

Stefan J Green

List of Publications by Year in descending order

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Version: 2024-02-01

188
papers

11,294
citations

31902

53
h-index

34900

98
g-index

200
all docs

200
docs citations

200
times ranked

16640
citing authors

#	ARTICLE	IF	CITATIONS
1	Colonic bacterial composition in Parkinson's disease. <i>Movement Disorders</i> , 2015, 30, 1351-1360.	2.2	932
2	Hydrocarbon-Degrading Bacteria and the Bacterial Community Response in Gulf of Mexico Beach Sands Impacted by the Deepwater Horizon Oil Spill. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7962-7974.	1.4	779
3	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. <i>Science</i> , 2019, 364, .	6.0	576
4	Massively parallel rRNA gene sequencing exacerbates the potential for biased community diversity comparisons due to variable library sizes. <i>Environmental Microbiology</i> , 2012, 14, 285-290.	1.8	386
5	Circadian Disorganization Alters Intestinal Microbiota. <i>PLoS ONE</i> , 2014, 9, e97500.	1.1	328
6	Taxa-specific changes in soil microbial community composition induced by pyrogenic carbon amendments. <i>Soil Biology and Biochemistry</i> , 2011, 43, 385-392.	4.2	323
7	Niche and host-associated functional signatures of the root surface microbiome. <i>Nature Communications</i> , 2014, 5, 4950.	5.8	305
8	Role of TLR4 in the gut-brain axis in Parkinson's disease: a translational study from men to mice. <i>Gut</i> , 2019, 68, 829-843.	6.1	290
9	Chronic oral application of a periodontal pathogen results in brain inflammation, neurodegeneration and amyloid beta production in wild type mice. <i>PLoS ONE</i> , 2018, 13, e0204941.	1.1	225
10	Ketogenic diet enhances neurovascular function with altered gut microbiome in young healthy mice. <i>Scientific Reports</i> , 2018, 8, 6670.	1.6	203
11	Burn Injury Alters the Intestinal Microbiome and Increases Gut Permeability and Bacterial Translocation. <i>PLoS ONE</i> , 2015, 10, e0129996.	1.1	195
12	Diversity of Sulfate-Reducing Bacteria in Oxidic and Anoxic Regions of a Microbial Mat Characterized by Comparative Analysis of Dissimilatory Sulfite Reductase Genes. <i>Applied and Environmental Microbiology</i> , 1999, 65, 4666-4671.	1.4	184
13	Denitrifying Bacteria from the Genus <i>Rhodanobacter</i> Dominate Bacterial Communities in the Highly Contaminated Subsurface of a Nuclear Legacy Waste Site. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1039-1047.	1.4	184
14	Circadian Rhythm and the Gut Microbiome. <i>International Review of Neurobiology</i> , 2016, 131, 193-205.	0.9	176
15	Deconstructing the Polymerase Chain Reaction: Understanding and Correcting Bias Associated with Primer Degeneracies and Primer-Template Mismatches. <i>PLoS ONE</i> , 2015, 10, e0128122.	1.1	172
16	Chronic stress-induced gut dysfunction exacerbates Parkinson's disease phenotype and pathology in a rotenone-induced mouse model of Parkinson's disease. <i>Neurobiology of Disease</i> , 2020, 135, 104352.	2.1	172
17	Dietary Fiber Treatment Corrects the Composition of Gut Microbiota, Promotes SCFA Production, and Suppresses Colon Carcinogenesis. <i>Genes</i> , 2018, 9, 102.	1.0	158
18	Unexpected Population Distribution in a Microbial Mat Community: Sulfate-Reducing Bacteria Localized to the Highly Oxidic Chemocline in Contrast to a Eukaryotic Preference for Anoxia. <i>Applied and Environmental Microbiology</i> , 1999, 65, 4659-4665.	1.4	156

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19	Microbial Community Structure and Activity Linked to Contrasting Biogeochemical Gradients in Bog and Fen Environments of the Glacial Lake Agassiz Peatland. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7023-7031.	1.4	149
20	Bioelectrochemical Perchlorate Reduction in a Microbial Fuel Cell. <i>Environmental Science & Technology</i> , 2010, 44, 4685-4691.	4.6	137
21	Denitrifying Bacteria Isolated from Terrestrial Subsurface Sediments Exposed to Mixed-Waste Contamination. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3244-3254.	1.4	136
22	<i>Rhodanobacter denitrificans</i> sp. nov., isolated from nitrate-rich zones of a contaminated aquifer. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 2457-2462.	0.8	135
23	The Circadian <i>Clock</i> Mutation Promotes Intestinal Dysbiosis. <i>Alcoholism: Clinical and Experimental Research</i> , 2016, 40, 335-347.	1.4	134
24	Making and Sequencing Heavily Multiplexed, High-Throughput 16S Ribosomal RNA Gene Amplicon Libraries Using a Flexible, Two-Stage PCR Protocol. <i>Methods in Molecular Biology</i> , 2018, 1783, 149-169.	0.4	130
25	The Gastrointestinal Microbiome: Alcohol Effects on the Composition of Intestinal Microbiota. , 2015, 37, 223-36.		130
26	Timing of food intake impacts daily rhythms of human salivary microbiota: a randomized, crossover study. <i>FASEB Journal</i> , 2018, 32, 2060-2072.	0.2	126
27	<i>APOE</i> modulated $A\beta$ -induced neuroinflammation in Alzheimer's disease: current landscape, novel data, and future perspective. <i>Journal of Neurochemistry</i> , 2015, 133, 465-488.	2.1	123
28	Molecular and morphological characterization of cyanobacterial diversity in the stromatolites of Highborne Cay, Bahamas. <i>ISME Journal</i> , 2009, 3, 573-587.	4.4	116
29	A Limited Microbial Consortium Is Responsible for Extended Bioreduction of Uranium in a Contaminated Aquifer. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5955-5965.	1.4	108
30	Lateral Gene Transfer in a Heavy Metal-Contaminated-Groundwater Microbial Community. <i>MBio</i> , 2016, 7, e02234-15.	1.8	105
31	Single-cell transcriptional changes associated with drug tolerance and response to combination therapies in cancer. <i>Nature Communications</i> , 2021, 12, 1628.	5.8	103
32	Microbial Metabolic Potential for Carbon Degradation and Nutrient (Nitrogen and Phosphorus) Acquisition in an Ombrotrophic Peatland. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3531-3540.	1.4	102
33	Effects of Nitrate on the Stability of Uranium in a Bioreduced Region of the Subsurface. <i>Environmental Science & Technology</i> , 2010, 44, 5104-5111.	4.6	100
34	Age Drives Distortion of Brain Metabolic, Vascular and Cognitive Functions, and the Gut Microbiome. <i>Frontiers in Aging Neuroscience</i> , 2017, 9, 298.	1.7	96
35	<i>Geobacter daltonii</i> sp. nov., an Fe(III)- and uranium(VI)-reducing bacterium isolated from a shallow subsurface exposed to mixed heavy metal and hydrocarbon contamination. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 546-553.	0.8	91
36	Similarity of bacterial communities in sawdust- and straw-amended cow manure composts. <i>FEMS Microbiology Letters</i> , 2004, 233, 115-123.	0.7	86

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37	Biogeochemical cycling and microbial diversity in the thrombolitic microbialites of Highborne Cay, Bahamas. <i>Geobiology</i> , 2010, 8, 337-354.	1.1	84
38	Human milk oligosaccharides protect against the development of autoimmune diabetes in NOD-mice. <i>Scientific Reports</i> , 2018, 8, 3829.	1.6	82
39	Gut microbiota varies by opioid use, circulating leptin and oxytocin in African American men with diabetes and high burden of chronic disease. <i>PLoS ONE</i> , 2018, 13, e0194171.	1.1	82
40	The <i>in vivo</i> lifestyle of bile acid 7 α -dehydroxylating bacteria: comparative genomics, metatranscriptomic, and bile acid metabolomics analysis of a defined microbial community in gnotobiotic mice. <i>Gut Microbes</i> , 2020, 11, 381-404.	4.3	80
41	Diazotroph Community Characterization via a High-Throughput <i>nifH</i> Amplicon Sequencing and Analysis Pipeline. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	78
42	Bacterial virulence against an oceanic bloom-forming phytoplankter is mediated by algal DMSP. <i>Science Advances</i> , 2018, 4, eaau5716.	4.7	78
43	Dietary inulin alters the gut microbiome, enhances systemic metabolism and reduces neuroinflammation in an APOE4 mouse model. <i>PLoS ONE</i> , 2019, 14, e0221828.	1.1	78
44	Competing Factors of Compost Concentration and Proximity to Root Affect the Distribution of Streptomycetes. <i>Microbial Ecology</i> , 2005, 50, 73-81.	1.4	76
45	An alkaline spring system within the Del Puerto Ophiolite (California, USA): A Mars analog site. <i>Planetary and Space Science</i> , 2009, 57, 533-540.	0.9	73
46	Succession of Bacterial Communities during Early Plant Development: Transition from Seed to Root and Effect of Compost Amendment. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3975-3983.	1.4	71
47	High Throughput Analysis of Integron Gene Cassettes in Wastewater Environments. <i>Environmental Science & Technology</i> , 2016, 50, 11825-11836.	4.6	68
48	The Potential Role of Gut-Derived Inflammation in Multiple System Atrophy. <i>Journal of Parkinson's Disease</i> , 2017, 7, 331-346.	1.5	68
49	Reproducible changes in the gut microbiome suggest a shift in microbial and host metabolism during spaceflight. <i>Microbiome</i> , 2019, 7, 113.	4.9	67
50	Genome Sequences for Six Rhodanobacter Strains, Isolated from Soils and the Terrestrial Subsurface, with Variable Denitrification Capabilities. <i>Journal of Bacteriology</i> , 2012, 194, 4461-4462.	1.0	62
51	Sleep fragmentation increases blood pressure and is associated with alterations in the gut microbiome and fecal metabolome in rats. <i>Physiological Genomics</i> , 2020, 52, 280-292.	1.0	61
52	Significant differences in fecal microbiota are associated with various stages of glucose tolerance in African American male veterans. <i>Translational Research</i> , 2015, 166, 401-411.	2.2	59
53	Longitudinal Survey of Microbiota in Hospitalized Preterm Very-Low-Birth-Weight Infants. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2016, 62, 292-303.	0.9	58
54	Contrasting patterns of seed and root colonization by bacteria from the genus <i>Chryseobacterium</i> and from the family Oxalobacteraceae. <i>ISME Journal</i> , 2007, 1, 291-299.	4.4	57

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55	The role of anaerobic respiration in the immobilization of uranium through biomineralization of phosphate minerals. <i>Geochimica Et Cosmochimica Acta</i> , 2013, 106, 344-363.	1.6	57
56	Shifts in methanogen community structure and function associated with long-term manipulation of sulfate and salinity in a hypersaline microbial mat. <i>Environmental Microbiology</i> , 2008, 10, 386-394.	1.8	56
57	The nasal microbiome in patients with chronic rhinosinusitis: Analyzing the effects of atopy and bacterial functional pathways in 111 patients. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 287-290.e4.	1.5	55
58	Root microbiome response to treated wastewater irrigation. <i>Science of the Total Environment</i> , 2019, 655, 899-907.	3.9	54
59	Genomic Methods and Microbiological Technologies for Profiling Novel and Extreme Environments for the Extreme Microbiome Project (XMP). <i>Journal of Biomolecular Techniques</i> , 2017, 28, 31-39.	0.8	53
60	Effects of tillage practices on soil microbiome and agricultural parameters. <i>Science of the Total Environment</i> , 2020, 705, 135791.	3.9	53
61	A salinity and sulfate manipulation of hypersaline microbial mats reveals stasis in the cyanobacterial community structure. <i>ISME Journal</i> , 2008, 2, 457-470.	4.4	48
62	Single-Arm, Non-randomized, Time Series, Single-Subject Study of Fecal Microbiota Transplantation in Multiple Sclerosis. <i>Frontiers in Neurology</i> , 2020, 11, 978.	1.1	48
63	Abnormal Eating Patterns Cause Circadian Disruption and Promote Alcohol-Associated Colon Carcinogenesis. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2020, 9, 219-237.	2.3	43
64	Suicide Polymerase Endonuclease Restriction, a Novel Technique for Enhancing PCR Amplification of Minor DNA Templates. <i>Applied and Environmental Microbiology</i> , 2005, 71, 4721-4727.	1.4	40
65	The Microbiome Composition of a Man's Penis Predicts Incident Bacterial Vaginosis in His Female Sex Partner With High Accuracy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 433.	1.8	40
66	Murine Gut Microbiome Association With APOE Alleles. <i>Frontiers in Immunology</i> , 2020, 11, 200.	2.2	37
67	<i>Thermodesulfobacterium geofontis</i> sp. nov., a hyperthermophilic, sulfate-reducing bacterium isolated from Obsidian Pool, Yellowstone National Park. <i>Extremophiles</i> , 2013, 17, 251-263.	0.9	36
68	Isolation and physiological characterization of psychrophilic denitrifying bacteria from permanently cold <sc>A</sc>rtic fjord sediments (<sc>S</sc>valbard, <sc>N</sc>orway). <i>Environmental Microbiology</i> , 2013, 15, 1606-1618.	1.8	36
69	Cyst Fluid Biosignature to Predict Intraductal Papillary Mucinous Neoplasms of the Pancreas with High Malignant Potential. <i>Journal of the American College of Surgeons</i> , 2019, 228, 721-729.	0.2	35
70	Microglia, inflammation and gut microbiota responses in a progressive monkey model of Parkinson's disease: A case series. <i>Neurobiology of Disease</i> , 2020, 144, 105027.	2.1	34
71	Synergistic effects of APOE and sex on the gut microbiome of young EFAD transgenic mice. <i>Molecular Neurodegeneration</i> , 2019, 14, 47.	4.4	33
72	Microbial Diversity in Modern Stromatolites. <i>Cellular Origin and Life in Extreme Habitats</i> , 2011, , 383-405.	0.3	33

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73	Decomposition of plankton-derived dissolved organic matter in permeable coastal sediments. <i>Limnology and Oceanography</i> , 2010, 55, 857-871.	1.6	32
74	Draft Genome Sequence of <i>Flavobacterium</i> sp. Strain F52, Isolated from the Rhizosphere of Bell Pepper (<i>Capsicum annuum</i> L. cv. Maccabi). <i>Journal of Bacteriology</i> , 2012, 194, 5462-5463.	1.0	32
75	Genomic and Epidemiological Evidence for Community Origins of Hospital-Onset Methicillin-Resistant <i>Staphylococcus aureus</i> Bloodstream Infections. <i>Journal of Infectious Diseases</i> , 2017, 215, 1640-1647.	1.9	30
76	A survey of deepwater horizon (DWH) oil-degrading bacteria from the Eastern oyster biome and its surrounding environment. <i>Frontiers in Microbiology</i> , 2014, 5, 149.	1.5	29
77	Host Genetic Factors Associated with Vaginal Microbiome Composition in Kenyan Women. <i>MSystems</i> , 2020, 5, .	1.7	29
78	Genomic Epidemiology of USA300 Methicillin-Resistant <i>Staphylococcus aureus</i> in an Urban Community. <i>Clinical Infectious Diseases</i> , 2016, 62, 37-44.	2.9	28
79	A New Era for Space Life Science: International Standards for Space Omics Processing. <i>Patterns</i> , 2020, 1, 100148.	3.1	28
80	Decomposition of plankton-derived dissolved organic matter in permeable coastal sediments. <i>Limnology and Oceanography</i> , 2010, 55, 857-871.	1.6	28
81	Microbial Diversity of Genital Ulcer Disease in Men Enrolled in a Randomized Trial of Male Circumcision in Kisumu, Kenya. <i>PLoS ONE</i> , 2012, 7, e38991.	1.1	27
82	Effect of temperature on methane oxidation and community composition in landfill cover soil. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 1283-1295.	1.4	27
83	Predictors of Obesity among Gut Microbiota Biomarkers in African American Men with and without Diabetes. <i>Microorganisms</i> , 2019, 7, 320.	1.6	27
84	Nasopharyngeal Microbiota in SARS-CoV-2 Positive and Negative Patients. <i>Biological Procedures Online</i> , 2021, 23, 10.	1.4	26
85	Whole-Genome Sequences of Five Oyster-Associated Bacteria Show Potential for Crude Oil Hydrocarbon Degradation. <i>Genome Announcements</i> , 2013, 1, .	0.8	25
86	MRSA Transmission in Intensive Care Units: Genomic Analysis of Patients, Their Environments, and Healthcare Workers. <i>Clinical Infectious Diseases</i> , 2021, 72, 1879-1887.	2.9	25
87	Metagenomic Evaluation of Bacterial and Archaeal Diversity in the Geothermal Hot Springs of Manikaran, India. <i>Genome Announcements</i> , 2015, 3, .	0.8	24
88	Effects of green tea on miRNA and microbiome of oral epithelium. <i>Scientific Reports</i> , 2018, 8, 5873.	1.6	24
89	The microbiome as a biosensor: functional profiles elucidate hidden stress in hosts. <i>Microbiome</i> , 2020, 8, 71.	4.9	24
90	Restriction site-associated DNA sequencing generates high-quality single nucleotide polymorphisms for assessing hybridization between bighead and silver carp in the United States and China. <i>Molecular Ecology Resources</i> , 2014, 14, 79-86.	2.2	23

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91	Effect of pH on Methane Oxidation and Community Composition in Landfill Cover Soil. <i>Journal of Environmental Engineering</i> , ASCE, 2020, 146, .	0.7	23
92	The Bacterial Composition within the <i>Sarracenia purpurea</i> Model System: Local Scale Differences and the Relationship with the Other Members of the Food Web. <i>PLoS ONE</i> , 2012, 7, e50969.	1.1	22
93	Molecular and lipid biomarker analysis of a gypsum-hosted endoevaporitic microbial community. <i>Geobiology</i> , 2014, 12, 62-82.	1.1	22
94	Deep Characterization of the Microbiomes of <i>Calophya</i> spp. (Hemiptera: Calophyidae) Gall-Inducing Psyllids Reveals the Absence of Plant Pathogenic Bacteria and Three Dominant Endosymbionts. <i>PLoS ONE</i> , 2015, 10, e0132248.	1.1	22
95	Draft Genome Sequences for Oil-Degrading Bacterial Strains from Beach Sands Impacted by the Deepwater Horizon Oil Spill. <i>Genome Announcements</i> , 2013, 1, .	0.8	21
96	Considerations When Designing a Microbiome Study: Implications for Nursing Science. <i>Biological Research for Nursing</i> , 2019, 21, 125-141.	1.0	21
97	Comparative Genomics and Metabolic Analysis Reveals Peculiar Characteristics of <i>Rhodococcus opacus</i> Strain M213 Particularly for Naphthalene Degradation. <i>PLoS ONE</i> , 2016, 11, e0161032.	1.1	21
98	Atopic dermatitis and food sensitization in South African toddlers. <i>Annals of Allergy, Asthma and Immunology</i> , 2017, 118, 742-743.e3.	0.5	20
99	Assessment of the impact of different fecal storage protocols on the microbiota diversity and composition: a pilot study. <i>BMC Microbiology</i> , 2019, 19, 145.	1.3	19
100	The Combination of 2- ² -Fucosyllactose with Short-Chain Galacto-Oligosaccharides and Long-Chain Fructo-Oligosaccharides that Enhance Influenza Vaccine Responses Is Associated with Mucosal Immune Regulation in Mice. <i>Journal of Nutrition</i> , 2019, 149, 856-869.	1.3	19
101	Detection of respiratory pathogens in clinical samples using metagenomic shotgun sequencing. <i>Journal of Medical Microbiology</i> , 2019, 68, 996-1002.	0.7	19
102	Molecular tools for isolate and community studies of Pyrenomycete fungi. <i>Mycologia</i> , 2004, 96, 439-451.	0.8	17
103	Microbial and Geochemical Assessment of Bauxitic Un-mined and Post-mined Chronosequence Soils from Mocho Mountains, Jamaica. <i>Microbial Ecology</i> , 2012, 64, 738-749.	1.4	17
104	Draft Genome Sequence of the Pathogenic Bacterium <i>Vibrio vulnificus</i> V252 Biotype 1, Isolated in Israel. <i>Genome Announcements</i> , 2015, 3, .	0.8	17
105	Microbial Community Structure Associated with Biogeochemical Processes in the Sulfate-Methane Transition Zone (SMTZ) of Gas-hydrate-bearing Sediment of the Ulleung Basin, East Sea. <i>Geomicrobiology Journal</i> , 2017, 34, 207-219.	1.0	17
106	APOE genetics influence murine gut microbiome. <i>Scientific Reports</i> , 2022, 12, 1906.	1.6	17
107	<i>Lactobacillus acidophilus</i> Mitigates Osteoarthritis-Associated Pain, Cartilage Disintegration and Gut Microbiota Dysbiosis in an Experimental Murine OA Model. <i>Biomedicine</i> , 2022, 10, 1298.	1.4	17
108	Denaturing Gradient Gel Electrophoresis (DGGE) for Microbial Community Analysis. <i>Springer Protocols</i> , 2015, , 77-99.	0.1	16

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109	Investigation of Respiratory Syncytial Virus Outbreak on an Adult Stem Cell Transplant Unit by Use of Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2017, 55, 2956-2963.	1.8	16
110	Frequent Methicillin-Resistant <i>Staphylococcus aureus</i> Introductions Into an Inner-city Jail: Indications of Community Transmission Networks. <i>Clinical Infectious Diseases</i> , 2020, 71, 323-331.	2.9	16
111	Hepatic deficiency of the pioneer transcription factor FoxA restricts hepatitis B virus biosynthesis by the developmental regulation of viral DNA methylation. <i>PLoS Pathogens</i> , 2017, 13, e1006239.	2.1	16
112	Watershed-Scale Fungal Community Characterization along a pH Gradient in a Subsurface Environment Cocontaminated with Uranium and Nitrate. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1810-1820.	1.4	15
113	Assessing the Efficiency of Cultivation Techniques To Recover Natural Product Biosynthetic Gene Populations from Sediment. <i>ACS Chemical Biology</i> , 2018, 13, 2074-2081.	1.6	15
114	Complete Genome of <i>Micromonospora</i> sp. Strain B006 Reveals Biosynthetic Potential of a Lake Michigan Actinomycete. <i>Journal of Natural Products</i> , 2018, 81, 2057-2068.	1.5	15
115	Apolipoprotein E genotype-dependent nutrigenetic effects to prebiotic inulin for modulating systemic metabolism and neuroprotection in mice via gut-brain axis. <i>Nutritional Neuroscience</i> , 2021, , 1-11.	1.5	14
116	Genome-centric evaluation of <i>Burkholderia</i> sp. strain SRS-W-2-2016 resistant to high concentrations of uranium and nickel isolated from the Savannah River Site (SRS), USA. <i>Genomics Data</i> , 2017, 12, 62-68.	1.3	13
117	Vaginal and Penile Microbiome Associations With Herpes Simplex Virus Type 2 in Women and Their Male Sex Partners. <i>Journal of Infectious Diseases</i> , 2022, 226, 644-654.	1.9	13
118	Abnormal food timing and predisposition to weight gain: Role of barrier dysfunction and microbiota. <i>Translational Research</i> , 2021, 231, 113-123.	2.2	13
119	Berberine alters gut microbial function through modulation of bile acids. <i>BMC Microbiology</i> , 2021, 21, 24.	1.3	13
120	High Prevalence of <i>Lactobacillus crispatus</i> Dominated Vaginal Microbiome Among Kenyan Secondary School Girls: Negative Effects of Poor Quality Menstrual Hygiene Management and Sexual Activity. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 716537.	1.8	13
121	Intestinal Barrier Dysfunction in the Absence of Systemic Inflammation Fails to Exacerbate Motor Dysfunction and Brain Pathology in a Mouse Model of Parkinson's Disease. <i>Frontiers in Neurology</i> , 2022, 13, .	1.1	13
122	Genome Sequences for Three Denitrifying Bacterial Strains Isolated from a Uranium- and Nitrate-Contaminated Subsurface Environment. <i>Genome Announcements</i> , 2013, 1, .	0.8	12
123	Fructose diet alleviates acetaminophen-induced hepatotoxicity in mice. <i>PLoS ONE</i> , 2017, 12, e0182977.	1.1	12
124	Stress-related ecophysiology of members of the genus <i>Rhodanobacter</i> isolated from a mixed waste contaminated subsurface. <i>Frontiers of Environmental Science and Engineering</i> , 2021, 15, 1.	3.3	12
125	Microbial Communities of Stored Product Mites: Variation by Species and Population. <i>Microbial Ecology</i> , 2021, 81, 506-522.	1.4	12
126	Starch-entrapped microsphere fibers improve bowel habit but do not exhibit prebiotic capacity in those with unsatisfactory bowel habits: a phase I, randomized, double-blind, controlled human trial. <i>Nutrition Research</i> , 2017, 44, 27-37.	1.3	11

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127	Effect of Dietary Fiber on the Composition of the Murine Dental Microbiome. Dentistry Journal, 2019, 7, 58.	0.9	11
128	Antimicrobial peptide cocktail activity in minced turkey meat. Food Microbiology, 2020, 92, 103580.	2.1	11
129	Deep nasal sinus cavity microbiota dysbiosis in Parkinson's disease. Npj Parkinson's Disease, 2021, 7, 111.	2.5	11
130	Draft Genome Sequence of Rhodococcus opacus Strain M213 Shows a Diverse Catabolic Potential. Genome Announcements, 2013, 1, .	0.8	10
131	High Frequency of MYD88 L265P Mutation in Primary Ocular Adnexal Marginal Zone Lymphoma and Its Clinicopathologic Correlation: A Study From a Single Institution. Archives of Pathology and Laboratory Medicine, 2019, 143, 483-493.	1.2	10
132	Raw Milk-Induced Protection against Food Allergic Symptoms in Mice Is Accompanied by Shifts in Microbial Community Structure. International Journal of Molecular Sciences, 2021, 22, 3417.	1.8	10
133	Microbiome variation during culture growth of the European house dust mite, <i>Dermatophagoides pteronyssinus</i> . FEMS Microbiology Ecology, 2021, 97, .	1.3	10
134	Faropenem resistance causes in vitro cross-resistance to carbapenems in ESBL-producing Escherichia coli. International Journal of Antimicrobial Agents, 2020, 55, 105902.	1.1	9
135	<i>Cardinium</i> inhibits <i>Wolbachia</i> in its mite host, <i>Tyrophagus putrescentiae</i> , and affects host fitness. FEMS Microbiology Ecology, 2021, 97, .	1.3	9
136	Compost Microbial Populations and Interactions with Plants. , 2010, , 231-251.		9
137	Proof-of-principle demonstration of endogenous circadian system and circadian misalignment effects on human oral microbiota. FASEB Journal, 2022, 36, e22043.	0.2	9
138	Draft Genome Sequence of Alicyclobacillus acidoterrestris Strain ATCC 49025. Genome Announcements, 2013, 1, .	0.8	8
139	Microbial Diversity of Genital Ulcers of HSV-2 Seropositive Women. Scientific Reports, 2017, 7, 15475.	1.6	8
140	Microorganisms and Processes Linked to Uranium Reduction and Immobilization. , 0, , 117-138.		8
141	Metagenomics Reveals Planktonic Bacterial Community Shifts across a Natural CO ₂ Gradient in the Mediterranean Sea. Genome Announcements, 2015, 3, .	0.8	6
142	The gut microbiota may be a novel pathogenic mechanism in loosening of orthopedic implants in rats. FASEB Journal, 2020, 34, 14302-14317.	0.2	6
143	Four Weeks of Treatment With Rifaximin Fails to Significantly Alter Microbial Diversity in Rectal Samples of HIV-Infected Immune Non-Responders (ACTG A5286) Which May be Attributed to Rectal Swab Use. Pathogens and Immunity, 2019, 4, 235.	1.4	6
144	Evaluation of Effects of Laboratory Disinfectants on Mouse Gut Microbiota. Comparative Medicine, 2021, 71, 492-501.	0.4	6

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145	Complete Genome Sequence of <i>Sulfitobacter</i> sp. Strain D7, a Virulent Bacterium Isolated from an <i>Emiliana huxleyi</i> Algal Bloom in the North Atlantic. Microbiology Resource Announcements, 2018, 7, .	0.3	5
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