

# Johan Bengtsson-Palme

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5519849/publications.pdf>

Version: 2024-02-01

74  
papers

14,351  
citations

117625

34  
h-index

98798

67  
g-index

84  
all docs

84  
docs citations

84  
times ranked

17546  
citing authors

#	ARTICLE	IF	CITATIONS
1	Towards a unified paradigm for sequence-based identification of fungi. <i>Molecular Ecology</i> , 2013, 22, 5271-5277.	3.9	2,997
2	The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. <i>Nucleic Acids Research</i> , 2019, 47, D259-D264.	14.5	2,072
3	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018, 560, 233-237.	27.8	1,370
4	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.	5.2	868
5	Concentrations of antibiotics predicted to select for resistant bacteria: Proposed limits for environmental regulation. <i>Environment International</i> , 2016, 86, 140-149.	10.0	612
6	Environmental factors influencing the development and spread of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , 2018, 42, .	8.6	612
7	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.	2.8	587
8	BacMet: antibacterial biocide and metal resistance genes database. <i>Nucleic Acids Research</i> , 2014, 42, D737-D743.	14.5	564
9	<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.	4.8	426
10	The structure and diversity of human, animal and environmental resistomes. <i>Microbiome</i> , 2016, 4, 54.	11.1	355
11	Maternal gut and breast milk microbiota affect infant gut antibiotic resistome and mobile genetic elements. <i>Nature Communications</i> , 2018, 9, 3891.	12.8	313
12	Critical knowledge gaps and research needs related to the environmental dimensions of antibiotic resistance. <i>Environment International</i> , 2018, 117, 132-138.	10.0	281
13	A Comprehensive, Automatically Updated Fungal ITS Sequence Dataset for Reference-Based Chimera Control in Environmental Sequencing Efforts. <i>Microbes and Environments</i> , 2015, 30, 145-150.	1.6	231
14	Elucidating selection processes for antibiotic resistance in sewage treatment plants using metagenomics. <i>Science of the Total Environment</i> , 2016, 572, 697-712.	8.0	213
15	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
16	Antibiotic resistance genes in the environment: prioritizing risks. <i>Nature Reviews Microbiology</i> , 2015, 13, 396-396.	28.6	194
17	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.	3.5	193
18	Minimal selective concentrations of tetracycline in complex aquatic bacterial biofilms. <i>Science of the Total Environment</i> , 2016, 553, 587-595.	8.0	166

#	ARTICLE	IF	CITATIONS
19	Five simple guidelines for establishing basic authenticity and reliability of newly generated fungal ITS sequences. <i>MycoKeys</i> , 0, 4, 37-63.	1.9	157
20	The Human Gut Microbiome as a Transporter of Antibiotic Resistance Genes between Continents. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 6551-6560.	3.2	155
21	<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.	4.8	152
22	Improving ITS sequence data for identification of plant pathogenic fungi. <i>Fungal Diversity</i> , 2014, 67, 11-19.	12.3	123
23	Industrial wastewater treatment plant enriches antibiotic resistance genes and alters the structure of microbial communities. <i>Water Research</i> , 2019, 162, 437-445.	11.3	95
24	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.	1.7	88
25	Using metagenomics to investigate human and environmental resistomes. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2690-2703.	3.0	87
26	Introducing ribosomal tandem repeat barcoding for fungi. <i>Molecular Ecology Resources</i> , 2019, 19, 118-127.	4.8	78
27	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.	8.0	76
28	Identification of 76 novel B1 metallo- $\beta$ -lactamases through large-scale screening of genomic and metagenomic data. <i>Microbiome</i> , 2017, 5, 134.	11.1	75
29	Selective concentration for ciprofloxacin resistance in <i>Escherichia coli</i> grown in complex aquatic bacterial biofilms. <i>Environment International</i> , 2018, 116, 255-268.	10.0	71
30	Does antifouling paint select for antibiotic resistance?. <i>Science of the Total Environment</i> , 2017, 590-591, 461-468.	8.0	70
31	Substrate-bound outward-open structure of a Na <sup>+</sup> -coupled sialic acid symporter reveals a new Na <sup>+</sup> site. <i>Nature Communications</i> , 2018, 9, 1753.	12.8	62
32	The relation between <i>Blastocystis</i> and the intestinal microbiota in Swedish travellers. <i>BMC Microbiology</i> , 2017, 17, 231.	3.3	56
33	<i>In Vivo</i> 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, .	2.2	55
34	Metagenomic sequencing of marine periphyton: taxonomic and functional insights into biofilm communities. <i>Frontiers in Microbiology</i> , 2015, 6, 1192.	3.5	49
35	The diversity of uncharacterized antibiotic resistance genes can be predicted from known gene variantsâ€”but not always. <i>Microbiome</i> , 2018, 6, 125.	11.1	39
36	Evaluating and optimizing the performance of software commonly used for the taxonomic classification of <scp>DNA</scp> metabarcoding sequence data. <i>Molecular Ecology Resources</i> , 2017, 17, 760-769.	4.8	38

#	ARTICLE	IF	CITATIONS
37	Metaxa2 Database Builder: enabling taxonomic identification from metagenomic or metabarcoding data using any genetic marker. <i>Bioinformatics</i> , 2018, 34, 4027-4033.	4.1	36
38	Metagenomics reveals that detoxification systems are underrepresented in marine bacterial communities. <i>BMC Genomics</i> , 2014, 15, 749.	2.8	35
39	Taxonomic annotation of public fungal ITS sequences from the built environment – a report from an April 10–11, 2017 workshop (Aberdeen, UK). <i>MycKeys</i> , 2018, 28, 65-82.	1.9	33
40	Diarrheal bacterial pathogens and multi-resistant enterobacteria in the Choqueyapu River in La Paz, Bolivia. <i>PLoS ONE</i> , 2019, 14, e0210735.	2.5	33
41	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.	1.6	31
42	Metaxa2 Diversity Tools: Easing microbial community analysis with Metaxa2. <i>Ecological Informatics</i> , 2016, 33, 45-50.	5.2	30
43	What Is the Role of the Environment in the Emergence of Novel Antibiotic Resistance Genes? A Modeling Approach. <i>Environmental Science &amp; Technology</i> , 2021, 55, 15734-15743.	10.0	28
44	Strategies to improve usability and preserve accuracy in biological sequence databases. <i>Proteomics</i> , 2016, 16, 2454-2460.	2.2	27
45	Microbial model communities: To understand complexity, harness the power of simplicity. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3987-4001.	4.1	27
46	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.	9.3	25
47	Computational discovery and functional validation of novel fluoroquinolone resistance genes in public metagenomic data sets. <i>BMC Genomics</i> , 2017, 18, 682.	2.8	24
48	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.	1.6	24
49	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>MycKeys</i> , 0, 16, 1-15.	1.9	16
50	Microbial Community Interactions Are Sensitive to Small Changes in Temperature. <i>Frontiers in Microbiology</i> , 2021, 12, 672910.	3.5	15
51	A reference cytochrome c oxidase subunit I database curated for hierarchical classification of arthropod metabarcoding data. <i>PeerJ</i> , 2018, 6, e5126.	2.0	14
52	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.	1.8	14
53	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 11: Sulfonamides. <i>EFSA Journal</i> , 2021, 19, e06863.	1.8	13
54	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.	2.1	12

#	ARTICLE	IF	CITATIONS
55	Protection goals must guide risk assessment for antibiotics. <i>Environment International</i> , 2018, 111, 352-353.	10.0	12
56	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.	1.8	12
57	Strategies for Taxonomic and Functional Annotation of Metagenomes. , 2018, , 55-79.		11
58	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.	1.8	11
59	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.	1.8	10
60	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.	1.8	9
61	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.	1.8	8
62	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.	1.8	8
63	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.	1.8	8
64	FARAO: the flexible all-round annotation organizer. <i>Bioinformatics</i> , 2016, 32, 3664-3666.	4.1	6
65	Assessment and Management of Risks Associated With Antibiotic Resistance in the Environment. , 2019, , 243-263.		6
66	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.	1.8	5
67	CAFE: a software suite for analysis of paired-sample transposon insertion sequencing data. <i>Bioinformatics</i> , 2021, 37, 121-122.	4.1	4
68	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.	1.8	4
69	Maximum levels of cross-contamination for 24 antimicrobial active substances in non-target feed. Part 4: Lactams: amoxicillin and penicillin V. <i>EFSA Journal</i> , 2021, 19, e06855.	1.8	3
70	The complete mitochondrial genome of the copepod <i>Calanus glacialis</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 506-507.	0.4	2
71	Mumame: a software tool for quantifying gene-specific point-mutations in shotgun metagenomic data. <i>Metabarcoding and Metagenomics</i> , 0, 3, .	0.0	2
72	Microbial retention and resistances in stormwater quality improvement devices treating road runoff. <i>FEMS Microbes</i> , 2021, 2, .	2.1	1

#	ARTICLE	IF	CITATIONS
73	Metaxa, Overview. , 2014, , 1-5.		1
74	Metaxa, Overview. , 2015, , 467-471.		0