

Anna Heintz-Buschart

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7075749/publications.pdf>

Version: 2024-02-01

66
papers

4,431
citations

201385

27
h-index

128067

60
g-index

79
all docs

79
docs citations

79
times ranked

7014
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome sequencing analysis of maize roots reveals the effects of substrate and root hair formation in a spatial context. <i>Plant and Soil</i> , 2022, 478, 211-228.	1.8	9
2	A beginner's guide to integrating multi-omics data from microbial communities. <i>Biochemist</i> , 2022, 44, 23-29.	0.2	5
3	Fungal guilds and soil functionality respond to tree community traits rather than to tree diversity in European forests. <i>Molecular Ecology</i> , 2021, 30, 572-591.	2.0	31
4	The multidimensionality of soil macroecology. <i>Global Ecology and Biogeography</i> , 2021, 30, 4-10.	2.7	16
5	Soil Texture, Sampling Depth and Root Hairs Shape the Structure of ACC Deaminase Bacterial Community Composition in Maize Rhizosphere. <i>Frontiers in Microbiology</i> , 2021, 12, 616828.	1.5	23
6	Targeting the Active Rhizosphere Microbiome of <i>Trifolium pratense</i> in Grassland Evidences a Stronger-Than-Expected Belowground Biodiversity-Ecosystem Functioning Link. <i>Frontiers in Microbiology</i> , 2021, 12, 629169.	1.5	18
7	PathoFact: a pipeline for the prediction of virulence factors and antimicrobial resistance genes in metagenomic data. <i>Microbiome</i> , 2021, 9, 49.	4.9	81
8	Amplicon Sequencing-Based Bipartite Network Analysis Confirms a High Degree of Specialization and Modularity for Fungi and Prokaryotes in Deadwood. <i>MSphere</i> , 2021, 6, .	1.3	10
9	Persistence of birth mode-dependent effects on gut microbiome composition, immune system stimulation and antimicrobial resistance during the first year of life. <i>ISME Communications</i> , 2021, 1, .	1.7	25
10	Organic agricultural practice enhances arbuscular mycorrhizal symbiosis in correspondence to soil warming and altered precipitation patterns. <i>Environmental Microbiology</i> , 2021, 23, 6163-6176.	1.8	24
11	Pathways linking biodiversity to human health: A conceptual framework. <i>Environment International</i> , 2021, 150, 106420.	4.8	210
12	Circulating bacterial signature is linked to metabolic disease and shifts with metabolic alleviation after bariatric surgery. <i>Genome Medicine</i> , 2021, 13, 105.	3.6	14
13	Structure of Chimpanzee Gut Microbiomes across Tropical Africa. <i>MSystems</i> , 2021, 6, e0126920.	1.7	8
14	Distinct effects of host and neighbour tree identity on arbuscular and ectomycorrhizal fungi along a tree diversity gradient. <i>ISME Communications</i> , 2021, 1, .	1.7	19
15	Large-scale drivers of relationships between soil microbial properties and organic carbon across Europe. <i>Global Ecology and Biogeography</i> , 2021, 30, 2070-2083.	2.7	32
16	Stool microRNA profiling " dumpster diving for a master marker?. <i>Gut</i> , 2021, , gutjnl-2021-325663.	6.1	0
17	Can We Estimate Functionality of Soil Microbial Communities from Structure-Derived Predictions? A Reality Test in Agricultural Soils. <i>Microbiology Spectrum</i> , 2021, 9, e0027821.	1.2	11
18	Back to the Future: Decomposability of a Biobased and Biodegradable Plastic in Field Soil Environments and Its Microbiome under Ambient and Future Climates. <i>Environmental Science & Technology</i> , 2021, 55, 12337-12351.	4.6	32

#	ARTICLE	IF	CITATIONS
19	Unraveling spatiotemporal variability of arbuscular mycorrhizal fungi in a temperate grassland plot. <i>Environmental Microbiology</i> , 2020, 22, 873-888.	1.8	27
20	Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. <i>Nature Communications</i> , 2020, 11, 5281.	5.8	57
21	Dietary cellulose induces anti-inflammatory immunity and transcriptional programs via maturation of the intestinal microbiota. <i>Gut Microbes</i> , 2020, 12, 1829962.	4.3	35
22	Effects of nitrogen and phosphorus addition on microbial community composition and element cycling in a grassland soil. <i>Soil Biology and Biochemistry</i> , 2020, 151, 108041.	4.2	103
23	Blind spots in global soil biodiversity and ecosystem function research. <i>Nature Communications</i> , 2020, 11, 3870.	5.8	192
24	The archives are half-empty: an assessment of the availability of microbial community sequencing data. <i>Communications Biology</i> , 2020, 3, 474.	2.0	22
25	Inhibition of Respiration of <i>Candida albicans</i> by Small Molecules Increases Phagocytosis Efficacy by Macrophages. <i>MSphere</i> , 2020, 5, .	1.3	6
26	Compatibility of X-ray computed tomography with plant gene expression, rhizosphere bacterial communities and enzyme activities. <i>Journal of Experimental Botany</i> , 2020, 71, 5603-5614.	2.4	17
27	Interactions of nitrogen and phosphorus cycling promote P acquisition and explain synergistic plant growth responses. <i>Ecology</i> , 2020, 101, e03003.	1.5	58
28	Putting soil invertebrate diversity on the map. <i>Molecular Ecology</i> , 2020, 29, 655-657.	2.0	5
29	Dadasnake, a Snakemake implementation of DADA2 to process amplicon sequencing data for microbial ecology. <i>GigaScience</i> , 2020, 9, .	3.3	39
30	Sample Preservation and Storage Significantly Impact Taxonomic and Functional Profiles in Metaproteomics Studies of the Human Gut Microbiome. <i>Microorganisms</i> , 2019, 7, 367.	1.6	32
31	Metabolites of lactic acid bacteria present in fermented foods are highly potent agonists of human hydroxycarboxylic acid receptor 3. <i>PLoS Genetics</i> , 2019, 15, e1008145.	1.5	85
32	Stoichiometric controls of soil carbon and nitrogen cycling after long-term nitrogen and phosphorus addition in a mesic grassland in South Africa. <i>Soil Biology and Biochemistry</i> , 2019, 135, 294-303.	4.2	77
33	Linking Soil Fungal Generality to Tree Richness in Young Subtropical Chinese Forests. <i>Microorganisms</i> , 2019, 7, 547.	1.6	10
34	Extensive transmission of microbes along the gastrointestinal tract. <i>ELife</i> , 2019, 8, .	2.8	313
35	257-LB: Long-Term Effects of Birth Mode on Gut Microbiome Colonization. <i>Diabetes</i> , 2019, 68, .	0.3	0
36	Extraction and Analysis of RNA Isolated from Pure Bacteria-Derived Outer Membrane Vesicles. <i>Methods in Molecular Biology</i> , 2018, 1737, 213-230.	0.4	22

#	ARTICLE	IF	CITATIONS
37	Mechanisms of Persistence of the Ammonia-Oxidizing Bacteria <i>Nitrosomonas</i> to the Biocide Free Nitrous Acid. <i>Environmental Science & Technology</i> , 2018, 52, 5386-5397.	4.6	52
38	The nasal and gut microbiome in Parkinson's disease and idiopathic rapid eye movement sleep behavior disorder. <i>Movement Disorders</i> , 2018, 33, 88-98.	2.2	428
39	Human Gut Microbiome: Function Matters. <i>Trends in Microbiology</i> , 2018, 26, 563-574.	3.5	458
40	Birth mode is associated with earliest strain-conferred gut microbiome functions and immunostimulatory potential. <i>Nature Communications</i> , 2018, 9, 5091.	5.8	190
41	Small RNA profiling of low biomass samples: identification and removal of contaminants. <i>BMC Biology</i> , 2018, 16, 52.	1.7	46
42	The RNA Complement of Outer Membrane Vesicles From <i>Salmonella enterica</i> Serovar Typhimurium Under Distinct Culture Conditions. <i>Frontiers in Microbiology</i> , 2018, 9, 2015.	1.5	62
43	Integrated meta-omic analyses of the gastrointestinal tract microbiome in patients undergoing allogeneic hematopoietic stem cell transplantation. <i>Translational Research</i> , 2017, 186, 79-94.e1.	2.2	27
44	Integrated multi-omics of the human gut microbiome in a case study of familial type 1 diabetes. <i>Nature Microbiology</i> , 2017, 2, 16180.	5.9	233
45	Colonization and Succession within the Human Gut Microbiome by Archaea, Bacteria, and Microeukaryotes during the First Year of Life. <i>Frontiers in Microbiology</i> , 2017, 8, 738.	1.5	207
46	Identification, Recovery, and Refinement of Hitherto Undescribed Population-Level Genomes from the Human Gastrointestinal Tract. <i>Frontiers in Microbiology</i> , 2016, 7, 884.	1.5	8
47	Regulation of <i>Candida albicans</i> Interaction with Macrophages through the Activation of HOG Pathway by Genistein. <i>Molecules</i> , 2016, 21, 162.	1.7	9
48	IMP: a pipeline for reproducible reference-independent integrated metagenomic and metatranscriptomic analyses. <i>Genome Biology</i> , 2016, 17, 260.	3.8	141
49	Sources and Functions of Extracellular Small RNAs in Human Circulation. <i>Annual Review of Nutrition</i> , 2016, 36, 301-336.	4.3	110
50	A decade of metaproteomics: Where we stand and what the future holds. <i>Proteomics</i> , 2015, 15, 3409-3417.	1.3	161
51	The extracellular RNA complement of <i>Escherichia coli</i> . <i>MicrobiologyOpen</i> , 2015, 4, 252-266.	1.2	162
52	Comparative integrated omics: identification of key functionalities in microbial community-wide metabolic networks. <i>Npj Biofilms and Microbiomes</i> , 2015, 1, 15007.	2.9	82
53	Method Optimization for Fecal Sample Collection and Fecal DNA Extraction. <i>Biopreservation and Biobanking</i> , 2015, 13, 79-93.	0.5	48
54	Rice responds to endophytic colonization which is independent of the common symbiotic signaling pathway. <i>New Phytologist</i> , 2015, 208, 531-543.	3.5	26

#	ARTICLE	IF	CITATIONS
55	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. <i>Nature Communications</i> , 2014, 5, 5603.	5.8	75
56	Sequential Isolation of Metabolites, RNA, DNA, and Proteins from the Same Unique Sample. <i>Methods in Enzymology</i> , 2013, 531, 219-236.	0.4	54
57	Identification of inhibitors of yeast-to-hyphae transition in <i>Candida albicans</i> by a reporter screening assay. <i>Journal of Biotechnology</i> , 2013, 164, 137-142.	1.9	17
58	Flagella Mediate Endophytic Competence Rather Than Act as MAMPS in Rice- <i>Azoarcus</i> sp. Strain BH72 Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 191-199.	1.4	42
59	A novel functional assay for fungal histidine kinases group III reveals the role of HAMP domains for fungicide sensitivity. <i>Journal of Biotechnology</i> , 2012, 157, 268-277.	1.9	23
60	The fungicide fludioxonil antagonizes fluconazole activity in the human fungal pathogen <i>Candida albicans</i> . <i>Journal of Medical Microbiology</i> , 2012, 61, 1696-1703.	0.7	6
61	Biotic interactions, community assembly, and eco-evolutionary dynamics as drivers of long-term biodiversity-ecosystem functioning relationships. <i>Research Ideas and Outcomes</i> , 0, 5, .	1.0	23
62	Microbial diversity-ecosystem function relationships across environmental gradients. <i>Research Ideas and Outcomes</i> , 0, 6, .	1.0	8
63	The sequential isolation of metabolites, RNA, DNA, and proteins from a single, undivided mixed microbial community sample. <i>Protocol Exchange</i> , 0, , .	0.3	0
64	Biotic Interactions as Mediators of Context-Dependent Biodiversity-Ecosystem Functioning Relationships. <i>Research Ideas and Outcomes</i> , 0, 8, .	1.0	10
65	Water Deficit History Selects Plant Beneficial Soil Bacteria Differently Under Conventional and Organic Farming. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
66	Effects of Tree Composition and Soil Depth on Structure and Functionality of Belowground Microbial Communities in Temperate European Forests. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	11