

# Sara Beier

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8956007/publications.pdf>

Version: 2024-02-01

25  
papers

1,186  
citations

567144

15  
h-index

610775

24  
g-index

27  
all docs

27  
docs citations

27  
times ranked

1925  
citing authors

#	ARTICLE	IF	CITATIONS
1	Niche breadth affects bacterial transcription patterns along a salinity gradient. <i>Molecular Ecology</i> , 2022, 31, 1216-1233.	2.0	10
2	Editorial: Advancements in the Understanding of Anthropogenic Impacts on the Microbial Ecology and Function of Aquatic Environments. <i>Frontiers in Microbiology</i> , 2021, 12, 820697.	1.5	0
3	The environment drives microbial trait variability in aquatic habitats. <i>Molecular Ecology</i> , 2020, 29, 4605-4617.	2.0	5
4	Ecosystem-wide metagenomic binning enables prediction of ecological niches from genomes. <i>Communications Biology</i> , 2020, 3, 119.	2.0	64
5	Cryopreservation and Resuscitation of Natural Aquatic Prokaryotic Communities. <i>Frontiers in Microbiology</i> , 2020, 11, 597653.	1.5	8
6	Microbial iron metabolism as revealed by gene expression profiles in contrasted Southern Ocean regimes. <i>Environmental Microbiology</i> , 2019, 21, 2360-2374.	1.8	27
7	Effect of large magnetotactic bacteria with polyphosphate inclusions on the phosphate profile of the suboxic zone in the Black Sea. <i>ISME Journal</i> , 2019, 13, 1198-1208.	4.4	59
8	Experimental insights into the importance of ecologically dissimilar bacteria to community assembly along a salinity gradient. <i>Environmental Microbiology</i> , 2018, 20, 1170-1184.	1.8	32
9	BARM and BalticMicrobeDB, a reference metagenome and interface to meta-omic data for the Baltic Sea. <i>Scientific Data</i> , 2018, 5, 180146.	2.4	54
10	A metatranscriptomics-based assessment of small-scale mixing of sulfidic and oxic waters on redoxline prokaryotic communities. <i>Environmental Microbiology</i> , 2018, 21, 584-602.	1.8	10
11	Interactions of Freshwater Cyanobacteria with Bacterial Antagonists. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	39
12	Lake bacterioplankton dynamics over diurnal timescales. <i>Freshwater Biology</i> , 2017, 62, 191-204.	1.2	11
13	Metatranscriptomic data reveal the effect of different community properties on multifunctional redundancy. <i>Molecular Ecology</i> , 2017, 26, 6813-6826.	2.0	18
14	Uptake of Leucine, Chitin, and Iron by Prokaryotic Groups during Spring Phytoplankton Blooms Induced by Natural Iron Fertilization off Kerguelen Island (Southern Ocean). <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	12
15	The transcriptional regulation of the glyoxylate cycle in <sc>SAR</sc>11 in response to iron fertilization in the <sc>S</sc>outhern <sc>O</sc>cean. <i>Environmental Microbiology Reports</i> , 2015, 7, 427-434.	1.0	20
16	Phenotypic plasticity in heterotrophic marine microbial communities in continuous cultures. <i>ISME Journal</i> , 2015, 9, 1141-1151.	4.4	20
17	The transcriptional response of prokaryotes to phytoplankton-derived dissolved organic matter in seawater. <i>Environmental Microbiology</i> , 2015, 17, 3466-3480.	1.8	55
18	Bacterial chitin degradation mechanisms and ecophysiological strategies. <i>Frontiers in Microbiology</i> , 2013, 4, 149.	1.5	368

#	ARTICLE	IF	CITATIONS
19	Pronounced seasonal dynamics of freshwater chitinase genes and chitin processing. <i>Environmental Microbiology</i> , 2012, 14, 2467-2479.	1.8	12
20	Function-specific response to depletion of microbial diversity. <i>ISME Journal</i> , 2011, 5, 351-361.	4.4	183
21	Global Phylogeography of Chitinase Genes in Aquatic Metagenomes. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1101-1106.	1.4	21
22	Uncoupling of chitinase activity and uptake of hydrolysis products in freshwater bacterioplankton. <i>Limnology and Oceanography</i> , 2011, 56, 1179-1188.	1.6	62
23	Betaproteobacterial ammonia oxidizers in root zones of aquatic macrophytes. <i>Fundamental and Applied Limnology</i> , 2010, 177, 241-255.	0.4	3
24	High Ratio of Bacteriochlorophyll Biosynthesis Genes to Chlorophyll Biosynthesis Genes in Bacteria of Humic Lakes. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7221-7228.	1.4	23
25	Bacterial Community Composition in Central European Running Waters Examined by Temperature Gradient Gel Electrophoresis and Sequence Analysis of 16S rRNA Genes. <i>Applied and Environmental Microbiology</i> , 2008, 74, 188-199.	1.4	69