

Janet K Jansson

List of Publications by Year in descending order

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203
papers

51,426
citations

5876

81
h-index

2439

197
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220
all docs

220
docs citations

220
times ranked

52870
citing authors

#	ARTICLE	IF	CITATIONS
1	Metagenomic analysis of microbial communities across a transect from low to highly hydrocarbon-contaminated soils in King George Island, Maritime Antarctica. <i>Geobiology</i> , 2022, 20, 98-111.	1.1	9
2	Trends in Microbial Community Composition and Function by Soil Depth. <i>Microorganisms</i> , 2022, 10, 540.	1.6	62
3	Permafrost as a potential pathogen reservoir. <i>One Earth</i> , 2022, 5, 351-360.	3.6	22
4	Mass spectral imaging showing the plant growth-promoting rhizobacteria's effect on the <i>Brachypodium</i> awn. <i>Biointerphases</i> , 2022, 17, .	0.6	3
5	Metadata harmonization—Standards are the key for a better usage of omics data for integrative microbiome analysis. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	13
6	Uncovering Hidden Members and Functions of the Soil Microbiome Using <i>De Novo</i> Metaproteomics. <i>Journal of Proteome Research</i> , 2022, 21, 2023-2035.	1.8	6
7	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
8	Activity-Based Protein Profiling of Chitin Catabolism. <i>ChemBioChem</i> , 2021, 22, 717-723.	1.3	8
9	Enrichment of potential pathogens in marine microbiomes with different degrees of anthropogenic activity. <i>Environmental Pollution</i> , 2021, 268, 115757.	3.7	12
10	Molecular imaging of plant-microbe interactions on the <i>Brachypodium</i> seed surface. <i>Analyst</i> , 2021, 146, 5855-5865.	1.7	9
11	Metabolic Interactions between <i>Brachypodium</i> and <i>Pseudomonas fluorescens</i> under Controlled Iron-Limited Conditions. <i>MSystems</i> , 2021, 6, .	1.7	13
12	MetFish: a Metabolomics Pipeline for Studying Microbial Communities in Chemically Extreme Environments. <i>MSystems</i> , 2021, 6, e0105820.	1.7	5
13	Moisture modulates soil reservoirs of active DNA and RNA viruses. <i>Communications Biology</i> , 2021, 4, 992.	2.0	33
14	Active virus-host interactions at sub-freezing temperatures in Arctic peat soil. <i>Microbiome</i> , 2021, 9, 208.	4.9	52
15	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
16	Soil microbiomes and climate change. <i>Nature Reviews Microbiology</i> , 2020, 18, 35-46.	13.6	725
17	Visualizing Microbial Community Dynamics via a Controllable Soil Environment. <i>MSystems</i> , 2020, 5, .	1.7	12
18	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.	0.7	10

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19	Terabase Metagenome Sequencing of Grassland Soil Microbiomes. Microbiology Resource Announcements, 2020, 9, .	0.3	4
20	Development and Analysis of a Stable, Reduced Complexity Model Soil Microbiome. Frontiers in Microbiology, 2020, 11, 1987.	1.5	18
21	The Specific Carbohydrate Diet and Diet Modification as Induction Therapy for Pediatric Crohn's Disease: A Randomized Diet Controlled Trial. Nutrients, 2020, 12, 3749.	1.7	62
22	Soil Microbiomes Under Climate Change and Implications for Carbon Cycling. Annual Review of Environment and Resources, 2020, 45, 29-59.	5.6	145
23	Earth microbial co-occurrence network reveals interconnection pattern across microbiomes. Microbiome, 2020, 8, 82.	4.9	239
24	Deconstructing the Soil Microbiome into Reduced-Complexity Functional Modules. MBio, 2020, 11, .	1.8	27
25	Integrated network modeling approach defines key metabolic responses of soil microbiomes to perturbations. Scientific Reports, 2020, 10, 10882.	1.6	9
26	Genetic and metabolic links between the murine microbiome and memory. Microbiome, 2020, 8, 53.	4.9	56
27	Light-Stress Influences the Composition of the Murine Gut Microbiome, Memory Function, and Plasma Metabolome. Frontiers in Molecular Biosciences, 2019, 6, 108.	1.6	26
28	Toward unrestricted use of public genomic data. Science, 2019, 363, 350-352.	6.0	45
29	Siderophore profiling of co-habiting soil bacteria by ultra-high resolution mass spectrometry. Metallomics, 2019, 11, 166-175.	1.0	19
30	Scientists' warning to humanity: microorganisms and climate change. Nature Reviews Microbiology, 2019, 17, 569-586.	13.6	1,138
31	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. Nature, 2019, 569, 655-662.	13.7	1,638
32	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. Cell, 2019, 177, 1600-1618.e17.	13.5	701
33	Metaphenomic Responses of a Native Prairie Soil Microbiome to Moisture Perturbations. MSystems, 2019, 4, .	1.7	56
34	Alterations in the relative abundance of <i>Faecalibacterium prausnitzii</i> correlate with changes in fecal calprotectin in patients with ileal Crohn's disease: a longitudinal study. Scandinavian Journal of Gastroenterology, 2019, 54, 577-585.	0.6	15
35	Selection, Succession, and Stabilization of Soil Microbial Consortia. MSystems, 2019, 4, .	1.7	64
36	Climate change microbiology – problems and perspectives. Nature Reviews Microbiology, 2019, 17, 391-396.	13.6	130

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37	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
38	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
39	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
40	Spatial distribution of prokaryotic communities in hypersaline soils. <i>Scientific Reports</i> , 2019, 9, 1769.	1.6	33
41	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
42	The soil microbiome "from metagenomics to metaproteomics". <i>Current Opinion in Microbiology</i> , 2018, 43, 162-168.	2.3	330
43	Landscape topography structures the soil microbiome in arctic polygonal tundra. <i>Nature Communications</i> , 2018, 9, 777.	5.8	105
44	Current understanding of the human microbiome. <i>Nature Medicine</i> , 2018, 24, 392-400.	15.2	1,593
45	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
46	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
47	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.	1.6	13
48	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.	0.8	7
49	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.	1.1	13
50	Metagenomic Insights into the Degradation of Resistant Starch by Human Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	63
51	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
52	Earth Microbiome Project and Global Systems Biology. <i>MSystems</i> , 2018, 3, .	1.7	65
53	The MPLEx Protocol for Multi-omic Analyses of Soil Samples. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	19
54	Microbial Community Structure and Functional Potential Along a Hypersaline Gradient. <i>Frontiers in Microbiology</i> , 2018, 9, 1492.	1.5	41

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55	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
56	A unified conceptual framework for prediction and control of microbiomes. <i>Current Opinion in Microbiology</i> , 2018, 44, 20-27.	2.3	42
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> , 2018, 125, 290-299.	4.2	37
58	Dispersal limitation and thermodynamic constraints govern spatial structure of permafrost microbial communities. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	62
59	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017, 2, 17004.	5.9	830
60	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
61	Indirect Interspecies Regulation: Transcriptional and Physiological Responses of a Cyanobacterium to Heterotrophic Partnership. <i>MSystems</i> , 2017, 2, .	1.7	20
62	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
63	Impact of Dietary Resistant Starch on the Human Gut Microbiome, Metaproteome, and Metabolome. <i>MBio</i> , 2017, 8, .	1.8	219
64	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
65	Trade-offs between microbiome diversity and productivity in a stratified microbial mat. <i>ISME Journal</i> , 2017, 11, 405-414.	4.4	26
66	Microbial and viral-like rhodopsins present in coastal marine sediments from four polar and subpolar regions. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw216.	1.3	9
67	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
68	Prospecting Biotechnologically-Relevant Monooxygenases from Cold Sediment Metagenomes: An In Silico Approach. <i>Marine Drugs</i> , 2017, 15, 114.	2.2	13
69	Gut Microbial Alterations Associated With Protection From Autoimmune Uveitis. , 2016, 57, 3747.		156
70	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 73.	1.5	120
71	Microbiome-wide association studies link dynamic microbial consortia to disease. <i>Nature</i> , 2016, 535, 94-103.	13.7	595
72	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

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73	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
74	Permafrost Meta-Omics and Climate Change. <i>Annual Review of Earth and Planetary Sciences</i> , 2016, 44, 439-462.	4.6	82
75	The past, present and future of microbiome analyses. <i>Nature Protocols</i> , 2016, 11, 2049-2053.	5.5	59
76	Molecular Long-Read Sequencing Facilitates Assembly and Genomic Binning from Complex Soil Metagenomes. <i>MSystems</i> , 2016, 1, .	1.7	89
77	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
78	A multi-omic future for microbiome studies. <i>Nature Microbiology</i> , 2016, 1, 16049.	5.9	112
79	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
80	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
81	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
82	Tools for the Microbiome: Nano and Beyond. <i>ACS Nano</i> , 2016, 10, 6-37.	7.3	137
83	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
84	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
85	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.	2.1	15
86	Microbial ecology of chlorinated solvent biodegradation. <i>Environmental Microbiology</i> , 2015, 17, 4835-4850.	1.8	21
87	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
88	Phyllostomid bat microbiome composition is associated to host phylogeny and feeding strategies. <i>Frontiers in Microbiology</i> , 2015, 6, 447.	1.5	92
89	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
90	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, .	0.8	14

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91	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, .	0.8	2
92	Multi-omics of permafrost, active layer and thermokarst bog soil microbiomes. <i>Nature</i> , 2015, 521, 208-212.	13.7	467
93	A unified initiative to harness Earth's microbiomes. <i>Science</i> , 2015, 350, 507-508.	6.0	195
94	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, .	0.8	4
95	Soil Metagenomics. , 2015, , 600-609.		0
96	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
97	Assessment of the Deepwater Horizon oil spill impact on Gulf coast microbial communities. <i>Frontiers in Microbiology</i> , 2014, 5, 130.	1.5	172
98	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
99	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
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, 4904-4909.	3.3	305
101	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	2.6	190
102	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
103	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
104	The founding charter of the Genomic Observatories Network. <i>GigaScience</i> , 2014, 3, 2.	3.3	51
105	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
106	The microbial ecology of permafrost. <i>Nature Reviews Microbiology</i> , 2014, 12, 414-425.	13.6	345
107	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2014, 8, 1464-1475.	4.4	325
108	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. <i>Microbiome</i> , 2014, 2, .	4.9	25

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109	The Earth Microbiome project: successes and aspirations. BMC Biology, 2014, 12, 69.	1.7	723
110	Metagenomes from two microbial consortia associated with Santa Barbara seep oil. Marine Genomics, 2014, 18, 97-99.	0.4	14
111	Metagenomic analysis of microbial consortium from natural crude oil that seeps into the marine ecosystem offshore Southern California. Standards in Genomic Sciences, 2014, 9, 1259-1274.	1.5	31
112	Meta-analyses of studies of the human microbiota. Genome Research, 2013, 23, 1704-1714.	2.4	352
113	Amino acid treatment enhances protein recovery from sediment and soils for metaproteomic studies. Proteomics, 2013, 13, 2776-2785.	1.3	18
114	Crystal ball " 2013. Microbial Biotechnology, 2013, 6, 3-16.	2.0	6
115	The life beneath our feet. Nature, 2013, 494, 40-41.	13.7	40
116	Soil Metagenomics. , 2013, , 1-11.		1
117	Structure, function and diversity of the healthy human microbiome. Nature, 2012, 486, 207-214.	13.7	9,614
118	A framework for human microbiome research. Nature, 2012, 486, 215-221.	13.7	2,249
119	Microbes in thawing permafrost: the unknown variable in the climate change equation. ISME Journal, 2012, 6, 709-712.	4.4	153
120	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. ISME Journal, 2012, 6, 1715-1727.	4.4	547
121	"Omics"™ of the mammalian gut " new insights into function. Current Opinion in Biotechnology, 2012, 23, 491-500.	3.3	31
122	Microbial gene functions enriched in the Deepwater Horizon deep-sea oil plume. ISME Journal, 2012, 6, 451-460.	4.4	240
123	Diversity, stability and resilience of the human gut microbiota. Nature, 2012, 489, 220-230.	13.7	4,114
124	Integrated Metagenomics/Metaproteomics Reveals Human Host-Microbiota Signatures of Crohn's Disease. PLoS ONE, 2012, 7, e49138.	1.1	374
125	Unlocking the potential of metagenomics through replicated experimental design. Nature Biotechnology, 2012, 30, 513-520.	9.4	250
126	Omics for understanding microbial functional dynamics. Environmental Microbiology, 2012, 14, 1-3.	1.8	71

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127	Deep-sea bacteria enriched by oil and dispersant from the Deepwater Horizon spill. <i>Environmental Microbiology</i> , 2012, 14, 2405-2416.	1.8	275
128	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
129	Metagenomic analysis of a permafrost microbial community reveals a rapid response to thaw. <i>Nature</i> , 2011, 480, 368-371.	13.7	601
130	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.	1.5	18
131	Towards "Tera-Terra" Terabase Sequencing of Terrestrial Metagenomes. <i>Microbe Magazine</i> , 2011, 6, 309-315.	0.4	12
132	Strategies for Metagenomic-Guided Whole-Community Proteomics of Complex Microbial Environments. <i>PLoS ONE</i> , 2011, 6, e27173.	1.1	58
133	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
134	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
135	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
136	Direct Cellular Lysis/Protein Extraction Protocol for Soil Metaproteomics. <i>Journal of Proteome Research</i> , 2010, 9, 6615-6622.	1.8	193
137	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
138	Stewards of a changing planet: commentaries from ISME13 Plenary Lecturers. <i>ISME Journal</i> , 2010, 4, 1079-1080.	4.4	3
139	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
140	Deep-Sea Oil Plume Enriches Indigenous Oil-Degrading Bacteria. <i>Science</i> , 2010, 330, 204-208.	6.0	1,109
141	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
142	Long-term impacts of antibiotic exposure on the human intestinal microbiota. <i>Microbiology (United Kingdom)</i> 177 Pt 10 2011, 177, 2859-2869.	9.7	859
143	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
144	Metabolomics Reveals Metabolic Biomarkers of Crohn's Disease. <i>PLoS ONE</i> , 2009, 4, e6386.	1.1	429

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145	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
146	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
147	Shotgun metaproteomics of the human distal gut microbiota. <i>ISME Journal</i> , 2009, 3, 179-189.	4.4	484
148	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
149	TerraGenome: a consortium for the sequencing of a soil metagenome. <i>Nature Reviews Microbiology</i> , 2009, 7, 252-252.	13.6	199
150	Impact of Phenolic Substrate and Growth Temperature on the <i>Arthrobacter chlorophenolicus</i> Proteome. <i>Journal of Proteome Research</i> , 2009, 8, 1953-1964.	1.8	13
151	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
152	Degradation of mixtures of phenolic compounds by <i>Arthrobacter chlorophenolicus</i> A6. <i>Biodegradation</i> , 2008, 19, 495-505.	1.5	55
153	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
154	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
155	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
156	Molecular analysis of the gut microbiota of identical twins with Crohn's disease. <i>ISME Journal</i> , 2008, 2, 716-727.	4.4	407
157	Active bacterial community structure along vertical redox gradients in Baltic Sea sediment. <i>Environmental Microbiology</i> , 2008, 10, 2051-2063.	1.8	74
158	The metagenomics of disease-suppressive soils – experiences from the METACONTROL project. <i>Trends in Biotechnology</i> , 2008, 26, 591-601.	4.9	99
159	Rapid lab-on-a-chip profiling of human gut bacteria. <i>Journal of Microbiological Methods</i> , 2008, 72, 82-90.	0.7	16
160	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
161	Long-term ecological impacts of antibiotic administration on the human intestinal microbiota. <i>ISME Journal</i> , 2007, 1, 56-66.	4.4	885
162	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

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163	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
164	Community Structure of Actively Growing Bacterial Populations in Plant Pathogen Suppressive Soil. <i>Microbial Ecology</i> , 2007, 53, 399-413.	1.4	60
165	Microbial community structure in polluted Baltic Sea sediments. <i>Environmental Microbiology</i> , 2006, 8, 223-232.	1.8	48
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