

# Shengjing Shi

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11353805/publications.pdf>

Version: 2024-02-01

14  
papers

3,070  
citations

687363

13  
h-index

1058476

14  
g-index

17  
all docs

17  
docs citations

17  
times ranked

3616  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamic root exudate chemistry and microbial substrate preferences drive patterns in rhizosphere microbial community assembly. <i>Nature Microbiology</i> , 2018, 3, 470-480.	13.3	1,268
2	The interconnected rhizosphere: High network complexity dominates rhizosphere assemblages. <i>Ecology Letters</i> , 2016, 19, 926-936.	6.4	803
3	Effects of selected root exudate components on soil bacterial communities. <i>FEMS Microbiology Ecology</i> , 2011, 77, 600-610.	2.7	316
4	Successional Trajectories of Rhizosphere Bacterial Communities over Consecutive Seasons. <i>MBio</i> , 2015, 6, e00746.	4.1	232
5	Stable isotope informed genome-resolved metagenomics reveals that Saccharibacteria utilize microbially-processed plant-derived carbon. <i>Microbiome</i> , 2018, 6, 122.	11.1	156
6	Elevated CO <sub>2</sub> shifts the functional structure and metabolic potentials of soil microbial communities in a C <sub>4</sub> agroecosystem. <i>Scientific Reports</i> , 2015, 5, 9316.	3.3	48
7	In situ sampling of low molecular weight organic anions from rhizosphere of radiata pine ( <i>Pinus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 4.2 43	4.2	43
8	Plant roots alter microbial functional genes supporting root litter decomposition. <i>Soil Biology and Biochemistry</i> , 2018, 127, 90-99.	8.8	35
9	Stable-Isotope-Informed, Genome-Resolved Metagenomics Uncovers Potential Cross-Kingdom Interactions in Rhizosphere Soil. <i>MSphere</i> , 2021, 6, e0008521.	2.9	34
10	Rhizosphere Carbon Turnover from Cradle to Grave: The Role of Microbe-Plant Interactions. <i>Rhizosphere Biology</i> , 2021, , 51-73.	0.6	33
11	Fungal-Bacterial Cooccurrence Patterns Differ between Arbuscular Mycorrhizal Fungi and Nonmycorrhizal Fungi across Soil Niches. <i>MBio</i> , 2021, 12, .	4.1	31
12	Investigation of organic anions in tree root exudates and rhizosphere microbial communities using in situ and destructive sampling techniques. <i>Plant and Soil</i> , 2012, 359, 149-163.	3.7	20
13	Microbial functional genes commonly respond to elevated carbon dioxide. <i>Environment International</i> , 2020, 144, 106068.	10.0	20
14	Impacts of pasture species and ruminant urine on N <sub>2</sub> O emissions and nitrogen transforming microbial communities in soil mesocosms. <i>New Zealand Journal of Agricultural Research</i> , 2022, 65, 42-62.	1.6	6