

Christoph C Tebbe

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141
papers

4,829
citations

38
h-index

67
g-index

149
ext. papers

5,673
ext. citations

4.4
avg, IF

5.64
L-index

#	Paper	IF	Citations
141	A new approach to utilize PCR-single-strand-conformation polymorphism for 16S rRNA gene-based microbial community analysis. <i>Applied and Environmental Microbiology</i> , 1998 , 64, 4870-6	4.8	551
140	Succession of microbial communities during hot composting as detected by PCR-single-strand-conformation polymorphism-based genetic profiles of small-subunit rRNA genes. <i>Applied and Environmental Microbiology</i> , 2000 , 66, 930-6	4.8	254
139	Field studies on the environmental fate of the Cry1Ab Bt-toxin produced by transgenic maize (MON810) and its effect on bacterial communities in the maize rhizosphere. <i>Molecular Ecology</i> , 2005 , 14, 2539-51	5.7	222
138	Effect of primers hybridizing to different evolutionarily conserved regions of the small-subunit rRNA gene in PCR-based microbial community analyses and genetic profiling. <i>Applied and Environmental Microbiology</i> , 2001 , 67, 3557-63	4.8	217
137	Bacterial diversity of soils assessed by DGGE, T-RFLP and SSCP fingerprints of PCR-amplified 16S rRNA gene fragments: do the different methods provide similar results?. <i>Journal of Microbiological Methods</i> , 2007 , 69, 470-9	2.8	186
136	Diversity and phylotype consistency of bacteria in the guts of three bee species (Apoidea) at an oilseed rape field. <i>Environmental Microbiology</i> , 2006 , 8, 258-72	5.2	183
135	Effect of field inoculation with <i>Sinorhizobium meliloti</i> L33 on the composition of bacterial communities in rhizospheres of a target plant (<i>Medicago sativa</i>) and a non-target plant (<i>Chenopodium album</i>)-linking of 16S rRNA gene-based single-strand conformation polymorphism community profiles to the diversity of cultivated bacteria. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 253-61	4.8	119
134	Degradation of o-xylene and m-xylene by a novel sulfate-reducer belonging to the genus <i>Desulfotomaculum</i> . <i>Archives of Microbiology</i> , 2004 , 181, 407-17	3	115
133	Bacterial diversity in a finished compost and vermicompost: differences revealed by cultivation-independent analyses of PCR-amplified 16S rRNA genes. <i>Applied Microbiology and Biotechnology</i> , 2006 , 71, 942-52	5.7	105
132	Bacterial diversity in maize rhizospheres: conclusions on the use of genetic profiles based on PCR-amplified partial small subunit rRNA genes in ecological studies. <i>Molecular Ecology</i> , 2003 , 12, 251-62	5.7	102
131	Intergeneric transfer of conjugative and mobilizable plasmids harbored by <i>Escherichia coli</i> in the gut of the soil microarthropod <i>Folsomia candida</i> (Collembola). <i>Applied and Environmental Microbiology</i> , 1998 , 64, 2652-9	4.8	102
130	Bacterial community composition in the rhizosphere of a transgenic, herbicide-resistant maize (<i>Zea mays</i>) and comparison to its non-transgenic cultivar Bosphore. <i>FEMS Microbiology Ecology</i> , 2002 , 40, 29-37	4.3	97
129	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , 2016 , 7, 73	5.7	82
128	Importance of rare taxa for bacterial diversity in the rhizosphere of Bt- and conventional maize varieties. <i>ISME Journal</i> , 2013 , 7, 37-49	11.9	81
127	Amphibian gut microbiota shifts differentially in community structure but converges on habitat-specific predicted functions. <i>Nature Communications</i> , 2016 , 7, 13699	17.4	79
126	The gut of the soil microarthropod <i>Folsomia candida</i> (Collembola) is a frequently changeable but selective habitat and a vector for microorganisms. <i>Applied and Environmental Microbiology</i> , 1998 , 64, 2660-9	4.8	78
125	Detection and phylogenetic analysis of <i>Wolbachia</i> in Collembola. <i>Environmental Microbiology</i> , 2004 , 6, 35-44	5.2	74

124	Response of microbial communities to long-term fertilization depends on their microhabitat. <i>FEMS Microbiology Ecology</i> , 2013 , 86, 71-84	4.3	72
123	Liming induces growth of a diverse flora of ammonia-oxidising bacteria in acid spruce forest soil as determined by SSCP and DGGE. <i>Soil Biology and Biochemistry</i> , 2003 , 35, 1337-1347	7.5	72
122	Changes of soil bacterial diversity as a consequence of agricultural land use in a semi-arid ecosystem. <i>PLoS ONE</i> , 2013 , 8, e59497	3.7	72
121	Release of the recombinant Cry3Bb1 protein of Bt maize MON88017 into field soil and detection of effects on the diversity of rhizosphere bacteria. <i>European Journal of Soil Biology</i> , 2010 , 46, 41-48	2.9	67
120	Guidance on allergenicity assessment of genetically modified plants. <i>EFSA Journal</i> , 2017 , 15, e04862	2.3	64
119	Microbial Community Dynamics During Composting of Organic Matter as Determined by 16S Ribosomal DNA Analysis. <i>Compost Science and Utilization</i> , 2002 , 10, 303-312	1.2	60
118	Impact of land-use change and soil organic carbon quality on microbial diversity in soils across Europe. <i>FEMS Microbiology Ecology</i> , 2017 , 93,	4.3	54
117	Origin and diversity of metabolically active gut bacteria from laboratory-bred larvae of <i>Manduca sexta</i> (Sphingidae, Lepidoptera, Insecta). <i>Applied and Environmental Microbiology</i> , 2008 , 74, 7189-96	4.8	54
116	Initial steps in the degradation of phosphinothricin (glufosinate) by soil bacteria. <i>Applied and Environmental Microbiology</i> , 1989 , 55, 711-6	4.8	54
115	Soil particle size fractions harbour distinct microbial communities and differ in potential for microbial mineralisation of organic pollutants. <i>Soil Biology and Biochemistry</i> , 2015 , 90, 255-265	7.5	53
114	Effect of elevated tropospheric ozone on the structure of bacterial communities inhabiting the rhizosphere of herbaceous plants native to Germany. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 7750-8	4.8	49
113	Bacterial Preferences for Specific Soil Particle Size Fractions Revealed by Community Analyses. <i>Frontiers in Microbiology</i> , 2018 , 9, 149	5.7	48
112	Bacterial communities and metabolic activity of faecal cultures from equol producer and non-producer menopausal women under treatment with soy isoflavones. <i>BMC Microbiology</i> , 2017 , 17, 93	4.5	47
111	Gut bacterial communities across tadpole ecomorphs in two diverse tropical anuran faunas. <i>Die Naturwissenschaften</i> , 2016 , 103, 25	2	46
110	In situ microcosms to evaluate natural attenuation potentials in contaminated aquifers. <i>Organic Geochemistry</i> , 2006 , 37, 1394-1410	3.1	46
109	Estimating the effects of Cry1F Bt-maize pollen on non-target Lepidoptera using a mathematical model of exposure. <i>Journal of Applied Ecology</i> , 2012 , 49, 29-37	5.8	45
108	Effects of transgenic corn and Cry1Ab protein on the nematode, <i>Caenorhabditis elegans</i> . <i>Ecotoxicology and Environmental Safety</i> , 2008 , 70, 334-40	7	45
107	Field study results on the probability and risk of a horizontal gene transfer from transgenic herbicide-resistant oilseed rape pollen to gut bacteria of bees. <i>Applied Microbiology and Biotechnology</i> , 2007 , 75, 573-82	5.7	43

106	Microbial community composition affects soil organic carbon turnover in mineral soils. <i>Biology and Fertility of Soils</i> , 2017 , 53, 445-456	6.1	41
105	Interaction of minerals, organic matter, and microorganisms during biogeochemical interface formation as shown by a series of artificial soil experiments. <i>Biology and Fertility of Soils</i> , 2017 , 53, 9-22	6.1	41
104	Diversity of bacteria associated with Collembola - a cultivation-independent survey based on PCR-amplified 16S rRNA genes. <i>FEMS Microbiology Ecology</i> , 2004 , 49, 217-27	4.3	41
103	Utilization of the herbicide phosphinothricin as a nitrogen source by soil bacteria. <i>Applied Microbiology and Biotechnology</i> , 1988 , 29, 103-105	5.7	38
102	Community richness of amphibian skin bacteria correlates with bioclimate at the global scale. <i>Nature Ecology and Evolution</i> , 2019 , 3, 381-389	12.3	37
101	Genetic profiling of noncultivated bacteria from the rhizospheres of sugar beet (<i>Beta vulgaris</i>) reveal field and annual variability but no effect of a transgenic herbicide resistance. <i>Canadian Journal of Microbiology</i> , 2003 , 49, 1-8	3.2	35
100	Importance of soil organic matter for the diversity of microorganisms involved in the degradation of organic pollutants. <i>ISME Journal</i> , 2014 , 8, 1289-300	11.9	34
99	Assessing the risk posed to free-living soil nematodes by a genetically modified maize expressing the insecticidal Cry3Bb1 protein. <i>Science of the Total Environment</i> , 2011 , 409, 2674-84	10.2	34
98	Amphibian skin microbiota exhibits temporal variation in community structure but stability of predicted Bd-inhibitory function. <i>ISME Journal</i> , 2017 , 11, 1521-1534	11.9	33
97	Artificial soil studies reveal domain-specific preferences of microorganisms for the colonisation of different soil minerals and particle size fractions. <i>FEMS Microbiology Ecology</i> , 2014 , 90, 770-82	4.3	31
96	Effect of stacked insecticidal Cry proteins from maize pollen on nurse bees (<i>Apis mellifera carnica</i>) and their gut bacteria. <i>PLoS ONE</i> , 2013 , 8, e59589	3.7	31
95	Increased microbial anabolism contributes to soil carbon sequestration by mineral fertilization in temperate grasslands. <i>Soil Biology and Biochemistry</i> , 2019 , 130, 167-176	7.5	31
94	Assessing environmental impacts of genetically modified plants on non-target organisms: The relevance of in planta studies. <i>Science of the Total Environment</i> , 2017 , 583, 123-132	10.2	30
93	Search of environmental descriptors to explain the variability of the bacterial diversity from maize rhizospheres across a regional scale. <i>European Journal of Soil Biology</i> , 2009 , 45, 383-393	2.9	29
92	Application of PCR-SSCP for molecular epidemiological studies on the exposure of farm children to bacteria in environmental dust. <i>Journal of Microbiological Methods</i> , 2008 , 73, 49-56	2.8	28
91	Earthworms of different functional groups affect the fate of the Bt-toxin Cry1Ab from transgenic maize in soil. <i>European Journal of Soil Biology</i> , 2008 , 44, 283-289	2.9	28
90	Structural differences in the rhizosphere communities of legumes are not equally reflected in community-level physiological profiles. <i>Soil Biology and Biochemistry</i> , 2003 , 35, 1405-1410	7.5	28
89	Fate of the insecticidal Cry1Ab protein of GM crops in two agricultural soils as revealed by ^{14}C -tracer studies. <i>Applied Microbiology and Biotechnology</i> , 2015 , 99, 7333-41	5.7	26

88	Salinity controls soil microbial community structure and function in coastal estuarine wetlands. <i>Environmental Microbiology</i> , 2021 , 23, 1020-1037	5.2	26
87	Cutaneous Bacterial Communities of a Poisonous Salamander: a Perspective from Life Stages, Body Parts and Environmental Conditions. <i>Microbial Ecology</i> , 2017 , 73, 455-465	4.4	24
86	Spatial heterogeneity of dechlorinating bacteria and limiting factors for in situ trichloroethene dechlorination revealed by analyses of sediment cores from a polluted field site. <i>FEMS Microbiology Ecology</i> , 2010 , 71, 444-59	4.3	21
85	Protocol for rapid fluorescence in situ hybridization of bacteria in cryosections of microarthropods. <i>Applied and Environmental Microbiology</i> , 2003 , 69, 2875-8	4.8	21
84	Bacterial community structure in experimental methanogenic bioreactors and search for pathogenic clostridia as community members. <i>Applied Microbiology and Biotechnology</i> , 2011 , 89, 1991-2004	5.7	19
83	Transgenic maize in the presence of ampicillin modifies the metabolic profile and microbial population structure of bovine rumen fluid in vitro. <i>British Journal of Nutrition</i> , 2006 , 96, 820-9	3.6	17
82	Two-dimensional single strand conformation polymorphism (SSCP) of 16S rRNA gene fragments reveals highly dissimilar bacterial communities in an acidic fen. <i>European Journal of Soil Biology</i> , 2008 , 44, 495-500	2.9	16
81	Field lysimeter investigation with luciferase-gene (luc)-tagged <i>Sinorhizobium meliloti</i> strains to evaluate the ecological significance of soil inoculation and a recA-mutation. <i>Soil Biology and Biochemistry</i> , 2000 , 32, 859-868	7.5	16
80	No evidence requiring change in the risk assessment of <i>Inachis io</i> larvae. <i>Ecological Modelling</i> , 2013 , 268, 103-122	3	15
79	Long-term field release of bioluminescent <i>Sinorhizobium meliloti</i> strains to assess the influence of a recA mutation on the strains survival. <i>Microbial Ecology</i> , 2006 , 52, 583-95	4.4	15
78	Fate of plasmid-bearing, luciferase marker gene tagged bacteria after feeding to the soil microarthropod <i>Onychiurus fimatus</i> (Collembola). <i>FEMS Microbiology Ecology</i> , 1999 , 30, 125-135	4.3	15
77	Taxon-specific fungal preference for distinct soil particle size fractions. <i>European Journal of Soil Biology</i> , 2019 , 94, 103103	2.9	14
76	Diversity responses of rumen microbial communities to <i>Fusarium</i> -contaminated feed, evaluated with rumen simulating technology. <i>Environmental Microbiology</i> , 2008 , 10, 483-96	5.2	14
75	Importance of soil texture to the fate of pathogens introduced by irrigation with treated wastewater. <i>Science of the Total Environment</i> , 2019 , 653, 886-896	10.2	14
74	Effects of concentrate proportion in the diet with or without <i>Fusarium</i> toxin-contaminated triticale on ruminal fermentation and the structural diversity of rumen microbial communities in vitro. <i>Archives of Animal Nutrition</i> , 2010 , 64, 467-83	2.7	13
73	Genetic profiling of bacterial communities from the rhizospheres of ozone damaged <i>Malva sylvestris</i> (Malvaceae). <i>European Journal of Soil Biology</i> , 2006 , 42, 191-199	2.9	13
72	Contrasting microbial community responses to salinization and straw amendment in a semiarid bare soil and its wheat rhizosphere. <i>Scientific Reports</i> , 2019 , 9, 9795	4.9	12
71	Varied responses in gene expression of culturable heterotrophic bacteria isolated from the environment. <i>Applied Microbiology and Biotechnology</i> , 1992 , 37, 818	5.7	12

70	Leaf-feeding larvae of <i>Manduca sexta</i> (Insecta, Lepidoptera) drastically reduce copy numbers of <i>aadA</i> antibiotic resistance genes from transplastomic tobacco but maintain intact <i>aadA</i> genes in their feces. <i>Environmental Biosafety Research</i> , 2007 , 6, 121-33		12
69	Technical Note on the quality of DNA sequencing for the molecular characterisation of genetically modified plants. <i>EFSA Journal</i> , 2018 , 16, e05345	2.3	11
68	Profiling the diversity of microbial communities with single-strand conformation polymorphism (SSCP). <i>Methods in Molecular Biology</i> , 2014 , 1096, 71-83	1.4	10
67	Temporary immersion bioreactors (TIB) provide a versatile, cost-effective and reproducible in vitro analysis of the response of pineapple shoots to salinity and drought. <i>Acta Physiologiae Plantarum</i> , 2017 , 39, 1	2.6	10
66	Soil texture and properties rather than irrigation water type shape the diversity and composition of soil microbial communities. <i>Applied Soil Ecology</i> , 2021 , 161, 103834	5	10
65	Clostridium cluster I and their pathogenic members in a full-scale operating biogas plant. <i>Applied Microbiology and Biotechnology</i> , 2015 , 99, 3585-98	5.7	9
64	Culture-Independent Analysis of Linuron-Mineralizing Microbiota and Functions in on-Farm Biopurification Systems via DNA-Stable Isotope Probing: Comparison with Enrichment Culture. <i>Environmental Science & Technology</i> , 2020 , 54, 9387-9397	10.3	9
63	Safety and efficacy of vitamin B (in the form of cyanocobalamin) produced by spp. as a feed additive for all animal species based on a dossier submitted by VITAC EEIG. <i>EFSA Journal</i> , 2018 , 16, e05336	3.3	9
62	Composition and variation of the skin microbiota in sympatric species of European newts (Salamandridae). <i>Amphibia - Reptilia</i> , 2015 , 36, 5-12	1.2	8
61	Fate of three genetically engineered, biotechnologically important microorganism species in soil: impact of soil properties and intraspecies competition with nonengineered strains. <i>Canadian Journal of Microbiology</i> , 1997 , 43, 827-834	3.2	8
60	Description of the structural diversity of rumen microbial communities in vitro using single-strand conformation polymorphism profiles. <i>Archives of Animal Nutrition</i> , 2008 , 62, 454-67	2.7	8
59	Resilience of a soil-established, genetically modified <i>Sinorhizobium meliloti</i> inoculant to soil management practices. <i>Applied Soil Ecology</i> , 2004 , 25, 161-167	5	8
58	Hidden heterogeneity and co-occurrence networks of soil prokaryotic communities revealed at the scale of individual soil aggregates. <i>MicrobiologyOpen</i> , 2021 , 10, e1144	3.4	8
57	Safety and efficacy of vitamin B (riboflavin) produced by ????? for all animal species based on a dossier submitted by BASF SE. <i>EFSA Journal</i> , 2018 , 16, e05337	2.3	7
56	Assessment of genetically modified maize MON87411 for food and feed uses, import and processing, under Regulation (EC) No 1829/2003 (application EFSA-GMO-NL-2015-124). <i>EFSA Journal</i> , 2018 , 16, e05310	2.3	7
55	Scientific Opinion on application EFSA-GMO-BE-2013-118 for authorisation of genetically modified maize MON87427/MON89034/507/MON88017/59122 and subcombinations independently of their origin, for food and feed uses, import and processing submitted under Regulation (EC) No 1829/2003 by Monsanto Company. <i>EFSA Journal</i> , 2017 , 15, e04921	2.3	7
54	Detection of monochlorobenzene metabolizing bacteria under anoxic conditions by DNA-stable isotope probing. <i>Biodegradation</i> , 2011 , 22, 973-82	4.1	7
53	Collembola as a Habitat for Microorganisms 2006 , 133-153		7

52	The third vegetative generation of a field-grown transgenic pineapple clone shows minor side effects of transformation on plant physiological parameters. <i>Plant Cell, Tissue and Organ Culture</i> , 2016 , 125, 303-308	2.7	7
51	Impact of common sample pre-treatments on key soil microbial properties. <i>Soil Biology and Biochemistry</i> , 2021 , 160, 108321	7.5	7
50	Inter-laboratory testing of the effect of DNA blocking reagent G2 on DNA extraction from low-biomass clay samples. <i>Scientific Reports</i> , 2018 , 8, 5711	4.9	6
49	The responses of soil nematode communities to Bt maize cultivation at four field sites across Europe. <i>Soil Biology and Biochemistry</i> , 2018 , 119, 194-202	7.5	6
48	Soil properties and habitats determine the response of bacterial communities to agricultural wastewater irrigation. <i>Pedosphere</i> , 2020 , 30, 146-158	5	6
47	Scientific Opinion on application EFSA-GMO-BE-2013-117 for authorisation of genetically modified maize MON87427/MON89034/NK603 and subcombinations independently of their origin, for food and feed uses, import and processing submitted under Regulation (EC) No 1829/2003 by Monsanto Company. <i>EFSA Journal</i> , 2017 , 15, e04822	2.3	5
46	Risk assessment of the cultivation of a stacked Bt-maize variety (MON89034/MON88017) for nematode communities. <i>Soil Biology and Biochemistry</i> , 2015 , 91, 109-118	7.5	5
45	Scientific Opinion on an application by Dow AgroSciences (EFSA-GMO-NL-2013-116) for placing on the market of genetically modified insect-resistant soybean DAS-81419-2 for food and feed uses, import and processing under Regulation (EC) No 1829/2003. <i>EFSA Journal</i> , 2016 , 14, e04642	2.3	4
44	Euclidean distance can identify the mannitol level that produces the most remarkable integral effect on sugarcane micropropagation in temporary immersion bioreactors. <i>Journal of Plant Research</i> , 2018 , 131, 719-724	2.6	4
43	Annual post-market environmental monitoring (PMEM) report on the cultivation of genetically modified maize MON810 in 2015 from Monsanto Europe S.A. <i>EFSA Journal</i> , 2017 , 15, e04805	2.3	4
42	Response to "The anglerfish deception". <i>EMBO Reports</i> , 2012 , 13, 481-2; author reply 482-3	6.5	4
41	Differences in the rhizosphere bacterial community of a transplastomic tobacco plant compared to its non-engineered counterpart. <i>Environmental Biosafety Research</i> , 2007 , 6, 113-9		4
40	No Tangible Effects of Field-Grown Cisgenic Potatoes on Soil Microbial Communities. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 603145	5.8	4
39	Response to Kruse-Plass et al. (2017) regarding the risk to non-target lepidopteran larvae exposed to pollen from one or more of three Bt maize events (MON810, Bt11 and 1507). <i>Environmental Sciences Europe</i> , 2017 , 29, 21	5	3
38	Mineral composition of a transgenic pineapple clone grown in the field for 8 yr. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2017 , 53, 489-493	2.3	3
37	Assessment of genetically modified maize MON87403 for food and feed uses, import and processing, under Regulation (EC) No 1829/2003 (application EFSA-GMO-BE-2015-125). <i>EFSA Journal</i> , 2018 , 16, e05225	2.3	3
36	Response of the rhizosphere prokaryotic community of barley (<i>Hordeum vulgare</i> L.) to elevated atmospheric CO concentration in open-top chambers. <i>MicrobiologyOpen</i> , 2017 , 6, e00462	3.4	3
35	Disentangling the impact of contrasting agricultural management practices on soil microbial communities Importance of rare bacterial community members. <i>Soil Biology and Biochemistry</i> , 2022 , 166, 108573	7.5	3

34	Reconstructing Genomes of Carbon Monoxide Oxidisers in Volcanic Deposits Including Members of the Class Ktedonobacteria. <i>Microorganisms</i> , 2020 , 8,	4.9	3
33	Annual replication is essential in evaluating the response of the soil microbiome to the genetic modification of maize in different biogeographical regions. <i>PLoS ONE</i> , 2019 , 14, e0222737	3.7	3
32	Assessment of genetically modified maize Bt11×MIR162×507×GA21 and three subcombinations independently of their origin, for food and feed uses under Regulation (EC) No 1829/2003 (application EFSA-GMO-DE-2010-86). <i>EFSA Journal</i> , 2018 , 16, e05309	2.3	3
31	Guidance for the risk assessment of the presence at low level of genetically modified plant material in imported food and feed under Regulation (EC) No 1829/2003. <i>EFSA Journal</i> , 2017 , 15, e05048	2.3	2
30	Assessment of genetically modified cotton GHB614×304-40×GHB119 for food and feed uses, import and processing under Regulation (EC) No 1829/2003 (application EFSA-GMO-NL-2014-122). <i>EFSA Journal</i> , 2018 , 16, e05349	2.3	2
29	Carotenoids in roots indicated the level of stress induced by mannitol and sodium azide treatment during the early stages of maize germination. <i>Acta Physiologiae Plantarum</i> , 2018 , 40, 1	2.6	2
28	Scientific opinion on application EFSA-GMO-NL-2013-120 for authorisation of genetically modified soybean FG72 ×A5547-127 for food and feed uses, import and processing submitted in accordance with Regulation (EC) No 1829/2003 by Bayer CropScience LP and M.S. Technologies LLC. <i>EFSA Journal</i> , 2017 , 15, e04744	2.3	2
27	Assessment of genetically modified maize 1507×B9122×MON810×NK603 and subcombinations, for food and feed uses, under Regulation (EC) No 1829/2003 (application EFSA-GMO-NL-2011-92). <i>EFSA Journal</i> , 2017 , 15, e05000	2.3	2
26	Production of the 14C-labeled insecticidal protein Cry1Ab for soil metabolic studies using a recombinant Escherichia coli in small-scale batch fermentations. <i>Applied Microbiology and Biotechnology</i> , 2012 , 96, 221-9	5.7	2
25	Freisetzung gentechnisch veränderter Bakterien: Leuchtmarkierte Zellen von Sinorhizobium melilotii im Boden. <i>Biologie in Unserer Zeit</i> , 2003 , 33, 162-175	0.1	2
24	Risk assessment of new sequencing information on GM maize event DAS-59122-7. <i>EFSA Journal</i> , 2016 , 14, e04639	2.3	2
23	Assessment of genetically modified maize 4114 for food and feed uses, under Regulation (EC) No 1829/2003 (application EFSA-GMO-NL-2014-123). <i>EFSA Journal</i> , 2018 , 16, e05280	2.3	2
22	Risk assessment of information on the subcombination Bt11×MIR162, related to the application of Syngenta (EFSA-GMO-DE-2009-66) for authorisation of food and feed containing, consisting and produced from genetically modified maize Bt11×MIR162×MIR604×GA21. <i>EFSA Journal</i> , 2017 , 15, e04745	2.3	1
21	Scientific Opinion on an application by Dow AgroSciences LLC (EFSA-GMO-NL-2011-91) for the placing on the market of genetically modified herbicide-tolerant soybean DAS-68416-4 for food and feed uses, import and processing under Regulation (EC) No 1829/2003. <i>EFSA Journal</i> , 2017 , 15, e04719	2.3	1
20	Assessment of genetically modified oilseed rape MS8, RF3 and MS8×RF3 for renewal of authorisation under regulation (EC) No 1829/2003 (application EFSA-GMO-RX-004). <i>EFSA Journal</i> , 2017 , 15, e05067	2.3	1
19	Scientific Opinion on application EFSA-GMO-NL-2013-119 for authorisation of genetically modified glufosinate-ammonium- and glyphosate-tolerant oilseed rape MON88302×MS8×RF3 and subcombinations independently of their origin, for food and feed uses, import and processing submitted in accordance with Regulation (EC) No 1829/2003 by Monsanto Company and Bayer CropScience. <i>EFSA Journal</i> , 2017 , 15, e04767	2.3	1
18	Microbial Community Profiling: SSCP and T-RFLP Techniques. <i>Springer Protocols</i> , 2015 , 101-126	0.3	1
17	Marker Genes As Tools To Study Deliberately Released Soil Bacteria 2006 , 421-447		1

16	Hidden heterogeneity and co-occurrence networks of soil prokaryotic communities revealed at the scale of individual soil aggregates		1
15	Scientific Opinion on an application by DOW AgroSciences LLC (EFSA-GMO-NL-2010-89) for placing on the market the genetically modified herbicide-tolerant maize DAS-40278-9 for food and feed uses, import and processing under Regulation (EC) No 1829/2003. <i>EFSA Journal</i> , 2016 , 14, e04633	2.3	1
14	Prokaryotic community assembly after 40 years of soda solonetz restoration by natural grassland and reclaimed farmland. <i>European Journal of Soil Biology</i> , 2020 , 100, 103213	2.9	1
13	Statement complementing the EFSA Scientific Opinion on application (EFSA-GMO-DE-2011-95) for the placing on the market of genetically modified maize 5307 for food and feed uses, import and processing under Regulation (EC) No 1829/2003 from Syngenta Crop Protection AG taking into consideration an additional toxicological study. <i>EFSA Journal</i> , 2018 , 16, e05233	2.3	1
12	Assessment of genetically modified soybean MON87751 for food and feed uses under Regulation (EC) No 1829/2003 (application EFSA-GMO-NL-2014-121). <i>EFSA Journal</i> , 2018 , 16, e05346	2.3	1
11	Assessment of genetically modified cotton GHB614/LLCotton25/MON5985 for food and feed uses, under Regulation (EC) No 1829/2003 (application EFSA-GMO-NL-2011-94). <i>EFSA Journal</i> , 2018 , 16, e05213	2.3	1
10	9. Artificial Soils as Tools for Microbial Ecology 2017 , 159-180		0
9	Scientific opinion on an application by Monsanto (EFSA-GMO-NL-2013-114) for the placing on the market of a herbicide-tolerant genetically modified cotton MON88701 for food and feed uses, import and processing under Regulation (EC) No 1829/2003. <i>EFSA Journal</i> , 2017 , 15, e04746	2.3	
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1	Annual replication is essential in evaluating the response of the soil microbiome to the genetic modification of maize in different biogeographical regions 2019 , 14, e0222737		