex aquatic bacterial biofilms. <i>Environment International</i> , 2018 , 116, 255-268	12.9	49
46	Introducing ribosomal tandem repeat barcoding for fungi. <i>Molecular Ecology Resources</i> , 2019 , 19, 118-128	7.4	46
45	Industrial wastewater treatment plant enriches antibiotic resistance genes and alters the structure of microbial communities. <i>Water Research</i> , 2019 , 162, 437-445	12.5	45
44	Identification of 76 novel B1 metallo- β -lactamases through large-scale screening of genomic and metagenomic data. <i>Microbiome</i> , 2017 , 5, 134	16.6	44
43	Does antifouling paint select for antibiotic resistance?. <i>Science of the Total Environment</i> , 2017 , 590-591, 461-468	10.2	42
42	Analysis of the Viable Microbiota and <i>Helicobacter pylori</i> Transcriptome in Gastric Infection and Early Stages of Carcinogenesis. <i>Infection and Immunity</i> , 2017 , 85,	3.7	40
41	The relation between <i>Blastocystis</i> and the intestinal microbiota in Swedish travellers. <i>BMC Microbiology</i> , 2017 , 17, 231	4.5	37
40	Substrate-bound outward-open structure of a Na-coupled sialic acid symporter reveals a new Na site. <i>Nature Communications</i> , 2018 , 9, 1753	17.4	36
39	Metagenomic sequencing of marine periphyton: taxonomic and functional insights into biofilm communities. <i>Frontiers in Microbiology</i> , 2015 , 6, 1192	5.7	33
38	Evaluating and optimizing the performance of software commonly used for the taxonomic classification of DNA metabarcoding sequence data. <i>Molecular Ecology Resources</i> , 2017 , 17, 760-769	8.4	30

37	The diversity of uncharacterized antibiotic resistance genes can be predicted from known gene variants-but not always. <i>Microbiome</i> , 2018 , 6, 125	16.6	27
36	Metaxa2 Database Builder: enabling taxonomic identification from metagenomic or metabarcoding data using any genetic marker. <i>Bioinformatics</i> , 2018 , 34, 4027-4033	7.2	26
35	Metagenomics reveals that detoxification systems are underrepresented in marine bacterial communities. <i>BMC Genomics</i> , 2014 , 15, 749	4.5	22
34	Can branding and price of pharmaceuticals guide informed choices towards improved pollution control during manufacturing?. <i>Journal of Cleaner Production</i> , 2018 , 171, 137-146	10.3	21
33	The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of antimicrobial resistance determinants using next generation sequencing technologies. <i>F1000Research</i> , 2018 , 7, 459	3.6	21
32	Strategies to improve usability and preserve accuracy in biological sequence databases. <i>Proteomics</i> , 2016 , 16, 2454-60	4.8	19
31	Taxonomic annotation of public fungal ITS sequences from the built environment - a report from an April 10-11, 2017 workshop (Aberdeen, UK). <i>MycoKeys</i> , 2018 , 65-82	2.4	18
30	Metaxa2 Diversity Tools: Easing microbial community analysis with Metaxa2. <i>Ecological Informatics</i> , 2016 , 33, 45-50	4.2	18
29	Computational discovery and functional validation of novel fluoroquinolone resistance genes in public metagenomic data sets. <i>BMC Genomics</i> , 2017 , 18, 682	4.5	16
28	Diarrheal bacterial pathogens and multi-resistant enterobacteria in the Choqueyapu River in La Paz, Bolivia. <i>PLoS ONE</i> , 2019 , 14, e0210735	3.7	14
27	Annotating public fungal ITS sequences from the built environment according to the MixS-Built Environment standard - a report from a May 23-24, 2016 workshop (Gothenburg, Sweden). <i>MycoKeys</i> , 2016 , 1-15	2.4	13
26	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 5:. <i>EFSA Journal</i> , 2021 , 19, e06856	2.3	13
25	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, 407-12	4	12
24	The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of antimicrobial resistance determinants using next generation sequencing technologies. <i>F1000Research</i> , 2018 , 7, 459	3.6	12
23	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 13:. <i>EFSA Journal</i> , 2021 , 19, e06865	2.3	12
22	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 11:. <i>EFSA Journal</i> , 2021 , 19, e06863	2.3	12
21	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 1:. <i>EFSA Journal</i> , 2021 , 19, e06852	2.3	10
20	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed.?Part 9:. <i>EFSA Journal</i> , 2021 , 19, e06861	2.3	10

19	A reference cytochrome c oxidase subunit I database curated for hierarchical classification of arthropod metabarcoding data. <i>PeerJ</i> , 2018 , 6, e5126	3.1	9
18	Microbial model communities: To understand complexity, harness the power of simplicity. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 3987-4001	6.8	9
17	Protection goals must guide risk assessment for antibiotics. <i>Environment International</i> , 2018 , 111, 352-353.	3.9	8
16	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 8:. <i>EFSA Journal</i> , 2021 , 19, e06860	2.3	8
15	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed.?Part 10:. <i>EFSA Journal</i> , 2021 , 19, e06862	2.3	8
14	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed.?Part 6:. <i>EFSA Journal</i> , 2021 , 19, e06858	2.3	8
13	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed.?Part 2:. <i>EFSA Journal</i> , 2021 , 19, e06853	2.3	8
12	Strategies for Taxonomic and Functional Annotation of Metagenomes 2018 , 55-79		6
11	Introducing ribosomal tandem repeat barcoding for fungi		6
10	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	10.3	5
9	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 7:. <i>EFSA Journal</i> , 2021 , 19, e06859	2.3	4
8	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 12:. <i>EFSA Journal</i> , 2021 , 19, e06864	2.3	4
7	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed.?Part 4:. <i>EFSA Journal</i> , 2021 , 19, e06855	2.3	3
6	The complete mitochondrial genome of the copepod. <i>Mitochondrial DNA Part B: Resources</i> , 2017 , 2, 506-507		2
5	Mumame: a software tool for quantifying gene-specific point-mutations in shotgun metagenomic data. <i>Metabarcoding and Metagenomics</i> ,3,		2
4	Assessment and Management of Risks Associated With Antibiotic Resistance in the Environment 2019 , 243-263		2
3	Microbial Community Interactions Are Sensitive to Small Changes in Temperature. <i>Frontiers in Microbiology</i> , 2021 , 12, 672910	5.7	1
2	FARAO: the flexible all-round annotation organizer. <i>Bioinformatics</i> , 2016 , 32, 3664-3666	7.2	1

1 Strategies to Reduce or Eliminate Resistant Pathogens in the Environment **2019**, 637-673

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