Johan Bengtsson-Palme

List of Publications by Year in Descending Order

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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	What Is the Role of the Environment in the Emergence of Novel Antibiotic Resistance Genes? A Modeling Approach. *Environmental Science & Technology*, **2021**, 55, 15734-15743	10.3	5
71	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 8:. *EFSA Journal*, **2021**, 19, e06860	2.3	8
70	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed.?Part 10:. *EFSA Journal*, **2021**, 19, e06862	2.3	8
69	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 1:. *EFSA Journal*, **2021**, 19, e06852	2.3	10
68	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 13:. *EFSA Journal*, **2021**, 19, e06865	2.3	12
67	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed.?Part 9:. *EFSA Journal*, **2021**, 19, e06861	2.3	10
66	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 7:. *EFSA Journal*, **2021**, 19, e06859	2.3	4
65	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 11:. *EFSA Journal*, **2021**, 19, e06863	2.3	12
64	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 12:. *EFSA Journal*, **2021**, 19, e06864	2.3	4
63	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed.?Part 6:. *EFSA Journal*, **2021**, 19, e06858	2.3	8
62	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed.?Part 2:. *EFSA Journal*, **2021**, 19, e06853	2.3	8
61	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed.?Part 4:. *EFSA Journal*, **2021**, 19, e06855	2.3	3
60	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 5:. *EFSA Journal*, **2021**, 19, e06856	2.3	13
59	Microbial Community Interactions Are Sensitive to Small Changes in Temperature. *Frontiers in Microbiology*, **2021**, 12, 672910	5.7	1
58	Microbial model communities: To understand complexity, harness the power of simplicity. *Computational and Structural Biotechnology Journal*, **2020**, 18, 3987-4001	6.8	9
57	Diarrheal bacterial pathogens and multi-resistant enterobacteria in the Choqueyapu River in La Paz, Bolivia. *PLoS ONE*, **2019**, 14, e0210735	3.7	14
56	Industrial wastewater treatment plant enriches antibiotic resistance genes and alters the structure of microbial communities. *Water Research*, **2019**, 162, 437-445	12.5	45

55	Strategies to Reduce or Eliminate Resistant Pathogens in the Environment **2019**, 637-673		0
54	Assessment and Management of Risks Associated With Antibiotic Resistance in the Environment **2019**, 243-263		2
53	The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. *Nucleic Acids Research*, **2019**, 47, D259-D264	20.1	864
52	Introducing ribosomal tandem repeat barcoding for fungi. *Molecular Ecology Resources*, **2019**, 19, 118-127	8.4	46
51	Selective concentration for ciprofloxacin resistance in Escherichia coli grown in complex aquatic bacterial biofilms. *Environment International*, **2018**, 116, 255-268	12.9	49
50	Protection goals must guide risk assessment for antibiotics. *Environment International*, **2018**, 111, 352-353	12.9	8
49	Environmental factors influencing the development and spread of antibiotic resistance. *FEMS Microbiology Reviews*, **2018**, 42,	15.1	361
48	Can branding and price of pharmaceuticals guide informed choices towards improved pollution control during manufacturing?. *Journal of Cleaner Production*, **2018**, 171, 137-146	10.3	21
47	Structure and function of the global topsoil microbiome. *Nature*, **2018**, 560, 233-237	50.4	654
46	The diversity of uncharacterized antibiotic resistance genes can be predicted from known gene variants-but not always. *Microbiome*, **2018**, 6, 125	16.6	27
45	Taxonomic annotation of public fungal ITS sequences from the built environment - a report from an April 10-11, 2017 workshop (Aberdeen, UK). *MycoKeys*, **2018**, 65-82	2.4	18
44	Substrate-bound outward-open structure of a Na-coupled sialic acid symporter reveals a new Na site. *Nature Communications*, **2018**, 9, 1753	17.4	36
43	Strategies for Taxonomic and Functional Annotation of Metagenomes **2018**, 55-79		6
42	Critical knowledge gaps and research needs related to the environmental dimensions of antibiotic resistance. *Environment International*, **2018**, 117, 132-138	12.9	183
41	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	3.6	12
40	A reference cytochrome c oxidase subunit I database curated for hierarchical classification of arthropod metabarcoding data. *PeerJ*, **2018**, 6, e5126	3.1	9
39	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	3.6	21
38	Maternal gut and breast milk microbiota affect infant gut antibiotic resistome and mobile genetic elements. *Nature Communications*, **2018**, 9, 3891	17.4	145

37	Metaxa2 Database Builder: enabling taxonomic identification from metagenomic or metabarcoding data using any genetic marker. *Bioinformatics*, **2018**, 34, 4027-4033	7.2	26
36	Antibiotic resistance in the food supply chain: where can sequencing and metagenomics aid risk assessment?. *Current Opinion in Food Science*, **2017**, 14, 66-71	9.8	58
35	Does antifouling paint select for antibiotic resistance?. *Science of the Total Environment*, **2017**, 590-591, 461-468	10.2	42
34	Computational discovery and functional validation of novel fluoroquinolone resistance genes in public metagenomic data sets. *BMC Genomics*, **2017**, 18, 682	4.5	16
33	The relation between Blastocystis and the intestinal microbiota in Swedish travellers. *BMC Microbiology*, **2017**, 17, 231	4.5	37
32	Identification of 76 novel B1 metallo-β-lactamases through large-scale screening of genomic and metagenomic data. *Microbiome*, **2017**, 5, 134	16.6	44
31	The complete mitochondrial genome of the copepod. *Mitochondrial DNA Part B: Resources*, **2017**, 2, 506-507	0.5	2
30	Analysis of the Viable Microbiota and Helicobacter pylori Transcriptome in Gastric Infection and Early Stages of Carcinogenesis. *Infection and Immunity*, **2017**, 85,	3.7	40
29	Using metagenomics to investigate human and environmental resistomes. *Journal of Antimicrobial Chemotherapy*, **2017**, 72, 2690-2703	5.1	63
28	Evaluating and optimizing the performance of software commonly used for the taxonomic classification of DNA metabarcoding sequence data. *Molecular Ecology Resources*, **2017**, 17, 760-769	8.4	30
27	Elucidating selection processes for antibiotic resistance in sewage treatment plants using metagenomics. *Science of the Total Environment*, **2016**, 572, 697-712	10.2	152
26	Strategies to improve usability and preserve accuracy in biological sequence databases. *Proteomics*, **2016**, 16, 2454-60	4.8	19
25	Minimal selective concentrations of tetracycline in complex aquatic bacterial biofilms. *Science of the Total Environment*, **2016**, 553, 587-595	10.2	116
24	Concentrations of antibiotics predicted to select for resistant bacteria: Proposed limits for environmental regulation. *Environment International*, **2016**, 86, 140-9	12.9	386
23	Metaxa2 Diversity Tools: Easing microbial community analysis with Metaxa2. *Ecological Informatics*, **2016**, 33, 45-50	4.2	18
22	The structure and diversity of human, animal and environmental resistomes. *Microbiome*, **2016**, 4, 54	16.6	239
21	FARAO: the flexible all-round annotation organizer. *Bioinformatics*, **2016**, 32, 3664-3666	7.2	1
20	Antibiotic resistance genes in the environment: prioritizing risks. *Nature Reviews Microbiology*, **2015**, 13, 396	22.2	134

19	The European technical report on aquatic effect-based monitoring tools under the water framework directive. *Environmental Sciences Europe*, **2015**, 27,		151
18	The Human Gut Microbiome as a Transporter of Antibiotic Resistance Genes between Continents. *Antimicrobial Agents and Chemotherapy*, **2015**, 59, 6551-60	5.9	120
17	ITS1: a DNA barcode better than ITS2 in eukaryotes?. *Molecular Ecology Resources*, **2015**, 15, 573-86	8.4	97
16	A Comprehensive, Automatically Updated Fungal ITS Sequence Dataset for Reference-Based Chimera Control in Environmental Sequencing Efforts. *Microbes and Environments*, **2015**, 30, 145-50	2.6	144
15	Co-occurrence of resistance genes to antibiotics, biocides and metals reveals novel insights into their co-selection potential. *BMC Genomics*, **2015**, 16, 964	4.5	370
14	METAXA2: improved identification and taxonomic classification of small and large subunit rRNA in metagenomic data. *Molecular Ecology Resources*, **2015**, 15, 1403-14	8.4	252
13	Metagenomic sequencing of marine periphyton: taxonomic and functional insights into biofilm communities. *Frontiers in Microbiology*, **2015**, 6, 1192	5.7	33
12	BacMet: antibacterial biocide and metal resistance genes database. *Nucleic Acids Research*, **2014**, 42, D737-43	20.1	310
11	Improving ITS sequence data for identification of plant pathogenic fungi. *Fungal Diversity*, **2014**, 67, 11-19	17.6	101
10	Metagenomics reveals that detoxification systems are underrepresented in marine bacterial communities. *BMC Genomics*, **2014**, 15, 749	4.5	22
9	Shotgun metagenomics reveals a wide array of antibiotic resistance genes and mobile elements in a polluted lake in India. *Frontiers in Microbiology*, **2014**, 5, 648	5.7	144
8	Improved software detection and extraction of ITS1 and ITS2 from ribosomal ITS sequences of fungi and other eukaryotes for analysis of environmental sequencing data. *Methods in Ecology and Evolution*, **2013**, 4, n/a-n/a	7.7	312
7	Towards a unified paradigm for sequence-based identification of fungi. *Molecular Ecology*, **2013**, 22, 5271-7	5.7	2019
6	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. *Research in Microbiology*, **2012**, 163, 407-12	4	12
5	Five simple guidelines for establishing basic authenticity and reliability of newly generated fungal ITS sequences. *MycoKeys*, **2012**, 4, 37-63	2.4	126
4	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. *Antonie Van Leeuwenhoek*, **2011**, 100, 471-5	2.1	61
3	Mumame: a software tool for quantifying gene-specific point-mutations in shotgun metagenomic data. *Metabarcoding and Metagenomics*,3,		2
2	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). *MycoKeys*,16, 1-15	2.4	13

1 Introducing ribosomal tandem repeat barcoding for fungi 6