

# Hyun S Gweon

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

2,869  
citations

471061

17  
h-index

433756

31  
g-index

35  
all docs

35  
docs citations

35  
times ranked

4092  
citing authors

#	ARTICLE	IF	CITATIONS
1	Accumulation of nylon microplastics and polybrominated diphenyl ethers and effects on gut microbial community of <i>Chironomus sancticaroli</i> . <i>Science of the Total Environment</i> , 2022, 832, 155089.	3.9	17
2	Neonicotinoid use on cereals and sugar beet is linked to continued low exposure risk in honeybees. <i>Agriculture, Ecosystems and Environment</i> , 2021, 308, 107205.	2.5	11
3	Interacting effects of land use type, microbes and plant traits on soil aggregate stability. <i>Soil Biology and Biochemistry</i> , 2021, 154, 108072.	4.2	38
4	Contrasting community assembly processes structure lotic bacteria metacommunities along the river continuum. <i>Environmental Microbiology</i> , 2021, 23, 484-498.	1.8	50
5	Genomic network analysis of environmental and livestock F-type plasmid populations. <i>ISME Journal</i> , 2021, 15, 2322-2335.	4.4	24
6	Characterization of communal sink drain communities of a university campus. <i>Environmental DNA</i> , 2021, 3, 901-911.	3.1	8
7	Niche and local geography shape the pangenome of wastewater- and livestock-associated Enterobacteriaceae. <i>Science Advances</i> , 2021, 7, .	4.7	47
8	Bacterial communities in larger islands have reduced temporal turnover. <i>ISME Journal</i> , 2021, 15, 2947-2955.	4.4	8
9	Population-level faecal metagenomic profiling as a tool to predict antimicrobial resistance in Enterobacterales isolates causing invasive infections: An exploratory study across Cambodia, Kenya, and the UK. <i>EClinicalMedicine</i> , 2021, 36, 100910.	3.2	10
10	Beyond Taxonomic Identification: Integration of Ecological Responses to a Soil Bacterial 16S rRNA Gene Database. <i>Frontiers in Microbiology</i> , 2021, 12, 682886.	1.5	6
11	Gut and faecal bacterial community of the terrestrial isopod <i>Porcellionides pruinosus</i> : potential use for monitoring exposure scenarios. <i>Ecotoxicology</i> , 2021, 30, 2096-2108.	1.1	1
12	Integration of DNA extraction, metabarcoding and an informatics pipeline to underpin a national citizen science honey monitoring scheme. <i>MethodsX</i> , 2021, 8, 101303.	0.7	4
13	A genomic epidemiological study shows that prevalence of antimicrobial resistance in Enterobacterales is associated with the livestock host, as well as antimicrobial usage. <i>Microbial Genomics</i> , 2021, 7, .	1.0	20
14	Equine grass sickness (a multiple systems neuropathy) is associated with alterations in the gastrointestinal mycobiome. <i>Animal Microbiome</i> , 2021, 3, 70.	1.5	6
15	Accumulation of polybrominated diphenyl ethers and microbiome response in the great pond snail <i>Lymnaea stagnalis</i> with exposure to nylon (polyamide) microplastics. <i>Ecotoxicology and Environmental Safety</i> , 2020, 188, 109882.	2.9	40
16	Rhizosphere bacteria are more strongly related to plant root traits than fungi in temperate montane forests: insights from closed and open forest patches along an elevational gradient. <i>Plant and Soil</i> , 2020, 450, 183-200.	1.8	24
17	Nutrients influence the dynamics of <i>Klebsiella pneumoniae</i> carbapenemase producing enterobacterales in transplanted hospital sinks. <i>Water Research</i> , 2020, 176, 115707.	5.3	17
18	Genomic surveillance of <i>Escherichia coli</i> and <i>Klebsiella</i> spp. in hospital sink drains and patients. <i>Microbial Genomics</i> , 2020, 6, .	1.0	26

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19	The pH optimum of soil exoenzymes adapt to long term changes in soil pH. <i>Soil Biology and Biochemistry</i> , 2019, 138, 107601.	4.2	73
20	Land use driven change in soil pH affects microbial carbon cycling processes. <i>Nature Communications</i> , 2018, 9, 3591.	5.8	380
21	Soil bacterial networks are less stable under drought than fungal networks. <i>Nature Communications</i> , 2018, 9, 3033.	5.8	992
22	Environment and host as large-scale controls of ectomycorrhizal fungi. <i>Nature</i> , 2018, 558, 243-248.	13.7	282
23	Environmental Metabarcoding Reveals Contrasting Belowground and Aboveground Fungal Communities from Poplar at a Hg Phytomanagement Site. <i>Microbial Ecology</i> , 2017, 74, 795-809.	1.4	37
24	Helminth burden and ecological factors associated with alterations in wild host gastrointestinal microbiota. <i>ISME Journal</i> , 2017, 11, 663-675.	4.4	30
25	Assessment of the bimodality in the distribution of bacterial genome sizes. <i>ISME Journal</i> , 2017, 11, 821-824.	4.4	10
26	Mapping and validating predictions of soil bacterial biodiversity using European and national scale datasets. <i>Applied Soil Ecology</i> , 2016, 97, 61-68.	2.1	62
27	Soil pH effects on the interactions between dissolved zinc, non-nano- and nano-ZnO with soil bacterial communities. <i>Environmental Science and Pollution Research</i> , 2016, 23, 4120-4128.	2.7	79
28	<sc>PIPITS</sc>: an automated pipeline for analyses of fungal internal transcribed spacer sequences from the <sc>I</sc>llumina sequencing platform. <i>Methods in Ecology and Evolution</i> , 2015, 6, 973-980.	2.2	277
29	Rearing and foraging affects bumblebee (<sc>B</sc>ombus terrestris</i>) gut microbiota. <i>Environmental Microbiology Reports</i> , 2015, 7, 634-641.	1.0	15
30	Catchment-scale biogeography of riverine bacterioplankton. <i>ISME Journal</i> , 2015, 9, 516-526.	4.4	202
31	Bio-Linux as a tool for bioinformatics training. , 2012, , .		1
32	Organisation of the pantothenate (vitamin B5) biosynthesis pathway in higher plants. <i>Plant Journal</i> , 2004, 37, 61-72.	2.8	64