

Andreas Brune

List of Publications by Year in descending order

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Version: 2024-02-01

160
papers

12,128
citations

20759

60
h-index

31759

101
g-index

180
all docs

180
docs citations

180
times ranked

8792
citing authors

#	ARTICLE	IF	CITATIONS
1	Symbiotic digestion of lignocellulose in termite guts. <i>Nature Reviews Microbiology</i> , 2014, 12, 168-180.	13.6	680
2	Role of Microorganisms in the Digestion of Lignocellulose by Termites. <i>Annual Review of Entomology</i> , 1994, 39, 453-487.	5.7	577
3	â€œMethanoplasmatales,â€-Thermoplasmatales-Related Archaea in Termite Guts and Other Environments, Are the Seventh Order of Methanogens. <i>Applied and Environmental Microbiology</i> , 2012, 78, 8245-8253.	1.4	331
4	Life at the oxicâ€“anoxic interface: microbial activities and adaptations. <i>FEMS Microbiology Reviews</i> , 2000, 24, 691-710.	3.9	322
5	Electron shuttling via humic acids in microbial iron(III) reduction in a freshwater sediment. <i>FEMS Microbiology Ecology</i> , 2004, 47, 85-92.	1.3	313
6	The Gut Microbiota of Termites: Digesting the Diversity in the Light of Ecology and Evolution. <i>Annual Review of Microbiology</i> , 2015, 69, 145-166.	2.9	312
7	New Mode of Energy Metabolism in the Seventh Order of Methanogens as Revealed by Comparative Genome Analysis of â€œCandidatus Methanoplasma termitumâ€-. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1338-1352.	1.4	235
8	Anaerobic and aerobic oxidation of ferrous iron at neutral pH by chemoheterotrophic nitrate-reducing bacteria. <i>Archives of Microbiology</i> , 1998, 169, 159-165.	1.0	234
9	The Cockroach Origin of the Termite Gut Microbiota: Patterns in Bacterial Community Structure Reflect Major Evolutionary Events. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2261-2269.	1.4	229
10	Termite guts: the world's smallest bioreactors. <i>Trends in Biotechnology</i> , 1998, 16, 16-21.	4.9	217
11	Microecology of the termite gut: structure and function on a microscale. <i>Current Opinion in Microbiology</i> , 2000, 3, 263-269.	2.3	208
12	Humic Acid Reduction by <i>Propionibacterium freudenreichii</i> and Other Fermenting Bacteria. <i>Applied and Environmental Microbiology</i> , 1998, 64, 4507-4512.	1.4	204
13	High-Resolution Analysis of Gut Environment and Bacterial Microbiota Reveals Functional Compartmentation of the Gut in Wood-Feeding Higher Termites (<i>Nasutitermes</i> spp.). <i>Applied and Environmental Microbiology</i> , 2012, 78, 4691-4701.	1.4	192
14	Microbial Community Structure in Midgut and Hindgut of the Humus-Feeding Larva of <i>Pachnoda ephippiata</i> (Coleoptera: Scarabaeidae). <i>Applied and Environmental Microbiology</i> , 2003, 69, 6659-6668.	1.4	186
15	The Ultramicrobacterium â€œ <i>Elusimicrobium minutum</i> â€-gen. nov., sp. nov., the First Cultivated Representative of the Termite Group 1 Phylum. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2831-2840.	1.4	162
16	Soilâ€“carbon preservation through habitat constraints and biological limitations on decomposer activity. <i>Journal of Plant Nutrition and Soil Science</i> , 2008, 171, 27-35.	1.1	156
17	Identifying the core microbial community in the gut of fungusâ€“growing termites. <i>Molecular Ecology</i> , 2014, 23, 4631-4644.	2.0	151
18	The Bacterial Community in the Gut of the Cockroach <i>Shelfordella lateralis</i> Reflects the Close Evolutionary Relatedness of Cockroaches and Termites. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2758-2767.	1.4	150

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19	Physicochemical Conditions and Microbial Activities in the Highly Alkaline Gut of the Humus-Feeding Larva of <i>Pachnoda ephippiata</i> (Coleoptera: Scarabaeidae). <i>Applied and Environmental Microbiology</i> , 2003, 69, 6650-6658.	1.4	145
20	Diet is the primary determinant of bacterial community structure in the guts of higher termites. <i>Molecular Ecology</i> , 2015, 24, 5284-5295.	2.0	143
21	pH profiles of the extremely alkaline hindguts of soil-feeding termites (Isoptera: Termitidae) determined with microelectrodes. <i>Journal of Insect Physiology</i> , 1996, 42, 1121-1127.	0.9	141
22	“Endomicrobia”: Cytoplasmic Symbionts of Termite Gut Protozoa Form a Separate Phylum of Prokaryotes. <i>Applied and Environmental Microbiology</i> , 2005, 71, 1473-1479.	1.4	140
23	Phylogenetic Diversity, Abundance, and Axial Distribution of Bacteria in the Intestinal Tract of Two Soil-Feeding Termites (<i>Cubitermes</i> spp.). <i>Applied and Environmental Microbiology</i> , 2003, 69, 6007-6017.	1.4	136
24	Life at the oxic-anoxic interface: microbial activities and adaptations. <i>FEMS Microbiology Reviews</i> , 2000, 24, 691-710.	3.9	134
25	Niche heterogeneity determines bacterial community structure in the termite gut (<i>Reticulitermes</i>) Tj ETQq1 1 0.784314 rgBT /Overload	1.8	127
26	<i>Endomicrobium proavitum</i> , the first isolate of <i>Endomicrobia</i> class. nov. (phylum <i>Endomicrobia</i>) “an ultramicrobacterium with an unusual cell cycle that fixes nitrogen with a <i>Group IV</i> nitrogenase. <i>Environmental Microbiology</i> , 2016, 18, 191-204.	1.8	125
27	Cospeciation of termite gut flagellates and their bacterial endosymbionts: <i>Trichonympha</i> species and <i>Candidatus Endomicrobium trichonymphae</i> ™. <i>Molecular Ecology</i> , 2009, 18, 332-342.	2.0	116
28	Axial Differences in Community Structure of Crenarchaeota and Euryarchaeota in the Highly Compartmentalized Gut of the Soil-Feeding Termite <i>Cubitermes orthognathus</i> . <i>Applied and Environmental Microbiology</i> , 2001, 67, 4880-4890.	1.4	114
29	The bacterial microbiota in the ceca of Capercaillie (<i>Tetrao urogallus</i>) differs between wild and captive birds. <i>Systematic and Applied Microbiology</i> , 2011, 34, 542-551.	1.2	106
30	Characterization of abundance and diversity of lactic acid bacteria in the hindgut of wood- and soil-feeding termites by molecular and culture-dependent techniques. <i>Archives of Microbiology</i> , 2000, 173, 126-137.	1.0	105
31	Structure and Topology of Microbial Communities in the Major Gut Compartments of <i>Melolontha melolontha</i> Larvae (Coleoptera: Scarabaeidae). <i>Applied and Environmental Microbiology</i> , 2005, 71, 4556-4566.	1.4	104
32	The gut microflora of <i>Reticulitermes flavipes</i> , its relation to oxygen, and evidence for oxygen-dependent acetogenesis by the most abundant <i>Enterococcus</i> sp.. <i>FEMS Microbiology Ecology</i> , 2006, 24, 137-149.	1.3	103
33	“ <i>Candidatus Arthromitus</i> ” revised: segmented filamentous bacteria in arthropod guts are members of <i>Lachnospiraceae</i> . <i>Environmental Microbiology</i> , 2012, 14, 1454-1465.	1.8	101
34	Rampant Host Switching Shaped the Termite Gut Microbiome. <i>Current Biology</i> , 2018, 28, 649-654.e2.	1.8	101
35	Hydrogen is the central free intermediate during lignocellulose degradation by termite gut symbionts. <i>ISME Journal</i> , 2007, 1, 551-565.	4.4	100
36	Ferrous iron oxidation by denitrifying bacteria in profundal sediments of a deep lake (Lake Constance). <i>FEMS Microbiology Ecology</i> , 2001, 37, 127-134.	1.3	98

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37	Biogeography of pelagic bacterioplankton across an antagonistic temperature-salinity gradient in the Red Sea. <i>Molecular Ecology</i> , 2012, 21, 388-405.	2.0	98
38	Genomic Analysis of <i>Elusimicrobium minutum</i> , the First Cultivated Representative of the Phylum Elusimicrobia (Formerly Termite Group 1). <i>Applied and Environmental Microbiology</i> , 2009, 75, 2841-2849.	1.4	95
39	Pyrogallol-to-phloroglucinol conversion and other hydroxyl-transfer reactions catalyzed by cell extracts of <i>Pelobacter acidigallici</i> . <i>Journal of Bacteriology</i> , 1990, 172, 1070-1076.	1.0	93
40	Hydrogen Profiles and Localization of Methanogenic Activities in the Highly Compartmentalized Hindgut of Soil-Feeding Higher Termites (<i>Cubitermes</i> spp.). <i>Applied and Environmental Microbiology</i> , 1999, 65, 4490-4496.	1.4	91
41	Fiber-associated spirochetes are major agents of hemicellulose degradation in the hindgut of wood-feeding higher termites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11996-E12004.	3.3	90
42	Phloroglucinol pathway in the strictly anaerobic <i>Pelobacter acidigallici</i> : fermentation of trihydroxybenzenes to acetate via triacetic acid. <i>Archives of Microbiology</i> , 1992, 157, 417-424.	1.0	88
43	Strict cospeciation of devescovineid flagellates and Bacteroidales ectosymbionts in the gut of dry-wood termites (<i>Kalotermitidae</i>). <i>Environmental Microbiology</i> , 2010, 12, 2120-2132.	1.8	88
44	Classifying the bacterial gut microbiota of termites and cockroaches: A curated phylogenetic reference database (DictDb). <i>Systematic and Applied Microbiology</i> , 2015, 38, 472-482.	1.2	87
45	pmoA-Based Analysis of Methanotrophs in a Littoral Lake Sediment Reveals a Diverse and Stable Community in a Dynamic Environment. <i>Applied and Environmental Microbiology</i> , 2004, 70, 3138-3142.	1.4	85
46	Cartwheel Architecture of <i>Trichonympha</i> Basal Body. <i>Science</i> , 2012, 337, 553-553.	6.0	84
47	Bacteroidales ectosymbionts of gut flagellates shape the nitrogen-fixing community in dry-wood termites. <i>ISME Journal</i> , 2012, 6, 1302-1313.	4.4	83
48	Impact of oxygen on metabolic fluxes and in situ rates of reductive acetogenesis in the hindgut of the wood-feeding termite <i>Reticulitermes flavipes</i> . <i>Environmental Microbiology</i> , 2000, 2, 436-449.	1.8	82
49	Axial Dynamics, Stability, and Interspecies Similarity of Bacterial Community Structure in the Highly Compartmentalized Gut of Soil-Feeding Termites (<i>Cubitermes</i> spp.). <i>Applied and Environmental Microbiology</i> , 2003, 69, 6018-6024.	1.4	81
50	<i>Candidatus Hepatoplasma crinochetorum</i> , a New, Stalk-Forming Lineage of Mollicutes Colonizing the Midgut Glands of a Terrestrial Isopod. <i>Applied and Environmental Microbiology</i> , 2004, 70, 6166-6172.	1.4	81
51	Differential enumeration and in situ localization of microorganisms in the hindgut of the lower termite <i>Mastotermes darwiniensis</i> by hybridization with rRNA-targeted probes. <i>Archives of Microbiology</i> , 1999, 172, 407-416.	1.0	80
52	Expression profiles of <i>fhs</i> (FTHFS) genes support the hypothesis that spirochaetes dominate reductive acetogenesis in the hindgut of lower termites. <i>Environmental Microbiology</i> , 2006, 8, 1261-1270.	1.8	77
53	Influence of gut alkalinity and oxygen status on mobilization and size-class distribution of humic acids in the hindgut of soil-feeding termites. <i>Applied Soil Ecology</i> , 1999, 13, 219-229.	2.1	76
54	Phylogenetic diversity of Endomicrobia and their specific affiliation with termite gut flagellates. <i>Microbiology (United Kingdom)</i> , 2007, 153, 3458-3465.	0.7	75

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55	Localization and In Situ Activities of Homoacetogenic Bacteria in the Highly Compartmentalized Hindgut of Soil-Feeding Higher Termites (<i>Cubitermes</i> spp.). <i>Applied and Environmental Microbiology</i> , 1999, 65, 4497-4505.	1.4	74
56	Transformation and mineralization of synthetic ¹⁴ C-labeled humic model compounds by soil-feeding termites. <i>Soil Biology and Biochemistry</i> , 2000, 32, 1281-1291.	4.2	73
57	Bacterial symbionts in the hepatopancreas of isopods: diversity and environmental transmission. <i>FEMS Microbiology Ecology</i> , 2007, 61, 141-152.	1.3	72
58	Selective digestion of the proteinaceous component of humic substances by the geophagous earthworms <i>Metaphire guillelmi</i> and <i>Amyntas corrugatus</i> . <i>Soil Biology and Biochemistry</i> , 2010, 42, 1455-1462.	4.2	70
59	Hydrogen-Dependent Oxygen Reduction by Homoacetogenic Bacteria Isolated from Termite Guts. <i>Applied and Environmental Microbiology</i> , 2003, 69, 779-786.	1.4	69
60	Metagenomic analysis of the microbiota in the highly compartmented hindguts of six wood- or soil-feeding higher termites. <i>Microbiome</i> , 2015, 3, 56.	4.9	65
61	? <i>Candidatus Hepatincola porcellionum</i> ? gen. nov., sp. nov., a new, stalk-forming lineage of Rickettsiales colonizing the midgut glands of a terrestrial isopod. <i>Archives of Microbiology</i> , 2004, 181, 299-304.	1.0	64
62	Digestion of peptidic residues in humic substances by an alkali-stable and humic-acid-tolerant proteolytic activity in the gut of soil-feeding termites. <i>Soil Biology and Biochemistry</i> , 2005, 37, 1648-1655.	4.2	63
63	Novel lineages of <i>Planctomycetes</i> densely colonize the alkaline gut of soil-feeding termites (<i>Cubitermes</i> spp.). <i>Environmental Microbiology</i> , 2008, 10, 1260-1270.	1.8	63
64	Pyrotag Sequencing of the Gut Microbiota of the Cockroach <i>Shelfordella lateralis</i> Reveals a Highly Dynamic Core but Only Limited Effects of Diet on Community Structure. <i>PLoS ONE</i> , 2014, 9, e85861.	1.1	63
65	Identification and localization of the multiple bacterial symbionts of the termite gut flagellate <i>Joenia annectens</i> . <i>Microbiology (United Kingdom)</i> , 2010, 156, 2068-2079.	0.7	61
66	Symbionts of the gut flagellate <i>Staurojoenia</i> sp. from <i>Neotermes cubanus</i> represent a novel, termite-associated lineage of Bacteroidales: description of <i>Candidatus Vestibaculum illigatum</i> ™. <i>Microbiology (United Kingdom)</i> , 2004, 150, 2229-2235.	0.7	60
67	Nitrogen Mineralization, Ammonia Accumulation, and Emission of Gaseous NH ₃ by Soil-feeding Termites. <i>Biogeochemistry</i> , 2006, 78, 267-283.	1.7	60
68	Deterministic Assembly of Complex Bacterial Communities in Guts of Germ-Free Cockroaches. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1256-1263.	1.4	59
69	Microenvironmental heterogeneity of gut compartments drives bacterial community structure in wood- and humus-feeding higher termites. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiv210.	1.3	59
70	Transformation and mineralization of ¹⁴ C-labeled cellulose, peptidoglycan, and protein by the soil-feeding termite <i>Cubitermes orthognathus</i> . <i>Biology and Fertility of Soils</i> , 2001, 33, 166-174.	2.3	58
71	Prokaryotic Symbionts of Termite Gut Flagellates: Phylogenetic and Metabolic Implications of a Tripartite Symbiosis. , 2006, 41, 39-60.		58
72	Preferential cultivation of type II methanotrophic bacteria from littoral sediments (Lake Constance). <i>FEMS Microbiology Ecology</i> , 2004, 47, 179-189.	1.3	57

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73	Nest specificity of the bacterial community in termite guts (<i>Hodotermes mossambicus</i>). <i>Insectes Sociaux</i> , 2006, 53, 339-344.	0.7	57
74	The fibre-associated cellulolytic bacterial community in the hindgut of wood-feeding higher termites (<i>Nasutitermes</i> spp.). <i>Environmental Microbiology</i> , 2014, 16, 2711-2722.	1.8	57
75	A strictly anaerobic nitrate-reducing bacterium growing with resorcinol and other aromatic compounds. <i>Archives of Microbiology</i> , 1992, 158, 48-53.	1.0	54
76	<i>Sporomusa aerivorans</i> sp. nov., an oxygen-reducing homoacetogenic bacterium from the gut of a soil-feeding termite. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 1397-1404.	0.8	54
77	Simultaneous methanogenesis and oxygen reduction by <i>Methanobrevibacter cuticularis</i> at low oxygen fluxes. <i>FEMS Microbiology Ecology</i> , 2007, 62, 303-312.	1.3	54
78	Symbiotic Associations Between Termites and Prokaryotes. , 2006, , 439-474.		53
79	Role of the Termite Gut Microbiota in Symbiotic Digestion. , 2010, , 439-475.		52
80	Inter- and intraspecific comparison of the bacterial assemblages in the hindgut of humivorous scarab beetle larvae (<i>Pachnoda</i> spp.). <i>FEMS Microbiology Ecology</i> , 2010, 74, 439-449.	1.3	51
81	Physicochemical conditions, metabolites and community structure of the bacterial microbiota in the gut of wood-feeding cockroaches (<i>Blaberidae</i> : <i>Panesthiinae</i>). <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-14.	1.3	50
82	<i>Candidatus</i> <i>Adiutrix intracellularis</i> TM , an endosymbiont of termite gut flagellates, is the first representative of a deep-branching clade of <i>Deltaproteobacteria</i> and a putative homoacetogen. <i>Environmental Microbiology</i> , 2016, 18, 2548-2564.	1.8	50
83	The hydrogen threshold of obligately methyl-reducing methanogens. <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	49
84	Dynamics of redox potential and changes in redox state of iron and humic acids during gut passage in soil-feeding termites (<i>Cubitermes</i> spp.). <i>Soil Biology and Biochemistry</i> , 2002, 34, 221-227.	4.2	46
85	The Termite Group I Phylum Is Highly Diverse and Widespread in the Environment. <i>Applied and Environmental Microbiology</i> , 2007, 73, 6682-6685.	1.4	46
86	Nitrate reduction, nitrous oxide formation, and anaerobic ammonia oxidation to nitrite in the gut of soil-feeding termites (<i>Cubitermes</i> and <i>Ophiotermes</i> spp.). <i>Environmental Microbiology</i> , 2012, 14, 860-871.	1.8	45
87	<i>Breznakia blatticola</i> gen. nov. sp. nov. and <i>Breznakia pachnodae</i> sp. nov., two fermenting bacteria isolated from insect guts, and emended description of the family <i>Erysipelotrichaceae</i> . <i>Systematic and Applied Microbiology</i> , 2016, 39, 319-329.	1.2	45
88	<i>Candidatus</i> <i>Ancillula trichonymphae</i> TM , a novel lineage of endosymbiotic <i>Actinobacteria</i> in termite gut flagellates of the genus <i>Trichonympha</i> . <i>Environmental Microbiology</i> , 2012, 14, 3259-3270.	1.8	43
89	Immune-modulating gut symbionts are not <i>Candidatus</i> <i>Arthromitus</i> . <i>Mucosal Immunology</i> , 2013, 6, 200-201.	2.7	43
90	Phylogenomic analysis of 589 metagenome-assembled genomes encompassing all major prokaryotic lineages from the gut of higher termites. <i>PeerJ</i> , 2020, 8, e8614.	0.9	43

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91	Degradation of hydroxyhydroquinone by the strictly anaerobic fermenting bacterium <i>Pelobacter massiliensis</i> sp. nov.. <i>Archives of Microbiology</i> , 1991, 155, 511-516.	1.0	42
92	<i>Propionivibrio limicola</i> sp. nov., a fermentative bacterium specialized in the degradation of hydroaromatic compounds, reclassification of <i>Propionibacter pelophilus</i> as <i>Propionivibrio pelophilus</i> comb. nov. and amended description of the genus <i>Propionivibrio</i> .. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 441-444.	0.8	42
93	Phylogenetic Diversity and Whole-Cell Hybridization of Oxymonad Flagellates from the Hindgut of the Wood-Feeding Lower Termite <i>Reticulitermes flavipes</i> . <i>Protist</i> , 2003, 154, 147-155.	0.6	42
94	Oxygen Affects Gut Bacterial Colonization and Metabolic Activities in a Gnotobiotic Cockroach Model. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1080-1089.	1.4	42
95	Diversity, Structure, and Evolution of the Termite Gut Microbial Community. , 2010, , 413-438.		40
96	Dynamics of Redox Changes of Iron Caused by Lightâ€“dark Variations in Littoral Sediment of a Freshwater Lake. <i>Biogeochemistry</i> , 2005, 74, 323-339.	1.7	38
97	<i>Sporotalea propionica</i> gen. nov. sp. nov., a hydrogen-oxidizing, oxygen-reducing, propionigenic firmicute from the intestinal tract of a soil-feeding termite. <i>Archives of Microbiology</i> , 2006, 187, 15-27.	1.0	38
98	Putatively freeâ€“living â€“ <i>Endomicrobia</i> â€“ ancestors of the intracellular symbionts of termite gut flagellates?. <i>Environmental Microbiology Reports</i> , 2010, 2, 554-559.	1.0	38
99	Woodworker's digest. <i>Nature</i> , 2007, 450, 487-488.	13.7	36
100	The functional evolution of termite gut microbiota. <i>Microbiome</i> , 2022, 10, .	4.9	35
101	A new family for â€“termite gut treponemesâ€“: description of <i>Brezhakiellaceae</i> fam. nov., <i>Gracilinema caldarium</i> gen. nov., comb. nov., <i>Leadbetteria azotonutricia</i> gen. nov., comb. nov., <i>Helmutkoenigia isopterocolens</i> gen. nov., comb. nov., and <i>Zuelzera stenostrepta</i> gen. nov., comb. nov., and proposal of <i>Rectinemataceae</i> fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	35
102	Physiological properties of the gut lumen of terrestrial isopods (Isopoda: Oniscidea): adaptive to digesting lignocellulose?. <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2005, 175, 275-283.	0.7	34
103	Digestion of microbial biomass, structural polysaccharides, and protein by the humivorous larva of <i>Pachnoda ephippiata</i> (Coleoptera: Scarabaeidae). <i>Soil Biology and Biochemistry</i> , 2005, 37, 107-116.	4.2	33
104	Gut pH, redox conditions and oxygen levels in an aquatic caterpillar: Potential effects on the fate of ingested tannins. <i>Journal of Insect Physiology</i> , 2008, 54, 462-471.	0.9	33
105	Nitrogen mineralization, denitrification, and nitrate ammonification by soil-feeding termites: a 15N-based approach. <i>Biogeochemistry</i> , 2011, 103, 355-369.	1.7	33
106	Age polyethism drives community structure of the bacterial gut microbiota in the fungusâ€“cultivating termite <i>Reticulitermes formosanus</i> . <i>Environmental Microbiology</i> , 2016, 18, 1440-1451.	1.8	33
107	Synthesis and characterization of specifically 14C-labeled humic model compounds for feeding trials with soil-feeding termites. <i>Soil Biology and Biochemistry</i> , 2000, 32, 1271-1280.	4.2	32
108	The gut microenvironment of helcid snails (Gastropoda: Pulmonata): in-situ profiles of pH, oxygen, and hydrogen determined by microsensors. <i>Canadian Journal of Zoology</i> , 2003, 81, 928-935.	0.4	32

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109	Efficient but occasionally imperfect vertical transmission of gut mutualistic protists in a wood-feeding termite. <i>Molecular Ecology</i> , 2020, 29, 308-324.	2.0	32
110	Methane Oxidation in Termite Hindguts: Absence of Evidence and Evidence of Absence. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2024-2028.	1.4	30
111	<i>Ereboglobus luteus</i> gen. nov. sp. nov. from cockroach guts, and new insights into the oxygen relationship of the genera <i>Opiritatus</i> and <i>Didymococcus</i> (Verrucomicrobia : Opiritutaceae). <i>Systematic and Applied Microbiology</i> , 2018, 41, 101-112.	1.2	30
112	Sequential Transhydroxylations Converting Hydroxyhydroquinone to Phloroglucinol in the Strictly Anaerobic, Fermentative Bacterium <i>Pelobacter massiliensis</i> . <i>Applied and Environmental Microbiology</i> , 1992, 58, 1861-1868.	1.4	30
113	Cross-Epithelial Hydrogen Transfer from the Midgut Compartment Drives Methanogenesis in the Hindgut of Cockroaches. <i>Applied and Environmental Microbiology</i> , 2001, 67, 4657-4661.	1.4	29
114	Population Structure of Endomicrobia in Single Host Cells of Termite Gut Flagellates (<i>Trichonympha</i> spp.). <i>Microbes and Environments</i> , 2015, 30, 92-98.	0.7	29
115	Methanogens in the Digestive Tract of Termites. <i>Microbiology Monographs</i> , 2010, , 81-100.	0.3	29
116	Exclusive Gut Flagellates of Serritermitidae Suggest a Major Transfaunation Event in Lower Termites: Description of <i>Heliconympha glossotermitis</i> gen. nov. spec. nov.. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 77-92.	0.8	29
117	Complete Genome Sequence of <i>Endomicrobium proavitum</i> , a Free-Living Relative of the Intracellular Symbionts of Termite Gut Flagellates (Phylum <i>Elusimicrobia</i>). <i>Genome Announcements</i> , 2015, 3, .	0.8	27
118	Synthesis of [13C]- and [14C]-labeled phenolic humus and lignin monomers. <i>Chemosphere</i> , 2005, 60, 1169-1181.	4.2	26
119	Microprofiles of oxygen, redox potential, and pH, and microbial fermentation products in the highly alkaline gut of the saprophagous larva of <i>Penthetria holosericea</i> (Diptera: Bibionidae). <i>Journal of Insect Physiology</i> , 2014, 67, 64-69.	0.9	26
120	Changes in amount of bacteria during gut passage of leaf litter and during coprophagy in three species of Bibionidae (Diptera) larvae. <i>Folia Microbiologica</i> , 2003, 48, 535-542.	1.1	25
121	High-resolution phylogenetic analysis of <i>Endomicrobia</i> reveals multiple acquisitions of endosymbiotic lineages by termite gut flagellates. <i>Environmental Microbiology Reports</i> , 2017, 9, 477-483.	1.0	25
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139	Characterization and phylogenomic analysis of <i>Breznakiella homolactica</i> gen. nov. sp. nov. indicate that termite gut treponemes evolved from non-acetogenic spirochetes in cockroaches. <i>Environmental Microbiology</i> , 2021, 23, 4228-4245.	1.8	15
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