

# Janet K Jansson

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

201 papers	35,748 citations	74 h-index	189 g-index
218 ext. papers	45,299 ext. citations	10.8 avg, IF	8.21 L-index

#	Paper	IF	Citations
201	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , <b>2012</b> , 486, 207-14	50.4	6938
200	Diversity, stability and resilience of the human gut microbiota. <i>Nature</i> , <b>2012</b> , 489, 220-30	50.4	2919
199	A framework for human microbiome research. <i>Nature</i> , <b>2012</b> , 486, 215-21	50.4	1722
198	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , <b>2017</b> , 551, 457-463	50.4	1076
197	Deep-sea oil plume enriches indigenous oil-degrading bacteria. <i>Science</i> , <b>2010</b> , 330, 204-8	33.3	906
196	Current understanding of the human microbiome. <i>Nature Medicine</i> , <b>2018</b> , 24, 392-400	50.5	823
195	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , <b>2019</b> , 569, 655-662	50.4	761
194	A pyrosequencing study in twins shows that gastrointestinal microbial profiles vary with inflammatory bowel disease phenotypes. <i>Gastroenterology</i> , <b>2010</b> , 139, 1844-1854.e1	13.3	731
193	Short-term antibiotic treatment has differing long-term impacts on the human throat and gut microbiome. <i>PLoS ONE</i> , <b>2010</b> , 5, e9836	3.7	714
192	Improved Bacterial 16S rRNA Gene (V4 and V4-5) and Fungal Internal Transcribed Spacer Marker Gene Primers for Microbial Community Surveys. <i>MSystems</i> , <b>2016</b> , 1,	7.6	703
191	Long-term ecological impacts of antibiotic administration on the human intestinal microbiota. <i>ISME Journal</i> , <b>2007</b> , 1, 56-66	11.9	693
190	Long-term impacts of antibiotic exposure on the human intestinal microbiota. <i>Microbiology (United Kingdom)</i> , <b>2010</b> , 156, 3216-3223	2.9	685
189	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , <b>2017</b> , 2, 17004	26.6	533
188	Scientists' warning to humanity: microorganisms and climate change. <i>Nature Reviews Microbiology</i> , <b>2019</b> , 17, 569-586	22.2	516
187	The Earth Microbiome project: successes and aspirations. <i>BMC Biology</i> , <b>2014</b> , 12, 69	7.3	501
186	Metagenomic analysis of a permafrost microbial community reveals a rapid response to thaw. <i>Nature</i> , <b>2011</b> , 480, 368-71	50.4	499
185	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> , <b>2010</b> , 44, 354-60	3	499

184	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MlxS) specifications. <i>Nature Biotechnology</i> , <b>2011</b> , 29, 415-20	44.5	445
183	Interactions between arbuscular mycorrhizal fungi and bacteria and their potential for stimulating plant growth. <i>Environmental Microbiology</i> , <b>2006</b> , 8, 1-10	5.2	444
182	Microbiome-wide association studies link dynamic microbial consortia to disease. <i>Nature</i> , <b>2016</b> , 535, 94-103	50.4	443
181	DNA Probe Method for the Detection of Specific Microorganisms in the Soil Bacterial Community. <i>Applied and Environmental Microbiology</i> , <b>1988</b> , 54, 703-711	4.8	423
180	Shotgun metaproteomics of the human distal gut microbiota. <i>ISME Journal</i> , <b>2009</b> , 3, 179-89	11.9	421
179	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. <i>ISME Journal</i> , <b>2012</b> , 6, 1715-27	11.9	420
178	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. <i>Cell</i> , <b>2019</b> , 177, 1600-1618.e17	56.2	379
177	Metabolomics reveals metabolic biomarkers of Crohn's disease. <i>PLoS ONE</i> , <b>2009</b> , 4, e6386	3.7	373
176	Molecular analysis of the gut microbiota of identical twins with Crohn's disease. <i>ISME Journal</i> , <b>2008</b> , 2, 716-27	11.9	354
175	Twin studies reveal specific imbalances in the mucosa-associated microbiota of patients with ileal Crohn's disease. <i>Inflammatory Bowel Diseases</i> , <b>2009</b> , 15, 653-60	4.5	346
174	Integrated metagenomics/metaproteomics reveals human host-microbiota signatures of Crohn's disease. <i>PLoS ONE</i> , <b>2012</b> , 7, e49138	3.7	320
173	Multi-omics of permafrost, active layer and thermokarst bog soil microbiomes. <i>Nature</i> , <b>2015</b> , 521, 208-13	50.4	305
172	Meta-analyses of studies of the human microbiota. <i>Genome Research</i> , <b>2013</b> , 23, 1704-14	9.7	289
171	Soil microbiomes and climate change. <i>Nature Reviews Microbiology</i> , <b>2020</b> , 18, 35-46	22.2	274
170	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , <b>2014</b> , 8, 1464-75	11.9	262
169	The microbial ecology of permafrost. <i>Nature Reviews Microbiology</i> , <b>2014</b> , 12, 414-25	22.2	243
168	Deep-sea bacteria enriched by oil and dispersant from the Deepwater Horizon spill. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 2405-16	5.2	231
167	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> , <b>2014</b> , 111, 4904-9	11.5	228

166	Microbial gene functions enriched in the Deepwater Horizon deep-sea oil plume. <i>ISME Journal</i> , <b>2012</b> , 6, 451-60	11.9	212
165	Unlocking the potential of metagenomics through replicated experimental design. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 513-20	44.5	212
164	Molecular characterization of the stomach microbiota in patients with gastric cancer and in controls. <i>Journal of Medical Microbiology</i> , <b>2009</b> , 58, 509-516	3.2	210
163	The soil microbiome-from metagenomics to metaphenomics. <i>Current Opinion in Microbiology</i> , <b>2018</b> , 43, 162-168	7.9	194
162	Meeting report: the terabase metagenomics workshop and the vision of an Earth microbiome project. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 243-8		187
161	Soft inertial microfluidics for high throughput separation of bacteria from human blood cells. <i>Lab on A Chip</i> , <b>2009</b> , 9, 1193-9	7.2	185
160	Responses of bacterial and archaeal ammonia oxidizers to soil organic and fertilizer amendments under long-term management. <i>Applied Soil Ecology</i> , <b>2010</b> , 45, 193-200	5	168
159	Simultaneous monitoring of cell number and metabolic activity of specific bacterial populations with a dual gfp-luxAB marker system. <i>Applied and Environmental Microbiology</i> , <b>1999</b> , 65, 813-21	4.8	167
158	Attachment of different soil bacteria to arbuscular mycorrhizal fungal extraradical hyphae is determined by hyphal vitality and fungal species. <i>FEMS Microbiology Letters</i> , <b>2006</b> , 254, 34-40	2.9	161
157	MICROBIOME. A unified initiative to harness Earth's microbiomes. <i>Science</i> , <b>2015</b> , 350, 507-8	33.3	155
156	Flow cytometric and microscopic analysis of GFP-tagged <i>Pseudomonas fluorescens</i> bacteria. <i>FEMS Microbiology Ecology</i> , <b>2006</b> , 22, 17-28	4.3	152
155	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , <b>2014</b> , 12, e1001920	9.7	146
154	The Earth Microbiome Project: Meeting report of the "1 EMP meeting on sample selection and acquisition" at Argonne National Laboratory October 6 2010. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 249-53		146
153	Direct cellular lysis/protein extraction protocol for soil metaproteomics. <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 6615-22	5.6	146
152	Impact of Dietary Resistant Starch on the Human Gut Microbiome, Metaproteome, and Metabolome. <i>MBio</i> , <b>2017</b> , 8,	7.8	145
151	Assessment of the Deepwater Horizon oil spill impact on Gulf coast microbial communities. <i>Frontiers in Microbiology</i> , <b>2014</b> , 5, 130	5.7	128
150	<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> , <b>2000</b> , 50 Pt 6, 2083-2092	2.2	127
149	Advances in preservation methods: keeping biosensor microorganisms alive and active. <i>Current Opinion in Biotechnology</i> , <b>2006</b> , 17, 43-9	11.4	121

148	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 499-509	44.5	120
147	In vivo study of trichoderma-pathogen-plant interactions, using constitutive and inducible green fluorescent protein reporter systems. <i>Applied and Environmental Microbiology</i> , <b>2004</b> , 70, 3073-81	4.8	116
146	Clindamycin-induced enrichment and long-term persistence of resistant <i>Bacteroides</i> spp. and resistance genes. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2006</b> , 58, 1160-7	5.1	115
145	Microbes in thawing permafrost: the unknown variable in the climate change equation. <i>ISME Journal</i> , <b>2012</b> , 6, 709-12	11.9	110
144	Metabolic Model-Based Integration of Microbiome Taxonomic and Metabolomic Profiles Elucidates Mechanistic Links between Ecological and Metabolic Variation. <i>MSystems</i> , <b>2016</b> , 1,	7.6	108
143	Impact of fire on active layer and permafrost microbial communities and metagenomes in an upland Alaskan boreal forest. <i>ISME Journal</i> , <b>2014</b> , 8, 1904-19	11.9	106
142	Use of bromodeoxyuridine immunocapture to identify active bacteria associated with arbuscular mycorrhizal hyphae. <i>Applied and Environmental Microbiology</i> , <b>2003</b> , 69, 6208-15	4.8	105
141	Molecular fingerprinting of the fecal microbiota of children raised according to different lifestyles. <i>Applied and Environmental Microbiology</i> , <b>2007</b> , 73, 2284-9	4.8	102
140	Gut Microbial Alterations Associated With Protection From Autoimmune Uveitis <b>2016</b> , 57, 3747-58		102
139	Tools for the Microbiome: Nano and Beyond. <i>ACS Nano</i> , <b>2016</b> , 10, 6-37	16.7	99
138	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> , <b>1999</b> , 65, 3674-80	4.8	96
137	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> , <b>2000</b> , 66, 3160-5	4.8	94
136	Novel 4-chlorophenol degradation gene cluster and degradation route via hydroxyquinol in <i>Arthrobacter chlorophenolicus</i> A6. <i>Applied and Environmental Microbiology</i> , <b>2005</b> , 71, 6538-44	4.8	93
135	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> , <b>2005</b> , 7, 1952-66	5.2	88
134	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 73	5.7	82
133	Earth microbial co-occurrence network reveals interconnection pattern across microbiomes. <i>Microbiome</i> , <b>2020</b> , 8, 82	16.6	80
132	Correction for Howe et al., 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> , <b>2014</b> , 111, 6115-6115	11.5	78
131	The metagenomics of disease-suppressive soils - experiences from the METACONTROL project. <i>Trends in Biotechnology</i> , <b>2008</b> , 26, 591-601	15.1	78

130	A multi-omic future for microbiome studies. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16049	26.6	77
129	Chitinase genes revealed and compared in bacterial isolates, DNA extracts and a metagenomic library from a phytopathogen-suppressive soil. <i>FEMS Microbiology Ecology</i> , <b>2010</b> , 71, 197-207	4.3	76
128	The Potential of Metagenomic Approaches for Understanding Soil Microbial Processes. <i>Soil Science Society of America Journal</i> , <b>2014</b> , 78, 3-10	2.5	73
127	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> , <b>2014</b> , 5, 332	5.7	72
126	Development of compost maturity and Actinobacteria populations during full-scale composting of organic household waste. <i>Journal of Applied Microbiology</i> , <b>2007</b> , 103, 487-98	4.7	69
125	Marker and reporter genes: illuminating tools for environmental microbiologists. <i>Current Opinion in Microbiology</i> , <b>2003</b> , 6, 310-6	7.9	69
124	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> , <b>2005</b> , 71, 501-6	4.8	69
123	Phyllostomid bat microbiome composition is associated to host phylogeny and feeding strategies. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 447	5.7	67
122	FOAM (Functional Ontology Assignments for Metagenomes): a Hidden Markov Model (HMM) database with environmental focus. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, e145	20.1	66
121	Active bacterial community structure along vertical redox gradients in Baltic Sea sediment. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 2051-63	5.2	65
120	Influence of early life exposure, host genetics and diet on the mouse gut microbiome and metabolome. <i>Nature Microbiology</i> , <b>2016</b> , 2, 16221	26.6	63
119	Climate change microbiology - problems and perspectives. <i>Nature Reviews Microbiology</i> , <b>2019</b> , 17, 391-396	26.2	62
118	Omics for understanding microbial functional dynamics. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 1-3	5.2	62
117	Permafrost Meta-Omics and Climate Change. <i>Annual Review of Earth and Planetary Sciences</i> , <b>2016</b> , 44, 439-462	15.3	62
116	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> , <b>2016</b> , 116, 2020-2029	3.6	61
115	Landscape topography structures the soil microbiome in arctic polygonal tundra. <i>Nature Communications</i> , <b>2018</b> , 9, 777	17.4	57
114	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> , <b>2015</b> , 6, 399	5.7	57
113	Community structure of actively growing bacterial populations in plant pathogen suppressive soil. <i>Microbial Ecology</i> , <b>2007</b> , 53, 399-413	4.4	56

112	Tracking genetically engineered microorganisms in nature. <i>Current Opinion in Biotechnology</i> , <b>1995</b> , 6, 275-83	11.4	55
111	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> , <b>2007</b> , 266, 138-43	2.9	54
110	The microbial nitrogen cycling potential is impacted by polyaromatic hydrocarbon pollution of marine sediments. <i>Frontiers in Microbiology</i> , <b>2014</b> , 5, 108	5.7	53
109	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> , <b>2001</b> , 3, 32-42	5.2	53
108	Antifungal and Root Surface Colonization Properties of GFP-Tagged <i>Paenibacillus brasiliensis</i> PB177. <i>World Journal of Microbiology and Biotechnology</i> , <b>2005</b> , 21, 1591-1597	4.4	51
107	Molecule Long-Read Sequencing Facilitates Assembly and Genomic Binning from Complex Soil Metagenomes. <i>MSystems</i> , <b>2016</b> , 1,	7.6	51
106	Quantification of the presence and activity of specific microorganisms in nature. <i>Molecular Biotechnology</i> , <b>1997</b> , 7, 103-20	3	49
105	Degradation of mixtures of phenolic compounds by <i>Arthrobacter chlorophenolicus</i> A6. <i>Biodegradation</i> , <b>2008</b> , 19, 495-505	4.1	49
104	Specific interactions between arbuscular mycorrhizal fungi and plant growth-promoting bacteria: as revealed by different combinations. <i>FEMS Microbiology Letters</i> , <b>2008</b> , 287, 174-80	2.9	46
103	Temporal dynamics of hot desert microbial communities reveal structural and functional responses to water input. <i>Scientific Reports</i> , <b>2016</b> , 6, 34434	4.9	45
102	Microbial community structure in polluted Baltic Sea sediments. <i>Environmental Microbiology</i> , <b>2006</b> , 8, 223-32	5.2	45
101	Quantification of genetically tagged cyanobacteria in Baltic Sea sediment by competitive PCR. <i>BioTechniques</i> , <b>1997</b> , 22, 512-8	2.5	43
100	Strategies for metagenomic-guided whole-community proteomics of complex microbial environments. <i>PLoS ONE</i> , <b>2011</b> , 6, e27173	3.7	43
99	The past, present and future of microbiome analyses. <i>Nature Protocols</i> , <b>2016</b> , 11, 2049-2053	18.8	40
98	Changes in active bacterial communities before and after dredging of highly polluted Baltic Sea sediments. <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 6800-7	4.8	38
97	Biomarkers for monitoring efficacy of bioremediation by microbial inoculants. <i>Environmental Pollution</i> , <b>2000</b> , 107, 217-23	9.3	38
96	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> , <b>2019</b> , 7, 18	16.6	37
95	Metagenomic Insights into the Degradation of Resistant Starch by Human Gut Microbiota. <i>Applied and Environmental Microbiology</i> , <b>2018</b> , 84,	4.8	37



94	Ion Mobility Spectrometry and the Omics: Distinguishing Isomers, Molecular Classes and Contaminant Ions in Complex Samples. <i>TrAC - Trends in Analytical Chemistry</i> , <b>2019</b> , 116, 292-299	14.6	35
93	Soil Microbiomes Under Climate Change and Implications for Carbon Cycling. <i>Annual Review of Environment and Resources</i> , <b>2020</b> , 45, 29-59	17.2	34
92	Dispersal limitation and thermodynamic constraints govern spatial structure of permafrost microbial communities. <i>FEMS Microbiology Ecology</i> , <b>2018</b> , 94,	4.3	33
91	Changes in microbial communities along redox gradients in polygonized Arctic wet tundra soils. <i>Environmental Microbiology Reports</i> , <b>2015</b> , 7, 649-57	3.7	32
90	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> , <b>2002</b> , 42, 387-97	4.3	32
89	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> , <b>2019</b> , 141, 42-47	16.4	31
88	Selection, Succession, and Stabilization of Soil Microbial Consortia. <i>MSystems</i> , <b>2019</b> , 4,	7.6	29
87	Use of bromodeoxyuridine immunocapture to identify psychrotolerant phenanthrene-degrading bacteria in phenanthrene-enriched polluted Baltic Sea sediments. <i>FEMS Microbiology Ecology</i> , <b>2008</b> , 65, 513-25	4.3	29
86	Diverse Bacterial Groups Contribute to the Alkane Degradation Potential of Chronically Polluted Subantarctic Coastal Sediments. <i>Microbial Ecology</i> , <b>2016</b> , 71, 100-12	4.4	28
85	Metagenomic analysis of microbial consortium from natural crude oil that seeps into the marine ecosystem offshore Southern California. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 1259-74		28
84	Identification of genetic factors that modify motor performance and body weight using Collaborative Cross mice. <i>Scientific Reports</i> , <b>2015</b> , 5, 16247	4.9	28
83	Metabolic and spatio-taxonomic response of uncultivated seafloor bacteria following the Deepwater Horizon oil spill. <i>ISME Journal</i> , <b>2017</b> , 11, 2569-2583	11.9	27
82	Complete genome sequence of the lignin-degrading bacterium <i>Klebsiella</i> sp. strain BRL6-2. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 19		27
81	'Omics' of the mammalian gut--new insights into function. <i>Current Opinion in Biotechnology</i> , <b>2012</b> , 23, 491-500	11.4	27
80	Monitoring of GFP-tagged bacterial cells. <i>Methods in Molecular Biology</i> , <b>1998</b> , 102, 285-98	1.4	27
79	Toward unrestricted use of public genomic data. <i>Science</i> , <b>2019</b> , 363, 350-352	33.3	25
78	Metaphenomic Responses of a Native Prairie Soil Microbiome to Moisture Perturbations. <i>MSystems</i> , <b>2019</b> , 4,	7.6	25
77	Advantages of the metagenomic approach for soil exploration: reply from Vogel et al.. <i>Nature Reviews Microbiology</i> , <b>2009</b> , 7, 756-757	22.2	25



76	Microbial Community Structure and Functional Potential in Cultivated and Native Tallgrass Prairie Soils of the Midwestern United States. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1775	5.7	25
75	The Specific Carbohydrate Diet and Diet Modification as Induction Therapy for Pediatric Crohn's Disease: A Randomized Diet Controlled Trial. <i>Nutrients</i> , <b>2020</b> , 12,	6.7	24
74	Identification and sequence of a nifJ-like gene in Rhodospirillum rubrum: partial characterization of a mutant unaffected in nitrogen fixation. <i>Molecular Microbiology</i> , <b>1996</b> , 20, 559-68	4.1	24
73	Disentangling the complexity of permafrost soil by using high resolution profiling of microbial community composition, key functions and respiration rates. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 4328-4342	5.2	23
72	Insights into the respiratory tract microbiota of patients with cystic fibrosis during early Pseudomonas aeruginosa colonization. <i>SpringerPlus</i> , <b>2015</b> , 4, 405		23
71	Metagenomics unveils the attributes of the alginolytic guilds of sediments from four distant cold coastal environments. <i>Environmental Microbiology</i> , <b>2016</b> , 18, 4471-4484	5.2	22
70	Metagenomic and Metatranscriptomic Analyses Reveal the Structure and Dynamics of a Dechlorinating Community Containing Dehalococcoides mccartyi and Corrinoid-Providing Microorganisms under Cobalamin-Limited Conditions. <i>Applied and Environmental Microbiology</i> , <b>2017</b> , 83,	4.8	21
69	A unified conceptual framework for prediction and control of microbiomes. <i>Current Opinion in Microbiology</i> , <b>2018</b> , 44, 20-27	7.9	21
68	Trade-offs between microbiome diversity and productivity in a stratified microbial mat. <i>ISME Journal</i> , <b>2017</b> , 11, 405-414	11.9	21
67	Monitoring physiological status of GFP-tagged Pseudomonas fluorescens SBW25 under different nutrient conditions and in soil by flow cytometry. <i>FEMS Microbiology Ecology</i> , <b>2004</b> , 51, 123-32	4.3	21
66	Degradation of 4-chlorophenol at low temperature and during extreme temperature fluctuations by Arthrobacter chlorophenolicus A6. <i>Microbial Ecology</i> , <b>2004</b> , 48, 246-53	4.4	21
65	Microbial Community Structure and Functional Potential Along a Hypersaline Gradient. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1492	5.7	20
64	Microbial ecology of chlorinated solvent biodegradation. <i>Environmental Microbiology</i> , <b>2015</b> , 17, 4835-50	5.2	20
63	Use of a novel nonantibiotic triple marker gene cassette to monitor high survival of Pseudomonas fluorescens SBW25 on winter wheat in the field. <i>FEMS Microbiology Ecology</i> , <b>2008</b> , 63, 156-68	4.3	20
62	Genetic and metabolic links between the murine microbiome and memory. <i>Microbiome</i> , <b>2020</b> , 8, 53	16.6	20
61	Micronutrient metal speciation is controlled by competitive organic chelation in grassland soils. <i>Soil Biology and Biochemistry</i> , <b>2018</b> , 120, 283-291	7.5	19
60	Impact of temperature on the physiological status of a potential bioremediation inoculant, Arthrobacter chlorophenolicus A6. <i>Applied and Environmental Microbiology</i> , <b>2004</b> , 70, 2952-8	4.8	19
59	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. <i>Microbiome</i> , <b>2014</b> , 2,	16.6	18

58	Amino acid treatment enhances protein recovery from sediment and soils for metaproteomic studies. <i>Proteomics</i> , <b>2013</b> , 13, 2776-85	4.8	17
57	Addressing the challenge of soil metaproteome complexity by improving metaproteome depth of coverage through two-dimensional liquid chromatography. <i>Soil Biology and Biochemistry</i> , <b>2018</b> , 125, 290-299	7.5	16
56	Rapid lab-on-a-chip profiling of human gut bacteria. <i>Journal of Microbiological Methods</i> , <b>2008</b> , 72, 82-90	2.8	16
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