

Janet K Jansson

List of Publications by Year in Descending Order

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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	Trends in Microbial Community Composition and Function by Soil Depth.. <i>Microorganisms</i> , 2022 , 10,	4.9	0
200	Permafrost as a potential pathogen reservoir. <i>One Earth</i> , 2022 , 5, 351-360	8.1	2
199	DNA Viral Diversity, Abundance, and Functional Potential Vary across Grassland Soils with a Range of Historical Moisture Regimes. <i>MBio</i> , 2021 , e0259521	7.8	1
198	Active virus-host interactions at sub-freezing temperatures in Arctic peat soil. <i>Microbiome</i> , 2021 , 9, 208	16.6	6
197	MetFish: a Metabolomics Pipeline for Studying Microbial Communities in Chemically Extreme Environments. <i>MSystems</i> , 2021 , 6, e0105820	7.6	0
196	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021 , 39, 499-509	44.5	120
195	Activity-Based Protein Profiling of Chitin Catabolism. <i>ChemBioChem</i> , 2021 , 22, 717-723	3.8	3
194	Enrichment of potential pathogens in marine microbiomes with different degrees of anthropogenic activity. <i>Environmental Pollution</i> , 2021 , 268, 115757	9.3	5
193	Molecular imaging of plant-microbe interactions on the seed surface. <i>Analyst, The</i> , 2021 , 146, 5855-5865		2
192	Metabolic Interactions between and <i>Pseudomonas fluorescens</i> under Controlled Iron-Limited Conditions. <i>MSystems</i> , 2021 , 6,	7.6	5
191	Moisture modulates soil reservoirs of active DNA and RNA viruses. <i>Communications Biology</i> , 2021 , 4, 992	6.7	5
190	Metagenomic analysis of microbial communities across a transect from low to highly hydrocarbon-contaminated soils in King George Island, Maritime Antarctica. <i>Geobiology</i> , 2021 ,	4.3	2
189	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,	6.7	24
188	Soil Microbiomes Under Climate Change and Implications for Carbon Cycling. <i>Annual Review of Environment and Resources</i> , 2020 , 45, 29-59	17.2	34
187	Earth microbial co-occurrence network reveals interconnection pattern across microbiomes. <i>Microbiome</i> , 2020 , 8, 82	16.6	80
186	Deconstructing the Soil Microbiome into Reduced-Complexity Functional Modules. <i>MBio</i> , 2020 , 11,	7.8	13
185	Integrated network modeling approach defines key metabolic responses of soil microbiomes to perturbations. <i>Scientific Reports</i> , 2020 , 10, 10882	4.9	5

184	Visualizing Microbial Community Dynamics via a Controllable Soil Environment. <i>MSystems</i> , 2020 , 5,	7.6	8
183	Xanthohumol microbiome and signature in healthy adults (the XMaS trial): a phase I triple-masked, placebo-controlled clinical trial. <i>Trials</i> , 2020 , 21, 835	2.8	5
182	Terabase Metagenome Sequencing of Grassland Soil Microbiomes. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	2
181	Development and Analysis of a Stable, Reduced Complexity Model Soil Microbiome. <i>Frontiers in Microbiology</i> , 2020 , 11, 1987	5.7	4
180	Soil microbiomes and climate change. <i>Nature Reviews Microbiology</i> , 2020 , 18, 35-46	22.2	274
179	Genetic and metabolic links between the murine microbiome and memory. <i>Microbiome</i> , 2020 , 8, 53	16.6	20
178	Toward unrestricted use of public genomic data. <i>Science</i> , 2019 , 363, 350-352	33.3	25
177	Siderophore profiling of co-habiting soil bacteria by ultra-high resolution mass spectrometry. <i>Metallomics</i> , 2019 , 11, 166-175	4.5	12
176	Scientists' warning to humanity: microorganisms and climate change. <i>Nature Reviews Microbiology</i> , 2019 , 17, 569-586	22.2	516
175	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019 , 569, 655-662	50.4	761
174	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. <i>Cell</i> , 2019 , 177, 1600-1618.e17	56.2	379
173	Metaphenomic Responses of a Native Prairie Soil Microbiome to Moisture Perturbations. <i>MSystems</i> , 2019 , 4,	7.6	25
172	Alterations in the relative abundance of correlate with changes in fecal calprotectin in patients with ileal Crohn's disease: a longitudinal study. <i>Scandinavian Journal of Gastroenterology</i> , 2019 , 54, 577-585	2.4	14
171	Selection, Succession, and Stabilization of Soil Microbial Consortia. <i>MSystems</i> , 2019 , 4,	7.6	29
170	Climate change microbiology - problems and perspectives. <i>Nature Reviews Microbiology</i> , 2019 , 17, 391-396	2.2	62
169	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	14.6	35
168	Diverse tumour susceptibility in Collaborative Cross mice: identification of a new mouse model for human gastric tumourigenesis. <i>Gut</i> , 2019 , 68, 1942-1952	19.2	12
167	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	16.6	37

166	Spatial distribution of prokaryotic communities in hypersaline soils. <i>Scientific Reports</i> , 2019 , 9, 1769	4.9	15
165	Light-Stress Influences the Composition of the Murine Gut Microbiome, Memory Function, and Plasma Metabolome. <i>Frontiers in Molecular Biosciences</i> , 2019 , 6, 108	5.6	14
164	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	16.4	31
163	The soil microbiome-from metagenomics to metaphenomics. <i>Current Opinion in Microbiology</i> , 2018 , 43, 162-168	7.9	194
162	Landscape topography structures the soil microbiome in arctic polygonal tundra. <i>Nature Communications</i> , 2018 , 9, 777	17.4	57
161	Current understanding of the human microbiome. <i>Nature Medicine</i> , 2018 , 24, 392-400	50.5	823
160	Micronutrient metal speciation is controlled by competitive organic chelation in grassland soils. <i>Soil Biology and Biochemistry</i> , 2018 , 120, 283-291	7.5	19
159	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	4.4	12
158	Temporal dynamics of CO ₂ and CH ₄ loss potentials in response to rapid hydrological shifts in tidal freshwater wetland soils. <i>Ecological Engineering</i> , 2018 , 114, 104-114	3.9	9
157	Microbial Community Structure and Functional Potential Along a Hypersaline Gradient. <i>Frontiers in Microbiology</i> , 2018 , 9, 1492	5.7	20
156	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	5.2	23
155	A unified conceptual framework for prediction and control of microbiomes. <i>Current Opinion in Microbiology</i> , 2018 , 44, 20-27	7.9	21
154	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	7.5	16
153	Dispersal limitation and thermodynamic constraints govern spatial structure of permafrost microbial communities. <i>FEMS Microbiology Ecology</i> , 2018 , 94,	4.3	33
152	Both the intratumoral immune and microbial microenvironment are linked to recurrence in human colon cancer: results from a prospective, multicenter nodal ultrastaging trial. <i>Oncotarget</i> , 2018 , 9, 23564-23576	4.3	1
151	Predominance and high diversity of genes associated to denitrification in metagenomes of subantarctic coastal sediments exposed to urban pollution. <i>PLoS ONE</i> , 2018 , 13, e0207606	3.7	6
150	Metagenomic Insights into the Degradation of Resistant Starch by Human Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2018 , 84,	4.8	37
149	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	5.7	25

148	The MPLEx Protocol for Multi-omic Analyses of Soil Samples. <i>Journal of Visualized Experiments</i> , 2018 ,	1.6	9
147	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017 , 2, 17004	26.6	533
146	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> , 2017 , 83,	4.8	21
145	Indirect Interspecies Regulation: Transcriptional and Physiological Responses of a Cyanobacterium to Heterotrophic Partnership. <i>MSystems</i> , 2017 , 2,	7.6	14
144	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4	1076
143	Impact of Dietary Resistant Starch on the Human Gut Microbiome, Metaproteome, and Metabolome. <i>MBio</i> , 2017 , 8,	7.8	145
142	Metabolic and spatio-taxonomic response of uncultivated seafloor bacteria following the Deepwater Horizon oil spill. <i>ISME Journal</i> , 2017 , 11, 2569-2583	11.9	27
141	Trade-offs between microbiome diversity and productivity in a stratified microbial mat. <i>ISME Journal</i> , 2017 , 11, 405-414	11.9	21
140	Microbial and viral-like rhodopsins present in coastal marine sediments from four polar and subpolar regions. <i>FEMS Microbiology Ecology</i> , 2017 , 93,	4.3	5
139	Prospecting Biotechnologically-Relevant Monooxygenases from Cold Sediment Metagenomes: An In Silico Approach. <i>Marine Drugs</i> , 2017 , 15,	6	12
138	Metagenomics unveils the attributes of the alginolytic guilds of sediments from four distant cold coastal environments. <i>Environmental Microbiology</i> , 2016 , 18, 4471-4484	5.2	22
137	A multi-omic future for microbiome studies. <i>Nature Microbiology</i> , 2016 , 1, 16049	26.6	77
136	Temporal dynamics of hot desert microbial communities reveal structural and functional responses to water input. <i>Scientific Reports</i> , 2016 , 6, 34434	4.9	45
135	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,	7.6	703
134	Diverse Bacterial Groups Contribute to the Alkane Degradation Potential of Chronically Polluted Subantarctic Coastal Sediments. <i>Microbial Ecology</i> , 2016 , 71, 100-12	4.4	28
133	Tools for the Microbiome: Nano and Beyond. <i>ACS Nano</i> , 2016 , 10, 6-37	16.7	99
132	Influence of early life exposure, host genetics and diet on the mouse gut microbiome and metabolome. <i>Nature Microbiology</i> , 2016 , 2, 16221	26.6	63
131	Gut Microbial Alterations Associated With Protection From Autoimmune Uveitis 2016 , 57, 3747-58		102

130	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , 2016 , 7, 73	5.7	82
129	Microbiome-wide association studies link dynamic microbial consortia to disease. <i>Nature</i> , 2016 , 535, 94-103	5.4	443
128	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	3.6	61
127	Metabolic Model-Based Integration of Microbiome Taxonomic and Metabolomic Profiles Elucidates Mechanistic Links between Ecological and Metabolic Variation. <i>MSystems</i> , 2016 , 1,	7.6	108
126	Permafrost Meta-Omics and Climate Change. <i>Annual Review of Earth and Planetary Sciences</i> , 2016 , 44, 439-462	15.3	62
125	The past, present and future of microbiome analyses. <i>Nature Protocols</i> , 2016 , 11, 2049-2053	18.8	40
124	Molecular Long-Read Sequencing Facilitates Assembly and Genomic Binning from Complex Soil Metagenomes. <i>MSystems</i> , 2016 , 1,	7.6	51
123	Multi-omics of permafrost, active layer and thermokarst bog soil microbiomes. <i>Nature</i> , 2015 , 521, 208-12	5.4	305
122	MICROBIOME. A unified initiative to harness Earth's microbiomes. <i>Science</i> , 2015 , 350, 507-8	33.3	155
121	Draft Genome Sequence of <i>Paenibacillus polymyxa</i> Strain Mc5Re-14, an Antagonistic Root Endophyte of <i>Matricaria chamomilla</i> . <i>Genome Announcements</i> , 2015 , 3,		3
120	Identification of genetic factors that modify motor performance and body weight using Collaborative Cross mice. <i>Scientific Reports</i> , 2015 , 5, 16247	4.9	28
119	Insights into the respiratory tract microbiota of patients with cystic fibrosis during early <i>Pseudomonas aeruginosa</i> colonization. <i>SpringerPlus</i> , 2015 , 4, 405		23
118	Fecal microbiome of growing pigs fed a cereal based diet including chicory (<i>Cichorium intybus</i> L.) or ribwort (<i>Plantago lanceolata</i> L.) forage. <i>Journal of Animal Science and Biotechnology</i> , 2015 , 6, 53	6	12
117	Microbial ecology of chlorinated solvent biodegradation. <i>Environmental Microbiology</i> , 2015 , 17, 4835-50	5.2	20
116	Changes in microbial communities along redox gradients in polygonized Arctic wet tundra soils. <i>Environmental Microbiology Reports</i> , 2015 , 7, 649-57	3.7	32
115	Phyllostomid bat microbiome composition is associated to host phylogeny and feeding strategies. <i>Frontiers in Microbiology</i> , 2015 , 6, 447	5.7	67
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> , 2015 , 6, 399	5.7	57
113	Draft Genome Sequence of <i>Streptomyces</i> sp. Strain Wb2n-11, a Desert Isolate with Broad-Spectrum Antagonism against Soilborne Phytopathogens. <i>Genome Announcements</i> , 2015 , 3,		13

112	Complete Genome Sequence of <i>Bacillus amyloliquefaciens</i> Strain Co1-6, a Plant Growth-Promoting Rhizobacterium of <i>Calendula officinalis</i> . <i>Genome Announcements</i> , 2015 , 3,		2
111	The microbial ecology of permafrost. <i>Nature Reviews Microbiology</i> , 2014 , 12, 414-25	22.2	243
110	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2014 , 8, 1464-75	11.9	262
109	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. <i>Microbiome</i> , 2014 , 2,	16.6	18
108	The Earth Microbiome project: successes and aspirations. <i>BMC Biology</i> , 2014 , 12, 69	7.3	501
107	Metagenomes from two microbial consortia associated with Santa Barbara seep oil. <i>Marine Genomics</i> , 2014 , 18 Pt B, 97-9	1.9	12
106	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, 1259-74		28
105	The microbial nitrogen cycling potential is impacted by polyaromatic hydrocarbon pollution of marine sediments. <i>Frontiers in Microbiology</i> , 2014 , 5, 108	5.7	53
104	Assessment of the Deepwater Horizon oil spill impact on Gulf coast microbial communities. <i>Frontiers in Microbiology</i> , 2014 , 5, 130	5.7	128
103	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> , 2014 , 111, 6115-6115	11.5	78
102	FOAM (Functional Ontology Assignments for Metagenomes): a Hidden Markov Model (HMM) database with environmental focus. <i>Nucleic Acids Research</i> , 2014 , 42, e145	20.1	66
101	Impact of fire on active layer and permafrost microbial communities and metagenomes in an upland Alaskan boreal forest. <i>ISME Journal</i> , 2014 , 8, 1904-19	11.9	106
100	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, 4904-9	11.5	228
99	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
98	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	5.7	72
97	Complete genome sequence of the lignin-degrading bacterium <i>Klebsiella</i> sp. strain BRL6-2. <i>Standards in Genomic Sciences</i> , 2014 , 9, 19		27
96	The Potential of Metagenomic Approaches for Understanding Soil Microbial Processes. <i>Soil Science Society of America Journal</i> , 2014 , 78, 3-10	2.5	73
95	Meta-analyses of studies of the human microbiota. <i>Genome Research</i> , 2013 , 23, 1704-14	9.7	289

94	Amino acid treatment enhances protein recovery from sediment and soils for metaproteomic studies. <i>Proteomics</i> , 2013 , 13, 2776-85	4.8	17
93	Crystal ball 2013. <i>Microbial Biotechnology</i> , 2013 , 6, 3-16	6.3	6
92	Deep-sea bacteria enriched by oil and dispersant from the Deepwater Horizon spill. <i>Environmental Microbiology</i> , 2012 , 14, 2405-16	5.2	231
91	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012 , 486, 207-14	50.4	6938
90	A framework for human microbiome research. <i>Nature</i> , 2012 , 486, 215-21	50.4	1722
89	Microbes in thawing permafrost: the unknown variable in the climate change equation. <i>ISME Journal</i> , 2012 , 6, 709-12	11.9	110
88	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2012 , 6, 1715-27	11.9	420
87	'Omics' of the mammalian gut--new insights into function. <i>Current Opinion in Biotechnology</i> , 2012 , 23, 491-500	11.4	27
86	Microbial gene functions enriched in the Deepwater Horizon deep-sea oil plume. <i>ISME Journal</i> , 2012 , 6, 451-60	11.9	212
85	Diversity, stability and resilience of the human gut microbiota. <i>Nature</i> , 2012 , 489, 220-30	50.4	2919
84	Integrated metagenomics/metaproteomics reveals human host-microbiota signatures of Crohn's disease. <i>PLoS ONE</i> , 2012 , 7, e49138	3.7	320
83	Unlocking the potential of metagenomics through replicated experimental design. <i>Nature Biotechnology</i> , 2012 , 30, 513-20	44.5	212
82	Omics for understanding microbial functional dynamics. <i>Environmental Microbiology</i> , 2012 , 14, 1-3	5.2	62
81	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , 2011 , 29, 415-20	44.5	445
80	Metagenomic analysis of a permafrost microbial community reveals a rapid response to thaw. <i>Nature</i> , 2011 , 480, 368-71	50.4	499
79	The Earth Microbiome Project: The Meeting Report for the 1st International Earth Microbiome Project Conference, Shenzhen, China, June 13th-15th 2011. <i>Standards in Genomic Sciences</i> , 2011 , 5, 243-247		13
78	Towards Peta-Terra-Terabase Sequencing of Terrestrial Metagenomes. <i>Microbe Magazine</i> , 2011 , 6, 309-315		10
77	Strategies for metagenomic-guided whole-community proteomics of complex microbial environments. <i>PLoS ONE</i> , 2011 , 6, e27173	3.7	43

76	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	4.3	76
75	Short-term antibiotic treatment has differing long-term impacts on the human throat and gut microbiome. <i>PLoS ONE</i> , 2010 , 5, e9836	3.7	714
74	Deep-sea oil plume enriches indigenous oil-degrading bacteria. <i>Science</i> , 2010 , 330, 204-8	33.3	906
73	A pyrosequencing study in twins shows that gastrointestinal microbial profiles vary with inflammatory bowel disease phenotypes. <i>Gastroenterology</i> , 2010 , 139, 1844-1854.e1	13.3	731
72	Long-term impacts of antibiotic exposure on the human intestinal microbiota. <i>Microbiology (United Kingdom)</i> , 2010 , 156, 3216-3223	2.9	685
71	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	5	168
70	Meeting report: the terabase metagenomics workshop and the vision of an Earth microbiome project. <i>Standards in Genomic Sciences</i> , 2010 , 3, 243-8		187
69	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> , 2010 , 3, 249-53		146
68	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, 354-60	3	499
67	Direct cellular lysis/protein extraction protocol for soil metaproteomics. <i>Journal of Proteome Research</i> , 2010 , 9, 6615-22	5.6	146
66	Metabolomics reveals metabolic biomarkers of Crohn's disease. <i>PLoS ONE</i> , 2009 , 4, e6386	3.7	373
65	Molecular characterization of the stomach microbiota in patients with gastric cancer and in controls. <i>Journal of Medical Microbiology</i> , 2009 , 58, 509-516	3.2	210
64	Twin studies reveal specific imbalances in the mucosa-associated microbiota of patients with ileal Crohn's disease. <i>Inflammatory Bowel Diseases</i> , 2009 , 15, 653-60	4.5	346
63	Shotgun metaproteomics of the human distal gut microbiota. <i>ISME Journal</i> , 2009 , 3, 179-89	11.9	421
62	Advantages of the metagenomic approach for soil exploration: reply from Vogel et al.. <i>Nature Reviews Microbiology</i> , 2009 , 7, 756-757	22.2	25
61	Impact of phenolic substrate and growth temperature on the <i>Arthrobacter chlorophenolicus</i> proteome. <i>Journal of Proteome Research</i> , 2009 , 8, 1953-64	5.6	12
60	Soft inertial microfluidics for high throughput separation of bacteria from human blood cells. <i>Lab on A Chip</i> , 2009 , 9, 1193-9	7.2	185
59	Molecular analysis of the gut microbiota of identical twins with Crohn's disease. <i>ISME Journal</i> , 2008 , 2, 716-27	11.9	354

58	Active bacterial community structure along vertical redox gradients in Baltic Sea sediment. <i>Environmental Microbiology</i> , 2008 , 10, 2051-63	5.2	65
57	The metagenomics of disease-suppressive soils - experiences from the METACONTROL project. <i>Trends in Biotechnology</i> , 2008 , 26, 591-601	15.1	78
56	Rapid lab-on-a-chip profiling of human gut bacteria. <i>Journal of Microbiological Methods</i> , 2008 , 72, 82-90	2.8	16
55	Degradation of mixtures of phenolic compounds by <i>Arthrobacter chlorophenolicus</i> A6. <i>Biodegradation</i> , 2008 , 19, 495-505	4.1	49
54	Specific interactions between arbuscular mycorrhizal fungi and plant growth-promoting bacteria: as revealed by different combinations. <i>FEMS Microbiology Letters</i> , 2008 , 287, 174-80	2.9	46
53	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, 156-68	4.3	20
52	Use of bromodeoxyuridine immunocapture to identify psychrotolerant phenanthrene-degrading bacteria in phenanthrene-enriched polluted Baltic Sea sediments. <i>FEMS Microbiology Ecology</i> , 2008 , 65, 513-25	4.3	29
51	Long-term ecological impacts of antibiotic administration on the human intestinal microbiota. <i>ISME Journal</i> , 2007 , 1, 56-66	11.9	693
50	Development of compost maturity and Actinobacteria populations during full-scale composting of organic household waste. <i>Journal of Applied Microbiology</i> , 2007 , 103, 487-98	4.7	69
49	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, 138-43	2.9	54
48	Community structure of actively growing bacterial populations in plant pathogen suppressive soil. <i>Microbial Ecology</i> , 2007 , 53, 399-413	4.4	56
47	Molecular fingerprinting of the fecal microbiota of children raised according to different lifestyles. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 2284-9	4.8	102
46	Clindamycin-induced enrichment and long-term persistence of resistant <i>Bacteroides</i> spp. and resistance genes. <i>Journal of Antimicrobial Chemotherapy</i> , 2006 , 58, 1160-7	5.1	115
45	Changes in active bacterial communities before and after dredging of highly polluted Baltic Sea sediments. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 6800-7	4.8	38
44	Microbial community structure in polluted Baltic Sea sediments. <i>Environmental Microbiology</i> , 2006 , 8, 223-32	5.2	45
43	Interactions between arbuscular mycorrhizal fungi and bacteria and their potential for stimulating plant growth. <i>Environmental Microbiology</i> , 2006 , 8, 1-10	5.2	444
42	Electron transport to nitrogenase in <i>Rhodospirillum rubrum</i> : the role of NAD(P)H as electron donor and the effect of fluoroacetate on nitrogenase activity. <i>FEMS Microbiology Letters</i> , 2006 , 150, 263-267	2.9	
41	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	2.9	161

40	Flow cytometric and microscopic analysis of GFP-tagged <i>Pseudomonas fluorescens</i> bacteria. <i>FEMS Microbiology Ecology</i> , 2006 , 22, 17-28	4.3	152
39	Advances in preservation methods: keeping biosensor microorganisms alive and active. <i>Current Opinion in Biotechnology</i> , 2006 , 17, 43-9	11.4	121
38	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, 1952-66	5.2	88
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