

Sren J Srensen

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.

350
papers

18,550
citations

66
h-index

123
g-index

386
ext. papers

23,348
ext. citations

6.7
avg, IF

6.83
L-index

#	Paper	IF	Citations
350	Gut microbiota in human adults with type 2 diabetes differs from non-diabetic adults. <i>PLoS ONE</i> , 2010 , 5, e9085	3.7	1768
349	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014 , 32, 822-8	44.5	624
348	Studying plasmid horizontal transfer in situ: a critical review. <i>Nature Reviews Microbiology</i> , 2005 , 3, 700-102.2	12.2	485
347	454 pyrosequencing analyses of bacterial and archaeal richness in 21 full-scale biogas digesters. <i>FEMS Microbiology Ecology</i> , 2013 , 85, 612-26	4.3	478
346	Enhanced biofilm formation and increased resistance to antimicrobial agents and bacterial invasion are caused by synergistic interactions in multispecies biofilms. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 3916-23	4.8	470
345	Ecosystem response of pasture soil communities to fumigation-induced microbial diversity reductions: an examination of the biodiversity↔ecosystem function relationship. <i>Oikos</i> , 2000 , 90, 279-294 ⁴		436
344	Critical Assessment of Metagenome Interpretation-a benchmark of metagenomics software. <i>Nature Methods</i> , 2017 , 14, 1063-1071	21.6	412
343	The interconnection between biofilm formation and horizontal gene transfer. <i>FEMS Immunology and Medical Microbiology</i> , 2012 , 65, 183-95		344
342	Early life treatment with vancomycin propagates <i>Akkermansia muciniphila</i> and reduces diabetes incidence in the NOD mouse. <i>Diabetologia</i> , 2012 , 55, 2285-94	10.3	337
341	Interactions in multispecies biofilms: do they actually matter?. <i>Trends in Microbiology</i> , 2014 , 22, 84-91	12.4	305
340	Conjugative plasmids: vessels of the communal gene pool. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009 , 364, 2275-89	5.8	297
339	Biofilms in chronic infections - a matter of opportunity - monospecies biofilms in multispecies infections. <i>FEMS Immunology and Medical Microbiology</i> , 2010 , 59, 324-36		269
338	Maturation of the gut microbiome and risk of asthma in childhood. <i>Nature Communications</i> , 2018 , 9, 14117.4	17.4	216
337	An examination of the biodiversity↔ecosystem function relationship in arable soil microbial communities. <i>Soil Biology and Biochemistry</i> , 2001 , 33, 1713-1722	7.5	210
336	Broad host range plasmids can invade an unexpectedly diverse fraction of a soil bacterial community. <i>ISME Journal</i> , 2015 , 9, 934-45	11.9	202
335	Microbial indicators for soil quality. <i>Biology and Fertility of Soils</i> , 2018 , 54, 1-10	6.1	189
334	Gut microbiota composition is correlated to grid floor induced stress and behavior in the BALB/c mouse. <i>PLoS ONE</i> , 2012 , 7, e46231	3.7	181

333	The microbiome of New World vultures. <i>Nature Communications</i> , 2014 , 5, 5498	17.4	177
332	Substrate specificity of the OqxAB multidrug resistance pump in <i>Escherichia coli</i> and selected enteric bacteria. <i>Journal of Antimicrobial Chemotherapy</i> , 2007 , 60, 145-7	5.1	176
331	High prevalence of biofilm synergy among bacterial soil isolates in cocultures indicates bacterial interspecific cooperation. <i>ISME Journal</i> , 2015 , 9, 81-9	11.9	172
330	Profiling of the metabolically active community from a production-scale biogas plant by means of high-throughput metatranscriptome sequencing. <i>Journal of Biotechnology</i> , 2012 , 158, 248-58	3.7	170
329	Loss of microbial diversity in soils is coincident with reductions in some specialized functions. <i>Environmental Microbiology</i> , 2014 , 16, 2408-20	5.2	164
328	Plasmid-encoded multidrug efflux pump conferring resistance to olaquinox in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2004 , 48, 3332-7	5.9	161
327	It is elemental: soil nutrient stoichiometry drives bacterial diversity. <i>Environmental Microbiology</i> , 2017 , 19, 1176-1188	5.2	154
326	The diversity and function of soil microbial communities exposed to different disturbances. <i>Microbial Ecology</i> , 2002 , 44, 49-58	4.4	146
325	Selection for Cu-tolerant bacterial communities with altered composition, but unaltered richness, via long-term Cu exposure. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 7438-46	4.8	141
324	Nitrogenase gene amplicons from global marine surface waters are dominated by genes of non-cyanobacteria. <i>PLoS ONE</i> , 2011 , 6, e19223	3.7	140
323	The effect of long-term mercury pollution on the soil microbial community 2001 , 36, 11-19		139
322	Application of a mer-lux biosensor for estimating bioavailable mercury in soil. <i>Soil Biology and Biochemistry</i> , 2000 , 32, 639-646	7.5	136
321	Effects of tylosin as a disturbance on the soil microbial community. <i>Soil Biology and Biochemistry</i> , 2001 , 33, 2061-2071	7.5	136
320	Nucleotide sequence of pOLA52: a conjugative IncX1 plasmid from <i>Escherichia coli</i> which enables biofilm formation and multidrug efflux. <i>Plasmid</i> , 2008 , 60, 59-74	3.3	119
319	Characterization of bacterial populations in Danish raw milk cheeses made with different starter cultures by denaturing gradient gel electrophoresis and pyrosequencing. <i>International Dairy Journal</i> , 2011 , 21, 142-148	3.5	117
318	The mycorrhizal fungus (<i>Glomus intraradices</i>) affects microbial activity in the rhizosphere of pea plants (<i>Pisum sativum</i>). <i>Soil Biology and Biochemistry</i> , 2003 , 35, 1349-1357	7.5	114
317	454-sequencing reveals stochastic local reassembly and high disturbance tolerance within arbuscular mycorrhizal fungal communities. <i>Journal of Ecology</i> , 2012 , 100, 151-160	6	110
316	Studying Bacterial Multispecies Biofilms: Where to Start?. <i>Trends in Microbiology</i> , 2016 , 24, 503-513	12.4	109

315	Identifying the core microbial community in the gut of fungus-growing termites. <i>Molecular Ecology</i> , 2014 , 23, 4631-44	5.7	108
314	Effects of mercury contamination on the culturable heterotrophic, functional and genetic diversity of the bacterial community in soil. <i>FEMS Microbiology Ecology</i> , 2001 , 36, 1-9	4.3	106
313	Making bio-sense of toxicity: new developments in whole-cell biosensors. <i>Current Opinion in Biotechnology</i> , 2006 , 17, 11-6	11.4	103
312	The fate of indigenous microbiota, starter cultures, <i>Escherichia coli</i> , <i>Listeria innocua</i> and <i>Staphylococcus aureus</i> in Danish raw milk and cheeses determined by pyrosequencing and quantitative real time (qRT)-PCR. <i>International Journal of Food Microbiology</i> , 2012 , 153, 192-202	5.8	101
311	Large-scale benchmarking reveals false discoveries and count transformation sensitivity in 16S rRNA gene amplicon data analysis methods used in microbiome studies. <i>Microbiome</i> , 2016 , 4, 62	16.6	93
310	The fate of mercury in Arctic terrestrial and aquatic ecosystems, a review. <i>Environmental Chemistry</i> , 2012 , 9, 321	3.2	92
309	Interspecific Bacterial Interactions are Reflected in Multispecies Biofilm Spatial Organization. <i>Frontiers in Microbiology</i> , 2016 , 7, 1366	5.7	92
308	Coping with copper: legacy effect of copper on potential activity of soil bacteria following a century of exposure. <i>FEMS Microbiology Ecology</i> , 2016 , 92,	4.3	91
307	Experimental methods and modeling techniques for description of cell population heterogeneity. <i>Biotechnology Advances</i> , 2011 , 29, 575-99	17.8	90
306	The Use of Whole-Cell Biosensors to Detect and Quantify Compounds or Conditions Affecting Biological Systems. <i>Microbial Ecology</i> , 2001 , 42, 483-494	4.4	86
305	Impact of DNA extraction method on bacterial community composition measured by denaturing gradient gel electrophoresis. <i>Soil Biology and Biochemistry</i> , 2004 , 36, 1607-1614	7.5	84
304	Versatile biosensor vectors for detection and quantification of mercury. <i>FEMS Microbiology Letters</i> , 2000 , 193, 123-7	2.9	84
303	Investigation of the relationship between lactococcal host cell wall polysaccharide genotype and 936 phage receptor binding protein phylogeny. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 4385-92	4.8	83
302	The murine lung microbiome in relation to the intestinal and vaginal bacterial communities. <i>BMC Microbiology</i> , 2013 , 13, 303	4.5	82
301	Type 3 fimbriae, encoded by the conjugative plasmid pOLA52, enhance biofilm formation and transfer frequencies in Enterobacteriaceae strains. <i>Microbiology (United Kingdom)</i> , 2008 , 154, 187-195	2.9	82
300	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , 2016 , 7, 73	5.7	82
299	Ecological patterns, diversity and core taxa of microbial communities in groundwater-fed rapid gravity filters. <i>ISME Journal</i> , 2016 , 10, 2209-22	11.9	81
298	How Microbial Aggregates Protect against Nanoparticle Toxicity. <i>Trends in Biotechnology</i> , 2018 , 36, 1171-1182	11.182	81

297	Cultivation-independent examination of horizontal transfer and host range of an IncP-1 plasmid among gram-positive and gram-negative bacteria indigenous to the barley rhizosphere. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 6687-92	4.8	81
296	Construction of a ColD cda promoter-based SOS-green fluorescent protein whole-cell biosensor with higher sensitivity toward genotoxic compounds than constructs based on recA, umuDC, or sulA promoters. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 2338-46	4.8	80
295	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021 , 53, 156-165	36.3	80
294	Effects of fertilization with urban and agricultural organic wastes in a field trial [Prokaryotic diversity investigated by pyrosequencing. <i>Soil Biology and Biochemistry</i> , 2013 , 57, 784-793	7.5	76
293	Antagonism correlates with metabolic similarity in diverse bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 10684-10688	11.5	74
292	Metabolic variability in bioprocessing: implications of microbial phenotypic heterogeneity. <i>Trends in Biotechnology</i> , 2014 , 32, 608-16	15.1	73
291	The effect of longterm exposure to mercury on the bacterial community in marine sediment. <i>Current Microbiology</i> , 1998 , 36, 291-7	2.4	70
290	Heavy metal exposure causes changes in the metabolic health-associated gut microbiome and metabolites. <i>Environment International</i> , 2019 , 126, 454-467	12.9	69
289	Hundreds of circular novel plasmids and DNA elements identified in a rat cecum metatranscriptome. <i>PLoS ONE</i> , 2014 , 9, e87924	3.7	69
288	Conjugative plasmid conferring resistance to olaquinox. <i>Antimicrobial Agents and Chemotherapy</i> , 2003 , 47, 798-9	5.9	69
287	Metal stressors consistently modulate bacterial conjugal plasmid uptake potential in a phylogenetically conserved manner. <i>ISME Journal</i> , 2017 , 11, 152-165	11.9	68
286	Presence of N-acyl homoserine lactones in soil detected by a whole-cell biosensor and flow cytometry. <i>Microbial Ecology</i> , 2003 , 45, 226-36	4.4	67
285	Detection of oxytetracycline production by <i>Streptomyces rimosus</i> in soil microcosms by combining whole-cell biosensors and flow cytometry. <i>Applied and Environmental Microbiology</i> , 2001 , 67, 239-44	4.8	66
284	Endolithic chlorophyll d-containing phototrophs. <i>ISME Journal</i> , 2011 , 5, 1072-6	11.9	64
283	All IncP-1 plasmid subgroups, including the novel epsilon subgroup, are prevalent in the influent of a Danish wastewater treatment plant. <i>Plasmid</i> , 2009 , 62, 134-9	3.3	64
282	Detection and quantification of tetracyclines by whole cell biosensors. <i>FEMS Microbiology Letters</i> , 2000 , 190, 273-8	2.9	64
281	High-throughput screening of multispecies biofilm formation and quantitative PCR-based assessment of individual species proportions, useful for exploring interspecific bacterial interactions. <i>Microbial Ecology</i> , 2014 , 68, 146-54	4.4	63
280	Microbial diversity of biofilm communities in microniches associated with the didemnid ascidian <i>Lissoclinum patella</i> . <i>ISME Journal</i> , 2012 , 6, 1222-37	11.9	63

279	Inducible gene expression by nonculturable bacteria in milk after pasteurization. <i>Applied and Environmental Microbiology</i> , 2002 , 68, 1988-93	4.8	63
278	Diversity and characterization of mercury-resistant bacteria in snow, freshwater and sea-ice brine from the High Arctic. <i>FEMS Microbiology Ecology</i> , 2011 , 75, 390-401	4.3	62
277	The multiple antibiotic resistance IncP-1 plasmid pKJK5 isolated from a soil environment is phylogenetically divergent from members of the previously established alpha, beta and delta sub-groups. <i>Plasmid</i> , 2007 , 58, 31-43	3.3	62
276	The prevalence of the OqxAB multidrug efflux pump amongst olaquinox-resistant <i>Escherichia coli</i> in pigs. <i>Microbial Drug Resistance</i> , 2005 , 11, 378-82	2.9	61
275	Estimating the Transfer Range of Plasmids Encoding Antimicrobial Resistance in a Wastewater Treatment Plant Microbial Community. <i>Environmental Science and Technology Letters</i> , 2018 , 5, 260-265	11	59
274	Complete genome sequence of the cystic fibrosis pathogen <i>Achromobacter xylosoxidans</i> NH44784-1996 complies with important pathogenic phenotypes. <i>PLoS ONE</i> , 2013 , 8, e68484	3.7	59
273	Impact of long-term agricultural management practices on soil prokaryotic communities. <i>Soil Biology and Biochemistry</i> , 2019 , 129, 17-28	7.5	59
272	Characterization of the gut microbiota in leptin deficient obese mice - Correlation to inflammatory and diabetic parameters. <i>Research in Veterinary Science</i> , 2014 , 96, 241-50	2.5	58
271	Assessment of the specificity of <i>Burkholderia</i> and <i>Pseudomonas</i> qPCR assays for detection of these genera in soil using 454 pyrosequencing. <i>FEMS Microbiology Letters</i> , 2012 , 333, 77-84	2.9	58
270	Predominant genera of fecal microbiota in children with atopic dermatitis are not altered by intake of probiotic bacteria <i>Lactobacillus acidophilus</i> NCFM and <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Bi-07. <i>FEMS Microbiology Ecology</i> , 2011 , 75, 482-96	4.3	57
269	Type IV CRISPR-Cas systems are highly diverse and involved in competition between plasmids. <i>Nucleic Acids Research</i> , 2020 , 48, 2000-2012	20.1	57
268	Bacterial chitinolytic communities respond to chitin and pH alteration in soil. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 263-72	4.8	56
267	Exploring the immediate and long-term impact on bacterial communities in soil amended with animal and urban organic waste fertilizers using pyrosequencing and screening for horizontal transfer of antibiotic resistance. <i>FEMS Microbiology Ecology</i> , 2014 , 90, 206-24	4.3	55
266	<i>Acromyrmex</i> Leaf-Cutting Ants Have Simple Gut Microbiota with Nitrogen-Fixing Potential. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 5527-37	4.8	55
265	Bacterial community structure in High-Arctic snow and freshwater as revealed by pyrosequencing of 16S rRNA genes and cultivation. <i>Polar Research</i> , 2013 , 32, 17390	2	55
264	Legacy Effects on the Recovery of Soil Bacterial Communities from Extreme Temperature Perturbation. <i>Frontiers in Microbiology</i> , 2017 , 8, 1832	5.7	54
263	Coexistence facilitates interspecific biofilm formation in complex microbial communities. <i>Environmental Microbiology</i> , 2016 , 18, 2565-74	5.2	53
262	Interspecies interactions result in enhanced biofilm formation by co-cultures of bacteria isolated from a food processing environment. <i>Food Microbiology</i> , 2015 , 51, 18-24	6	52

261	Long-term industrial metal contamination unexpectedly shaped diversity and activity response of sediment microbiome. <i>Journal of Hazardous Materials</i> , 2018 , 344, 299-307	12.8	52
260	Infant airway microbiota and topical immune perturbations in the origins of childhood asthma. <i>Nature Communications</i> , 2019 , 10, 5001	17.4	52
259	Physiological heterogeneities in microbial populations and implications for physical stress tolerance. <i>Microbial Cell Factories</i> , 2012 , 11, 94	6.4	52
258	The effect of the lacY gene on the induction of IPTG inducible promoters, studied in <i>Escherichia coli</i> and <i>Pseudomonas fluorescens</i> . <i>Current Microbiology</i> , 1998 , 36, 341-7	2.4	52
257	Similar sponge-associated bacteria can be acquired via both vertical and horizontal transmission. <i>Environmental Microbiology</i> , 2015 , 17, 3807-21	5.2	51
256	Specificity and stability of the <i>Acromyrmex</i> - <i>Pseudonocardia</i> symbiosis. <i>Molecular Ecology</i> , 2013 , 22, 4307-4321	5.4	51
255	The effect of long-term mercury pollution on the soil microbial community. <i>FEMS Microbiology Ecology</i> , 2001 , 36, 11-19	4.3	51
254	Autogenic succession and deterministic recovery following disturbance in soil bacterial communities. <i>Scientific Reports</i> , 2017 , 7, 45691	4.9	50
253	Characterisation, dissemination and persistence of gentamicin resistant <i>Escherichia coli</i> from a Danish university hospital to the waste water environment. <i>Environment International</i> , 2008 , 34, 108-15	12.9	50
252	Effect of tetracycline on transfer and establishment of the tetracycline-inducible conjugative transposon Tn916 in the guts of gnotobiotic rats. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 758-64	4.8	50
251	Shifts in the microbial community structure explain the response of soil respiration to land-use change but not to climate warming. <i>Soil Biology and Biochemistry</i> , 2015 , 89, 123-134	7.5	49
250	Microbiomes associated with infective stages of root-knot and lesion nematodes in soil. <i>PLoS ONE</i> , 2017 , 12, e0177145	3.7	49
249	Microbial degradation of street dust polycyclic aromatic hydrocarbons in microcosms simulating diffuse pollution of urban soil. <i>Environmental Microbiology</i> , 2006 , 8, 535-45	5.2	49
248	Shifts in abundance and diversity of mobile genetic elements after the introduction of diverse pesticides into an on-farm biopurification system over the course of a year. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 4012-20	4.8	48
247	Facultative control of matrix production optimizes competitive fitness in <i>Pseudomonas aeruginosa</i> PA14 biofilm models. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 8414-26	4.8	47
246	Chromosomal insertion of the entire <i>Escherichia coli</i> lactose operon, into two strains of <i>Pseudomonas</i> , using a modified mini-Tn5 delivery system. <i>Gene</i> , 1997 , 186, 167-73	3.8	47
245	High diversity of bacterial mercuric reductase genes from surface and sub-surface floodplain soil (Oak Ridge, USA). <i>ISME Journal</i> , 2007 , 1, 453-67	11.9	47
244	Establishment and early succession of a multispecies biofilm composed of soil bacteria. <i>Microbial Ecology</i> , 2007 , 54, 352-62	4.4	47

243	Mercuric reductase genes (<i>merA</i>) and mercury resistance plasmids in High Arctic snow, freshwater and sea-ice brine. <i>FEMS Microbiology Ecology</i> , 2014 , 87, 52-63	4.3	46
242	A low-cost, multiplexable, automated flow cytometry procedure for the characterization of microbial stress dynamics in bioreactors. <i>Microbial Cell Factories</i> , 2013 , 12, 100	6.4	46
241	Effect of genomic location on horizontal transfer of a recombinant gene cassette between <i>Pseudomonas</i> strains in the rhizosphere and spermosphere of barley seedlings. <i>Current Microbiology</i> , 2001 , 42, 160-7	2.4	44
240	Bacterial social interactions and the emergence of community-intrinsic properties. <i>Current Opinion in Microbiology</i> , 2018 , 42, 104-109	7.9	44
239	Impact of conjugal transfer on the stability of IncP-1 plasmid pKJK5 in bacterial populations. <i>FEMS Microbiology Letters</i> , 2007 , 266, 250-6	2.9	43
238	Biodegradation, bioaccessibility, and genotoxicity of diffuse polycyclic aromatic hydrocarbon (PAH) pollution at a motorway site. <i>Environmental Science & Technology</i> , 2006 , 40, 3293-8	10.3	42
237	Enhanced degradation of phenoxyacetic acid in soil by horizontal transfer of the <i>tfdA</i> gene encoding a 2,4-dichlorophenoxyacetic acid dioxygenase. <i>FEMS Microbiology Ecology</i> , 2001 , 35, 75-84	4.3	42
236	High frequencies of antibiotic resistance genes in infants' meconium and early fecal samples. <i>Journal of Developmental Origins of Health and Disease</i> , 2016 , 7, 35-44	2.4	42
235	Deciphering conjugative plasmid permissiveness in wastewater microbiomes. <i>Molecular Ecology</i> , 2017 , 26, 3556-3571	5.7	41
234	Direct detection and quantification of horizontal gene transfer by using flow cytometry and <i>gfp</i> as a reporter gene. <i>Current Microbiology</i> , 2003 , 47, 129-33	2.4	41
233	Bias in bacterial diversity as a result of Nycodenz extraction from bulk soil. <i>Soil Biology and Biochemistry</i> , 2011 , 43, 2152-2159	7.5	40
232	Cultivation of hard-to-culture subsurface mercury-resistant bacteria and discovery of new <i>merA</i> gene sequences. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 3795-803	4.8	39
231	Low-abundant species facilitates specific spatial organization that promotes multispecies biofilm formation. <i>Environmental Microbiology</i> , 2017 , 19, 2893-2905	5.2	38
230	Chlorophyll <i>f</i> -driven photosynthesis in a cavernous cyanobacterium. <i>ISME Journal</i> , 2015 , 9, 2108-11	11.9	38
229	Effects of Soil Pre-Treatment with Basamid [®] Granules, , and on Bacterial and Fungal Communities at Two Apple Replant Disease Sites. <i>Frontiers in Microbiology</i> , 2017 , 8, 1604	5.7	38
228	Bioinformatic approaches reveal metagenomic characterization of soil microbial community. <i>PLoS ONE</i> , 2014 , 9, e93445	3.7	38
227	Adaptation of the bacterial community to mercury contamination. <i>FEMS Microbiology Letters</i> , 2001 , 204, 49-53	2.9	38
226	Natural decay process affects the abundance and community structure of Bacteria and Archaea in <i>Picea abies</i> logs. <i>FEMS Microbiology Ecology</i> , 2016 , 92,	4.3	37

225	Short- and long-term impacts of azithromycin treatment on the gut microbiota in children: A double-blind, randomized, placebo-controlled trial. <i>EBioMedicine</i> , 2018 , 38, 265-272	8.8	37
224	Comparison of antibiotic-resistant bacteria and antibiotic resistance genes abundance in hospital and community wastewater: A systematic review. <i>Science of the Total Environment</i> , 2020 , 743, 140804	10.2	36
223	Sequentially aerated membrane biofilm reactors for autotrophic nitrogen removal: microbial community composition and dynamics. <i>Microbial Biotechnology</i> , 2014 , 7, 32-43	6.3	36
222	Mining of unexplored habitats for novel chitinases--chiA as a helper gene proxy in metagenomics. <i>Applied Microbiology and Biotechnology</i> , 2012 , 94, 1347-58	5.7	36
221	Mineralisation of 2,6-dichlorobenzamide (BAM) in dichlobenil-exposed soils and isolation of a BAM-mineralising <i>Aminobacter</i> sp. <i>Environmental Pollution</i> , 2006 , 144, 289-95	9.3	36
220	In vivo detection and quantification of tetracycline by use of a whole-cell biosensor in the rat intestine. <i>Antimicrobial Agents and Chemotherapy</i> , 2004 , 48, 1112-7	5.9	36
219	Use of a whole-cell biosensor and flow cytometry to detect AHL production by an indigenous soil community during decomposition of litter. <i>Microbial Ecology</i> , 2005 , 50, 221-9	4.4	36
218	A meta-proteomics approach to study the interspecies interactions affecting microbial biofilm development in a model community. <i>Scientific Reports</i> , 2017 , 7, 16483	4.9	35
217	Distinct gene expression profile of <i>Xanthomonas retroflexus</i> engaged in synergistic multispecies biofilm formation. <i>ISME Journal</i> , 2017 , 11, 300-303	11.9	35
216	Persistence mechanisms of conjugative plasmids. <i>Methods in Molecular Biology</i> , 2009 , 532, 73-102	1.4	35
215	A flow cytometry-optimized assay using an SOS-green fluorescent protein (SOS-GFP) whole-cell biosensor for the detection of genotoxins in complex environments. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2006 , 603, 164-72	3	35
214	Current strategies for mobilome research. <i>Frontiers in Microbiology</i> , 2014 , 5, 750	5.7	34
213	Rifaximin has minor effects on bacterial composition, inflammation, and bacterial translocation in cirrhosis: A randomized trial. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2018 , 33, 307-314	4	34
212	DPS - a rapid method for genome sequencing of DNA-containing bacteriophages directly from a single plaque. <i>Journal of Virological Methods</i> , 2014 , 196, 152-6	2.6	34
211	The developing hypopharyngeal microbiota in early life. <i>Microbiome</i> , 2016 , 4, 70	16.6	34
210	Monitoring plasmid-mediated horizontal gene transfer in microbiomes: recent advances and future perspectives. <i>Plasmid</i> , 2018 , 99, 56-67	3.3	33
209	The genome sequence of the lactic acid bacterium, <i>Carnobacterium maltaromaticum</i> ATCC 35586 encodes potential virulence factors. <i>International Journal of Food Microbiology</i> , 2012 , 152, 107-15	5.8	33
208	Construction of an extended range whole-cell tetracycline biosensor by use of the tet(M) resistance gene. <i>FEMS Microbiology Letters</i> , 2005 , 253, 201-5	2.9	33

207	Adaptation of the bacterial community to mercury contamination. <i>FEMS Microbiology Letters</i> , 2001 , 204, 49-53	2.9	33
206	Delivery mode and gut microbial changes correlate with an increased risk of childhood asthma. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	33
205	Natural hot spots for gain of multiple resistances: arsenic and antibiotic resistances in heterotrophic, aerobic bacteria from marine hydrothermal vent fields. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 2534-43	4.8	32
204	Sequencing of IncX-plasmids suggests ubiquity of mobile forms of a biofilm-promoting gene cassette recruited from <i>Klebsiella pneumoniae</i> . <i>PLoS ONE</i> , 2012 , 7, e41259	3.7	32
203	An unexpected location of the arginine catabolic mobile element (ACME) in a USA300-related MRSA strain. <i>PLoS ONE</i> , 2011 , 6, e16193	3.7	32
202	Transfer of plasmid RP4 in the spermosphere and rhizosphere of barley seedling. <i>Antonie Van Leeuwenhoek</i> , 1998 , 73, 69-77	2.1	32
201	Biocontrol of Bacterial Wilt Disease Through Complex Interaction Between Tomato Plant, Antagonists, the Indigenous Rhizosphere Microbiota, and. <i>Frontiers in Microbiology</i> , 2019 , 10, 2835	5.7	32
200	A community resource for paired genomic and metabolomic data mining. <i>Nature Chemical Biology</i> , 2021 , 17, 363-368	11.7	32
199	Maize lines with different nitrogen use efficiency select bacterial communities with different β -glucosidase-encoding genes and glucosidase activity in the rhizosphere. <i>Biology and Fertility of Soils</i> , 2015 , 51, 995-1004	6.1	31
198	Microbial Diversity and Putative Opportunistic Pathogens in Dishwasher Biofilm Communities. <i>Applied and Environmental Microbiology</i> , 2018 , 84,	4.8	31
197	Investigation of diversity of plasmids carrying the blaTEM-52 gene. <i>Journal of Antimicrobial Chemotherapy</i> , 2011 , 66, 2465-74	5.1	31
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37	Effects of mercury contamination on the culturable heterotrophic, functional and genetic diversity of the bacterial community in soil		2
36	Detection and quantification of tetracyclines by whole cell biosensors		2
35	Discovery of multiple anti-CRISPRs uncovers anti-defense gene clustering in mobile genetic elements		2
34	The microbiome of captive hamadryas baboons. <i>Animal Microbiome</i> , 2020 , 2, 25	4.1	2
33	Genome Sequence of <i>Kocuria varians</i> G6 Isolated from a Slaughterhouse in Denmark. <i>Genome Announcements</i> , 2016 , 4,		2
32	Microbial community analysis of soils under different soybean cropping regimes in the Argentinean south-eastern Humid Pampas. <i>FEMS Microbiology Ecology</i> , 2021 , 97,	4.3	2
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30	Importance of microbial communities at the root-soil interface for extracellular polymeric substances and soil aggregation in semiarid grasslands. <i>Soil Biology and Biochemistry</i> , 2021 , 159, 108301	7.5	2
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27	Draft Genome Sequences of Two <i>Kocuria</i> Isolates, <i>K. salsicia</i> G1 and <i>K. rhizophila</i> G2, Isolated from a Slaughterhouse in Denmark. <i>Genome Announcements</i> , 2016 , 4,		1
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