

Janet K Jansson

List of Publications by Year in descending order

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Version: 2024-02-01

203
papers

51,426
citations

5876

81
h-index

2439

197
g-index

220
all docs

220
docs citations

220
times ranked

52870
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.	13.7	9,614
2	Diversity, stability and resilience of the human gut microbiota. <i>Nature</i> , 2012, 489, 220-230.	13.7	4,114
3	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	13.7	2,249
4	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
5	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	13.7	1,638
6	Current understanding of the human microbiome. <i>Nature Medicine</i> , 2018, 24, 392-400.	15.2	1,593
7	Improved Bacterial 16S rRNA Gene (V4 and V4-5) and Fungal Internal Transcribed Spacer Marker Gene Primers for Microbial Community Surveys. <i>MSystems</i> , 2016, 1, .	1.7	1,364
8	Scientists's warning to humanity: microorganisms and climate change. <i>Nature Reviews Microbiology</i> , 2019, 17, 569-586.	13.6	1,138
9	Deep-Sea Oil Plume Enriches Indigenous Oil-Degrading Bacteria. <i>Science</i> , 2010, 330, 204-208.	6.0	1,109
10	Short-Term Antibiotic Treatment Has Differing Long-Term Impacts on the Human Throat and Gut Microbiome. <i>PLoS ONE</i> , 2010, 5, e9836.	1.1	936
11	A Pyrosequencing Study in Twins Shows That Gastrointestinal Microbial Profiles Vary With Inflammatory Bowel Disease Phenotypes. <i>Gastroenterology</i> , 2010, 139, 1844-1854.e1.	0.6	916
12	Long-term ecological impacts of antibiotic administration on the human intestinal microbiota. <i>ISME Journal</i> , 2007, 1, 56-66.	4.4	885
13	Long-term impacts of antibiotic exposure on the human intestinal microbiota. <i>Microbiology (United Kingdom)</i> 157, 1077-1085. doi:10.1099/mic/0/01571077-1077-1085	0.7	859
14	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017, 2, 17004.	5.9	830
15	Soil microbiomes and climate change. <i>Nature Reviews Microbiology</i> , 2020, 18, 35-46.	13.6	725
16	The Earth Microbiome project: successes and aspirations. <i>BMC Biology</i> , 2014, 12, 69.	1.7	723
17	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. <i>Cell</i> , 2019, 177, 1600-1618.e17.	13.5	701
18	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	9.4	608

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19	Metagenomic analysis of a permafrost microbial community reveals a rapid response to thaw. <i>Nature</i> , 2011, 480, 368-371.	13.7	601
20	Changes in the Composition of the Human Fecal Microbiome After Bacteriotherapy for Recurrent <i>Clostridium difficile</i> -associated Diarrhea. <i>Journal of Clinical Gastroenterology</i> , 2010, 44, 354-360.	1.1	595
21	Microbiome-wide association studies link dynamic microbial consortia to disease. <i>Nature</i> , 2016, 535, 94-103.	13.7	595
22	DNA Probe Method for the Detection of Specific Microorganisms in the Soil Bacterial Community. <i>Applied and Environmental Microbiology</i> , 1988, 54, 703-711.	1.4	577
23	Interactions between arbuscular mycorrhizal fungi and bacteria and their potential for stimulating plant growth. <i>Environmental Microbiology</i> , 2006, 8, 1-10.	1.8	567
24	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2012, 6, 1715-1727.	4.4	547
25	Shotgun metaproteomics of the human distal gut microbiota. <i>ISME Journal</i> , 2009, 3, 179-189.	4.4	484
26	Multi-omics of permafrost, active layer and thermokarst bog soil microbiomes. <i>Nature</i> , 2015, 521, 208-212.	13.7	467
27	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
28	Metabolomics Reveals Metabolic Biomarkers of Crohn's Disease. <i>PLoS ONE</i> , 2009, 4, e6386.	1.1	429
29	Molecular analysis of the gut microbiota of identical twins with Crohn's disease. <i>ISME Journal</i> , 2008, 2, 716-727.	4.4	407
30	Twin studies reveal specific imbalances in the mucosa-associated microbiota of patients with ileal Crohn's disease. <i>Inflammatory Bowel Diseases</i> , 2009, 15, 653-660.	0.9	407
31	Integrated Metagenomics/Metaproteomics Reveals Human Host-Microbiota Signatures of Crohn's Disease. <i>PLoS ONE</i> , 2012, 7, e49138.	1.1	374
32	Meta-analyses of studies of the human microbiota. <i>Genome Research</i> , 2013, 23, 1704-1714.	2.4	352
33	The microbial ecology of permafrost. <i>Nature Reviews Microbiology</i> , 2014, 12, 414-425.	13.6	345
34	The soil microbiome – from metagenomics to metaproteomics. <i>Current Opinion in Microbiology</i> , 2018, 43, 162-168.	2.3	330
35	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2014, 8, 1464-1475.	4.4	325
36	Tackling soil diversity with the assembly of large, complex metagenomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4904-4909.	3.3	305

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37	Deep-sea bacteria enriched by oil and dispersant from the Deepwater Horizon spill. <i>Environmental Microbiology</i> , 2012, 14, 2405-2416.	1.8	275
38	Molecular characterization of the stomach microbiota in patients with gastric cancer and in controls. <i>Journal of Medical Microbiology</i> , 2009, 58, 509-516.	0.7	260
39	Unlocking the potential of metagenomics through replicated experimental design. <i>Nature Biotechnology</i> , 2012, 30, 513-520.	9.4	250
40	Microbial gene functions enriched in the Deepwater Horizon deep-sea oil plume. <i>ISME Journal</i> , 2012, 6, 451-460.	4.4	240
41	Earth microbial co-occurrence network reveals interconnection pattern across microbiomes. <i>Microbiome</i> , 2020, 8, 82.	4.9	239
42	Meeting Report: The Terabase Metagenomics Workshop and the Vision of an Earth Microbiome Project. <i>Standards in Genomic Sciences</i> , 2010, 3, 243-248.	1.5	228
43	Soft inertial microfluidics for high throughput separation of bacteria from human blood cells. <i>Lab on A Chip</i> , 2009, 9, 1193.	3.1	222
44	Impact of Dietary Resistant Starch on the Human Gut Microbiome, Metaproteome, and Metabolome. <i>MBio</i> , 2017, 8, .	1.8	219
45	TerraGenome: a consortium for the sequencing of a soil metagenome. <i>Nature Reviews Microbiology</i> , 2009, 7, 252-252.	13.6	199
46	Attachment of different soil bacteria to arbuscular mycorrhizal fungal extraradical hyphae is determined by hyphal vitality and fungal species. <i>FEMS Microbiology Letters</i> , 2006, 254, 34-40.	0.7	197
47	A unified initiative to harness Earth's microbiomes. <i>Science</i> , 2015, 350, 507-508.	6.0	195
48	Direct Cellular Lysis/Protein Extraction Protocol for Soil Metaproteomics. <i>Journal of Proteome Research</i> , 2010, 9, 6615-6622.	1.8	193
49	Responses of bacterial and archaeal ammonia oxidizers to soil organic and fertilizer amendments under long-term management. <i>Applied Soil Ecology</i> , 2010, 45, 193-200.	2.1	190
50	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	2.6	190
51	Simultaneous Monitoring of Cell Number and Metabolic Activity of Specific Bacterial Populations with a Dual <i>gfp-luxAB</i> Marker System. <i>Applied and Environmental Microbiology</i> , 1999, 65, 813-821.	1.4	177
52	Flow cytometric and microscopic analysis of GFP-tagged <i>Pseudomonas fluorescens</i> bacteria. <i>FEMS Microbiology Ecology</i> , 2006, 22, 17-28.	1.3	177
53	The Earth Microbiome Project: Meeting report of the 1st EMP meeting on sample selection and acquisition at Argonne National Laboratory October 6th 2010.. <i>Standards in Genomic Sciences</i> , 2010, 3, 249-253.	1.5	176
54	Assessment of the Deepwater Horizon oil spill impact on Gulf coast microbial communities. <i>Frontiers in Microbiology</i> , 2014, 5, 130.	1.5	172

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55	Metabolic Model-Based Integration of Microbiome Taxonomic and Metabolomic Profiles Elucidates Mechanistic Links between Ecological and Metabolic Variation. <i>MSystems</i> , 2016, 1, .	1.7	167
56	In Vivo Study of Trichoderma -Pathogen-Plant Interactions, Using Constitutive and Inducible Green Fluorescent Protein Reporter Systems. <i>Applied and Environmental Microbiology</i> , 2004, 70, 3073-3081.	1.4	157
57	Gut Microbial Alterations Associated With Protection From Autoimmune Ulceritis. , 2016, 57, 3747.		156
58	Microbes in thawing permafrost: the unknown variable in the climate change equation. <i>ISME Journal</i> , 2012, 6, 709-712.	4.4	153
59	<i>Arthrobacter chlorophenolicus</i> sp. nov., a new species capable of degrading high concentrations of 4-chlorophenol.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2000, 50, 2083-2092.	0.8	150
60	Impact of fire on active layer and permafrost microbial communities and metagenomes in an upland Alaskan boreal forest. <i>ISME Journal</i> , 2014, 8, 1904-1919.	4.4	150
61	Soil Microbiomes Under Climate Change and Implications for Carbon Cycling. <i>Annual Review of Environment and Resources</i> , 2020, 45, 29-59.	5.6	145
62	Advances in preservation methods: keeping biosensor microorganisms alive and active. <i>Current Opinion in Biotechnology</i> , 2006, 17, 43-49.	3.3	138
63	Clindamycin-induced enrichment and long-term persistence of resistant <i>Bacteroides</i> spp. and resistance genes. <i>Journal of Antimicrobial Chemotherapy</i> , 2006, 58, 1160-1167.	1.3	138
64	Influence of early life exposure, host genetics and diet on the mouse gut microbiome and metabolome. <i>Nature Microbiology</i> , 2017, 2, 16221.	5.9	138
65	Tools for the Microbiome: Nano and Beyond. <i>ACS Nano</i> , 2016, 10, 6-37.	7.3	137
66	Climate change microbiology – problems and perspectives. <i>Nature Reviews Microbiology</i> , 2019, 17, 391-396.	13.6	130
67	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 73.	1.5	120
68	Use of Bromodeoxyuridine Immunocapture To Identify Active Bacteria Associated with Arbuscular Mycorrhizal Hyphae. <i>Applied and Environmental Microbiology</i> , 2003, 69, 6208-6215.	1.4	119
69	Novel 4-Chlorophenol Degradation Gene Cluster and Degradation Route via Hydroxyquinol in <i>Arthrobacter chlorophenolicus</i> A6. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6538-6544.	1.4	113
70	Colonization Pattern of the Biocontrol Strain <i>Pseudomonas chlororaphis</i> MA 342 on Barley Seeds Visualized by Using Green Fluorescent Protein. <i>Applied and Environmental Microbiology</i> , 1999, 65, 3674-3680.	1.4	113
71	Molecular Fingerprinting of the Fecal Microbiota of Children Raised According to Different Lifestyles. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2284-2289.	1.4	112
72	A multi-omic future for microbiome studies. <i>Nature Microbiology</i> , 2016, 1, 16049.	5.9	112

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73	Effect of Starvation and the Viable-but-Nonculturable State on Green Fluorescent Protein (GFP) Fluorescence in GFP-Tagged <i>Pseudomonas fluorescens</i> A506. <i>Applied and Environmental Microbiology</i> , 2000, 66, 3160-3165.	1.4	108
74	Single-cell genomics reveals features of a <i>Colwellia</i> species that was dominant during the Deepwater Horizon oil spill. <i>Frontiers in Microbiology</i> , 2014, 5, 332.	1.5	106
75	The Potential of Metagenomic Approaches for Understanding Soil Microbial Processes. <i>Soil Science Society of America Journal</i> , 2014, 78, 3-10.	1.2	105
76	Landscape topography structures the soil microbiome in arctic polygonal tundra. <i>Nature Communications</i> , 2018, 9, 777.	5.8	105
77	Combined bromodeoxyuridine immunocapture and terminal-restriction fragment length polymorphism analysis highlights differences in the active soil bacterial metagenome due to <i>Glomus mosseae</i> inoculation or plant species. <i>Environmental Microbiology</i> , 2005, 7, 1952-1966.	1.8	99
78	The metagenomics of disease-suppressive soils – experiences from the METACONTROL project. <i>Trends in Biotechnology</i> , 2008, 26, 591-601.	4.9	99
79	Chitinase genes revealed and compared in bacterial isolates, DNA extracts and a metagenomic library from a phytopathogen-suppressive soil. <i>FEMS Microbiology Ecology</i> , 2010, 71, 197-207.	1.3	96
80	Distinct summer and winter bacterial communities in the active layer of Svalbard permafrost revealed by DNA- and RNA-based analyses. <i>Frontiers in Microbiology</i> , 2015, 6, 399.	1.5	94
81	Phyllostomid bat microbiome composition is associated to host phylogeny and feeding strategies. <i>Frontiers in Microbiology</i> , 2015, 6, 447.	1.5	92
82	FOAM (Functional Ontology Assignments for Metagenomes): a Hidden Markov Model (HMM) database with environmental focus. <i>Nucleic Acids Research</i> , 2014, 42, e145-e145.	6.5	90
83	MolecuLo Long-Read Sequencing Facilitates Assembly and Genomic Binning from Complex Soil Metagenomes. <i>MSystems</i> , 2016, 1, .	1.7	89
84	Diets high in resistant starch increase plasma levels of trimethylamine-N-oxide, a gut microbiome metabolite associated with CVD risk. <i>British Journal of Nutrition</i> , 2016, 116, 2020-2029.	1.2	86
85	Monitoring of Antibiotic-Induced Alterations in the Human Intestinal Microflora and Detection of Probiotic Strains by Use of Terminal Restriction Fragment Length Polymorphism. <i>Applied and Environmental Microbiology</i> , 2005, 71, 501-506.	1.4	85
86	Permafrost Meta-Omics and Climate Change. <i>Annual Review of Earth and Planetary Sciences</i> , 2016, 44, 439-462.	4.6	82
87	Development of compost maturity and Actinobacteria populations during full-scale composting of organic household waste. <i>Journal of Applied Microbiology</i> , 2007, 103, 487-498.	1.4	78
88	Marker and reporter genes: illuminating tools for environmental microbiologists. <i>Current Opinion in Microbiology</i> , 2003, 6, 310-316.	2.3	77
89	The microbial nitrogen cycling potential is impacted by polyaromatic hydrocarbon pollution of marine sediments. <i>Frontiers in Microbiology</i> , 2014, 5, 108.	1.5	76
90	Active bacterial community structure along vertical redox gradients in Baltic Sea sediment. <i>Environmental Microbiology</i> , 2008, 10, 2051-2063.	1.8	74

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91	Temporal dynamics of hot desert microbial communities reveal structural and functional responses to water input. <i>Scientific Reports</i> , 2016, 6, 34434.	1.6	74
92	Omics for understanding microbial functional dynamics. <i>Environmental Microbiology</i> , 2012, 14, 1-3.	1.8	71
93	Ion mobility spectrometry and the omics: Distinguishing isomers, molecular classes and contaminant ions in complex samples. <i>TrAC - Trends in Analytical Chemistry</i> , 2019, 116, 292-299.	5.8	71
94	Earth Microbiome Project and Global Systems Biology. <i>MSystems</i> , 2018, 3, .	1.7	65
95	Tracking genetically engineered microorganisms in nature. <i>Current Opinion in Biotechnology</i> , 1995, 6, 275-283.	3.3	64
96	Selection, Succession, and Stabilization of Soil Microbial Consortia. <i>MSystems</i> , 2019, 4, .	1.7	64
97	Metagenomic Insights into the Degradation of Resistant Starch by Human Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	63
98	Use of green fluorescent protein and luciferase biomarkers to monitor survival and activity of <i>Arthrobacter chlorophenolicus</i> A6 cells during degradation of 4-chlorophenol in soil. <i>Environmental Microbiology</i> , 2001, 3, 32-42.	1.8	62
99	Adaptation of the psychrotroph <i>Arthrobacter chlorophenolicus</i> A6 to growth temperature and the presence of phenols by changes in the anteiso/iso ratio of branched fatty acids. <i>FEMS Microbiology Letters</i> , 2007, 266, 138-143.	0.7	62
100	The Specific Carbohydrate Diet and Diet Modification as Induction Therapy for Pediatric Crohn's Disease: A Randomized Diet Controlled Trial. <i>Nutrients</i> , 2020, 12, 3749.	1.7	62
101	Dispersal limitation and thermodynamic constraints govern spatial structure of permafrost microbial communities. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	62
102	Trends in Microbial Community Composition and Function by Soil Depth. <i>Microorganisms</i> , 2022, 10, 540.	1.6	62
103	Community Structure of Actively Growing Bacterial Populations in Plant Pathogen Suppressive Soil. <i>Microbial Ecology</i> , 2007, 53, 399-413.	1.4	60
104	Specific interactions between arbuscular mycorrhizal fungi and plant growth-promoting bacteria: as revealed by different combinations. <i>FEMS Microbiology Letters</i> , 2008, 287, 174-180.	0.7	59
105	The past, present and future of microbiome analyses. <i>Nature Protocols</i> , 2016, 11, 2049-2053.	5.5	59
106	Strategies for Metagenomic-Guided Whole-Community Proteomics of Complex Microbial Environments. <i>PLoS ONE</i> , 2011, 6, e27173.	1.1	58
107	Metaphenomic Responses of a Native Prairie Soil Microbiome to Moisture Perturbations. <i>MSystems</i> , 2019, 4, .	1.7	56
108	Genetic and metabolic links between the murine microbiome and memory. <i>Microbiome</i> , 2020, 8, 53.	4.9	56

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109	Degradation of mixtures of phenolic compounds by <i>Arthrobacter chlorophenolicus</i> A6. <i>Biodegradation</i> , 2008, 19, 495-505.	1.5	55
110	Antifungal and Root Surface Colonization Properties of GFP-Tagged <i>Paenibacillus brasilensis</i> PB177. <i>World Journal of Microbiology and Biotechnology</i> , 2005, 21, 1591-1597.	1.7	54
111	Quantification of the presence and activity of specific microorganisms in nature. <i>Molecular Biotechnology</i> , 1997, 7, 103-120.	1.3	52
112	Active virus-host interactions at sub-freezing temperatures in Arctic peat soil. <i>Microbiome</i> , 2021, 9, 208.	4.9	52
113	Quantification of Genetically Tagged Cyanobacteria in Baltic Sea Sediment by Competitive PCR. <i>BioTechniques</i> , 1997, 22, 512-518.	0.8	51
114	The founding charter of the Genomic Observatories Network. <i>GigaScience</i> , 2014, 3, 2.	3.3	51
115	Metaproteomics reveals persistent and phylum-redundant metabolic functional stability in adult human gut microbiomes of Crohn's remission patients despite temporal variations in microbial taxa, genomes, and proteomes. <i>Microbiome</i> , 2019, 7, 18.	4.9	51
116	Microbial community structure in polluted Baltic Sea sediments. <i>Environmental Microbiology</i> , 2006, 8, 223-232.	1.8	48
117	A Probe-Enabled Approach for the Selective Isolation and Characterization of Functionally Active Subpopulations in the Gut Microbiome. <i>Journal of the American Chemical Society</i> , 2019, 141, 42-47.	6.6	48
118	Identification of genetic factors that modify motor performance and body weight using Collaborative Cross mice. <i>Scientific Reports</i> , 2015, 5, 16247.	1.6	47
119	Changes in Active Bacterial Communities before and after Dredging of Highly Polluted Baltic Sea Sediments. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6800-6807.	1.4	46
120	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	6.0	45
121	Changes in microbial communities along redox gradients in polygonized Arctic wet tundra soils. <i>Environmental Microbiology Reports</i> , 2015, 7, 649-657.	1.0	42
122	A unified conceptual framework for prediction and control of microbiomes. <i>Current Opinion in Microbiology</i> , 2018, 44, 20-27.	2.3	42
123	Microbial Community Structure and Functional Potential Along a Hypersaline Gradient. <i>Frontiers in Microbiology</i> , 2018, 9, 1492.	1.5	41
124	The life beneath our feet. <i>Nature</i> , 2013, 494, 40-41.	13.7	40
125	Complete genome sequence of the lignin-degrading bacterium <i>Klebsiella</i> sp. strain BRL6-2. <i>Standards in Genomic Sciences</i> , 2014, 9, 19.	1.5	40
126	Biomarkers for monitoring efficacy of bioremediation by microbial inoculants. <i>Environmental Pollution</i> , 2000, 107, 217-223.	3.7	39

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127	Metabolic and spatio-taxonomic response of uncultivated seafloor bacteria following the Deepwater Horizon oil spill. <i>ISME Journal</i> , 2017, 11, 2569-2583.	4.4	39
128	Disentangling the complexity of permafrost soil by using high resolution profiling of microbial community composition, key functions and respiration rates. <i>Environmental Microbiology</i> , 2018, 20, 4328-4342.	1.8	37
129	Addressing the challenge of soil metaproteome complexity by improving metaproteome depth of coverage through two-dimensional liquid chromatography. <i>Soil Biology and Biochemistry</i> , 2018, 125, 290-299.	4.2	37
130	Monitoring of GFP-Tagged Bacterial Cells. , 1998, 102, 285-298.		36
131	Metagenomics unveils the attributes of the alginolytic guilds of sediments from four distant cold coastal environments. <i>Environmental Microbiology</i> , 2016, 18, 4471-4484.	1.8	36
132	Diverse Bacterial Groups Contribute to the Alkane Degradation Potential of Chronically Polluted Subantarctic Coastal Sediments. <i>Microbial Ecology</i> , 2016, 71, 100-112.	1.4	36
133	Microbial Community Structure and Functional Potential in Cultivated and Native Tallgrass Prairie Soils of the Midwestern United States. <i>Frontiers in Microbiology</i> , 2018, 9, 1775.	1.5	36
134	Impact of 4-chlorophenol contamination and/or inoculation with the 4-chlorophenol-degrading strain, <i>Arthrobacter chlorophenolicus</i> A6L, on soil bacterial community structure. <i>FEMS Microbiology Ecology</i> , 2002, 42, 387-397.	1.3	35
135	Use of bromodeoxyuridine immunocapture to identify psychrotolerant phenanthrene-degrading bacteria in phenanthrene-enriched polluted Baltic Sea sediments. <i>FEMS Microbiology Ecology</i> , 2008, 65, 513-525.	1.3	35
136	Advantages of the metagenomic approach for soil exploration: reply from Vogel et al.. <i>Nature Reviews Microbiology</i> , 2009, 7, 756-757.	13.6	35
137	Spatial distribution of prokaryotic communities in hypersaline soils. <i>Scientific Reports</i> , 2019, 9, 1769.	1.6	33
138	Moisture modulates soil reservoirs of active DNA and RNA viruses. <i>Communications Biology</i> , 2021, 4, 992.	2.0	33
139	“Omics” of the mammalian gut – new insights into function. <i>Current Opinion in Biotechnology</i> , 2012, 23, 491-500.	3.3	31
140	Metagenomic analysis of microbial consortium from natural crude oil that seeps into the marine ecosystem offshore Southern California. <i>Standards in Genomic Sciences</i> , 2014, 9, 1259-1274.	1.5	31
141	Micronutrient metal speciation is controlled by competitive organic chelation in grassland soils. <i>Soil Biology and Biochemistry</i> , 2018, 120, 283-291.	4.2	31
142	Metagenomic Analysis of Subtidal Sediments from Polar and Subpolar Coastal Environments Highlights the Relevance of Anaerobic Hydrocarbon Degradation Processes. <i>Microbial Ecology</i> , 2018, 75, 123-139.	1.4	30
143	Metagenomic and Metatranscriptomic Analyses Reveal the Structure and Dynamics of a Dechlorinating Community Containing <i>Dehalococcoides mccartyi</i> and Corrinoid-Providing Microorganisms under Cobalamin-Limited Conditions. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	29
144	Deconstructing the Soil Microbiome into Reduced-Complexity Functional Modules. <i>MBio</i> , 2020, 11, .	1.8	27

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145	Identification and sequence of a nifH like gene in Rhodospirillum rubrum : partial characterization of a mutant unaffected in nitrogen fixation. <i>Molecular Microbiology</i> , 1996, 20, 559-568.	1.2	26
146	Monitoring physiological status of GFP-tagged <i>Pseudomonas fluorescens</i> SBW25 under different nutrient conditions and in soil by flow cytometry. <i>FEMS Microbiology Ecology</i> , 2004, 51, 123-132.	1.3	26
147	Trade-offs between microbiome diversity and productivity in a stratified microbial mat. <i>ISME Journal</i> , 2017, 11, 405-414.	4.4	26
148	Light-Stress Influences the Composition of the Murine Gut Microbiome, Memory Function, and Plasma Metabolome. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 108.	1.6	26
149	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. <i>Microbiome</i> , 2014, 2, .	4.9	25
150	Insights into the respiratory tract microbiota of patients with cystic fibrosis during early <i>Pseudomonas aeruginosa</i> colonization. <i>SpringerPlus</i> , 2015, 4, 405.	1.2	25
151	Degradation of 4-Chlorophenol at Low Temperature and during Extreme Temperature Fluctuations by <i>Arthrobacter chlorophenolicus</i> A6. <i>Microbial Ecology</i> , 2004, 48, 246-253.	1.4	24
152	Diverse tumour susceptibility in Collaborative Cross mice: identification of a new mouse model for human gastric tumourigenesis. <i>Gut</i> , 2019, 68, 1942-1952.	6.1	24
153	DNA Viral Diversity, Abundance, and Functional Potential Vary across Grassland Soils with a Range of Historical Moisture Regimes. <i>MBio</i> , 2021, 12, e0259521.	1.8	24
154	Permafrost as a potential pathogen reservoir. <i>One Earth</i> , 2022, 5, 351-360.	3.6	22
155	Use of a novel nonantibiotic triple marker gene cassette to monitor high survival of <i>Pseudomonas fluorescens</i> SBW25 on winter wheat in the field. <i>FEMS Microbiology Ecology</i> , 2008, 63, 156-168.	1.3	21
156	Microbial ecology of chlorinated solvent biodegradation. <i>Environmental Microbiology</i> , 2015, 17, 4835-4850.	1.8	21
157	Impact of Temperature on the Physiological Status of a Potential Bioremediation Inoculant, <i>Arthrobacter chlorophenolicus</i> A6. <i>Applied and Environmental Microbiology</i> , 2004, 70, 2952-2958.	1.4	20
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