

# Garret Suen

## List of Publications by Year in Descending Order

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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.

120  
papers

4,807  
citations

36  
h-index

67  
g-index

130  
ext. papers

6,488  
ext. citations

6.6  
avg, IF

5.42  
L-index

#	Paper	IF	Citations
120	Nitrogen recycling via gut symbionts increases in ground squirrels over the hibernation season.. <i>Science</i> , <b>2022</b> , 375, 460-463	33.3	5
119	Characterization of captive and wild 13-lined ground squirrel cecal microbiotas using Illumina-based sequencing.. <i>Animal Microbiome</i> , <b>2022</b> , 4, 1	4.1	0
118	Integrative interactomics applied to bovine fescue toxicosis.. <i>Scientific Reports</i> , <b>2022</b> , 12, 4899	4.9	0
117	Assessing the effects of experimental bacterial challenge with <i>Pasteurella multocida</i> and ampicillin on the respiratory microbiota of pre-weaned Holstein calves.. <i>Veterinary Microbiology</i> , <b>2022</b> , 269, 109428 <sup>3,3</sup>		
116	Assessing the microbiota of recycled bedding sand on a Wisconsin dairy farm. <i>Journal of Animal Science and Biotechnology</i> , <b>2021</b> , 12, 114	6	1
115	Assessing the Response of Ruminal Bacterial and Fungal Microbiota to Whole-Rumen Contents Exchange in Dairy Cows. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 665776	5.7	1
114	Assessing the relationship between the rumen microbiota and feed efficiency in Nellore steers. <i>Journal of Animal Science and Biotechnology</i> , <b>2021</b> , 12, 79	6	4
113	Characterizing the microbiota of wooden boards used for cheese ripening. <i>JDS Communications</i> , <b>2021</b> , 2, 171-176	1.4	2
112	Multimomics analysis reveals the presence of a microbiome in the gut of fetal lambs. <i>Gut</i> , <b>2021</b> , 70, 853-864 <sup>4,2</sup>	4.2	19
111	A <i>Sarcina</i> bacterium linked to lethal disease in sanctuary chimpanzees in Sierra Leone. <i>Nature Communications</i> , <b>2021</b> , 12, 763	17.4	5
110	The Rumen Bacterial Community in Dairy Cows Is Correlated to Production Traits During Freshening Period. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 630605	5.7	4
109	The genomic basis of army ant chemosensory adaptations. <i>Molecular Ecology</i> , <b>2021</b> , 30, 6627-6641	5.7	3
108	Assessing the impact of storage time on the stability of stool microbiota richness, diversity, and composition.. <i>Gut Pathogens</i> , <b>2021</b> , 13, 75	5.4	1
107	Wisconsin dairy farm worker perceptions and practices related to antibiotic use, resistance, and infection prevention using a systems engineering framework.. <i>PLoS ONE</i> , <b>2021</b> , 16, e0258290	3.7	0
106	A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. <i>Nature Communications</i> , <b>2020</b> , 11, 6389	17.4	26
105	Effect of stevia on the gut microbiota and glucose tolerance in a murine model of diet-induced obesity. <i>FEMS Microbiology Ecology</i> , <b>2020</b> , 96,	4.3	7
104	Crop rotation, but not cover crops, influenced soil bacterial community composition in a corn-soybean system in southern Wisconsin. <i>Applied Soil Ecology</i> , <b>2020</b> , 154, 103603	5	17

103	Changes in the host transcriptome and microbial metatranscriptome of the ileum of dairy calves subjected to artificial dosing of exogenous rumen contents. <i>Physiological Genomics</i> , <b>2020</b> , 52, 333-346	3.6	1
102	Household Pet Ownership and the Microbial Diversity of the Human Gut Microbiota. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2020</b> , 10, 73	5.9	17
101	Fecal microbiota transplantation for patients on antibiotic treatment with infection history (GRAFT): Study protocol for a phase II, randomized, double-blind, placebo-controlled trial to prevent recurrent infections. <i>Contemporary Clinical Trials Communications</i> , <b>2020</b> , 18, 100576	1.8	
100	Validating the Use of Bovine Buccal Sampling as a Proxy for the Rumen Microbiota by Using a Time Course and Random Forest Classification Approach. <i>Applied and Environmental Microbiology</i> , <b>2020</b> , 86,	4.8	3
99	The bovine epimural microbiota displays compositional and structural heterogeneity across different ruminal locations. <i>Journal of Dairy Science</i> , <b>2020</b> , 103, 3636-3647	4	4
98	Toxic tall fescue grazing increases susceptibility of the Angus steer fecal microbiota and plasma/urine metabolome to environmental effects. <i>Scientific Reports</i> , <b>2020</b> , 10, 2497	4.9	6
97	166 Altering the ruminal microbiota in dairy calves using rumen contents dosing. <i>Journal of Animal Science</i> , <b>2020</b> , 98, 135-136	0.7	
96	PSIX-25 Documenting succession of the rumen microbial community in dairy calves. <i>Journal of Animal Science</i> , <b>2020</b> , 98, 331-331	0.7	
95	PSXII-1 High-throughput Phenotyping of Rumen Microbial Contents Using Buccal Swabs. <i>Journal of Animal Science</i> , <b>2020</b> , 98, 444-445	0.7	
94	PSVI-17 Evaluating the impact of a high-starch and high-forage diet on the ruminal solid, liquid, and epimural microbiota of dairy cows. <i>Journal of Animal Science</i> , <b>2020</b> , 98, 435-435	0.7	
93	Use of a systems engineering framework to assess perceptions and practices about antimicrobial resistance of workers on large dairy farms in Wisconsin <b>2020</b> ,		2
92	Characterization of microbial communities in ethanol biorefineries. <i>Journal of Industrial Microbiology and Biotechnology</i> , <b>2020</b> , 47, 183-195	4.2	4
91	Assessing the Beneficial Effects of the Immunomodulatory Glycan LNFPIII on Gut Microbiota and Health in a Mouse Model of Gulf War Illness. <i>International Journal of Environmental Research and Public Health</i> , <b>2020</b> , 17,	4.6	8
90	Ruminal Fermentation Pattern, Bacterial Community Composition, and Nutrient Digestibility of Nellore Cattle Submitted to Either Nutritional Restriction or Intake of Concentrate Feedstuffs Prior to Adaptation Period. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 1865	5.7	3
89	Multiplexed Competition in a Synthetic Squid Light Organ Microbiome Using Barcode-Tagged Gene Deletions. <i>MSystems</i> , <b>2020</b> , 5,	7.6	3
88	Urinary lead concentration and composition of the adult gut microbiota in a cross-sectional population-based sample. <i>Environment International</i> , <b>2019</b> , 133, 105122	12.9	27
87	Transcriptomics analysis of host liver and meta-transcriptome analysis of rumen epimural microbial community in young calves treated with artificial dosing of rumen content from adult donor cow. <i>Scientific Reports</i> , <b>2019</b> , 9, 790	4.9	9
86	Response of Beef Cattle Fecal Microbiota to Grazing on Toxic Tall Fescue. <i>Applied and Environmental Microbiology</i> , <b>2019</b> , 85,	4.8	10

85	The Bacterial and Fungal Microbiota of Nelore Steers Is Dynamic Across the Gastrointestinal Tract and Its Fecal-Associated Microbiota Is Correlated to Feed Efficiency. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 1263	5.7	13
84	Laryngotracheal Microbiota in Adult Laryngotracheal Stenosis. <i>MSphere</i> , <b>2019</b> , 4,	5	15
83	Effects of corn silage inclusion in preweaning calf diets. <i>Journal of Dairy Science</i> , <b>2019</b> , 102, 4131-4137	4	6
82	Feeding modes shape the acquisition and structure of the initial gut microbiota in newborn lambs. <i>Environmental Microbiology</i> , <b>2019</b> , 21, 2333-2346	5.2	20
81	Compositional and structural dynamics of the ruminal microbiota in dairy heifers and its relationship to methane production. <i>Journal of the Science of Food and Agriculture</i> , <b>2019</b> , 99, 210-218	4.3	8
80	The ruminal bacterial community in lactating dairy cows has limited variation on a day-to-day basis. <i>Journal of Animal Science and Biotechnology</i> , <b>2019</b> , 10, 66	6	9
79	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation. <i>Genome Biology</i> , <b>2019</b> , 20, 153	18.3	38
78	Characterising the gut microbiome in veterans with Gulf War Illness: a protocol for a longitudinal, prospective cohort study. <i>BMJ Open</i> , <b>2019</b> , 9, e031114	3	6
77	Diet Influences Early Microbiota Development in Dairy Calves without Long-Term Impacts on Milk Production. <i>Applied and Environmental Microbiology</i> , <b>2019</b> , 85,	4.8	39
76	Bacterial Community Dynamics across the Gastrointestinal Tracts of Dairy Calves during Preweaning Development. <i>Applied and Environmental Microbiology</i> , <b>2018</b> , 84,	4.8	44
75	The Ruminococci: key symbionts of the gut ecosystem. <i>Journal of Microbiology</i> , <b>2018</b> , 56, 199-208	3	83
74	Influence of sampling technique and bedding type on the milk microbiota: Results of a pilot study. <i>Journal of Dairy Science</i> , <b>2018</b> , 101, 6346-6356	4	33
73	Wisconsin microbiome study, a cross-sectional investigation of dietary fibre, microbiome composition and antibiotic-resistant organisms: rationale and methods. <i>BMJ Open</i> , <b>2018</b> , 8, e019450	3	18
72	Dietary changes during weaning shape the gut microbiota of red pandas () <b>2018</b> , 6, cox075		8
71	Addressing Global Ruminant Agricultural Challenges Through Understanding the Rumen Microbiome: Past, Present, and Future. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 2161	5.7	123
70	Bacterial Communities in the Alpaca Gastrointestinal Tract Vary With Diet and Body Site. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 3334	5.7	2
69	The Phylogenomic Diversity of Herbivore-Associated spp. Is Correlated to Lignocellulose-Degrading Potential. <i>MSphere</i> , <b>2018</b> , 3,	5	18
68	A global analysis of gene expression in S85 grown on cellulose and soluble sugars at different growth rates. <i>Biotechnology for Biofuels</i> , <b>2018</b> , 11, 295	7.8	7

67	Oral probiotic combination of Lactobacillus and Bifidobacterium alters the gastrointestinal microbiota during antibiotic treatment for Clostridium difficile infection. <i>PLoS ONE</i> , <b>2018</b> , 13, e0204253	3.7	24
66	A Cohort Study of the Milk Microbiota of Healthy and Inflamed Bovine Mammary Glands From Dryoff Through 150 Days in Milk. <i>Frontiers in Veterinary Science</i> , <b>2018</b> , 5, 247	3.1	18
65	Understanding the Milk Microbiota. <i>Veterinary Clinics of North America - Food Animal Practice</i> , <b>2018</b> , 34, 427-438	4.6	16
64	Microbial succession in the gastrointestinal tract of dairy cows from 2 weeks to first lactation. <i>Scientific Reports</i> , <b>2017</b> , 7, 40864	4.9	84
63	Fibrobacter communities in the gastrointestinal tracts of diverse hindgut-fermenting herbivores are distinct from those of the rumen. <i>Environmental Microbiology</i> , <b>2017</b> , 19, 3768-3783	5.2	12
62	Assessing the impact of rumen microbial communities on methane emissions and production traits in Holstein cows in a tropical climate. <i>Systematic and Applied Microbiology</i> , <b>2017</b> , 40, 492-499	4.2	19
61	Transient changes in milk production efficiency and bacterial community composition resulting from near-total exchange of ruminal contents between high- and low-efficiency Holstein cows. <i>Journal of Dairy Science</i> , <b>2017</b> , 100, 7165-7182	4	36
60	Effect of Pre-weaning Diet on the Ruminal Archaeal, Bacterial, and Fungal Communities of Dairy Calves. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 1553	5.7	43
59	Camelina Seed Supplementation at Two Dietary Fat Levels Change Ruminal Bacterial Community Composition in a Dual-Flow Continuous Culture System. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 2147	5.7	11
58	The human laryngeal microbiome: effects of cigarette smoke and reflux. <i>Scientific Reports</i> , <b>2016</b> , 6, 35882	4.9	24
57	Diet specialization selects for an unusual and simplified gut microbiota in two- and three-toed sloths. <i>Environmental Microbiology</i> , <b>2016</b> , 18, 1391-402	5.2	30
56	Bears Arouse Interest in Microbiota's Role in Health. <i>Trends in Microbiology</i> , <b>2016</b> , 24, 245-246	12.4	5
55	Small genome of the fungus Escovopsis weberi, a specialized disease agent of ant agriculture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 3567-72	11.5	49
54	Detection of short-term cropping system-induced changes to soil bacterial communities differs among four molecular characterization methods. <i>Soil Biology and Biochemistry</i> , <b>2016</b> , 96, 160-168	7.5	13
53	Sequence-based analysis of the genus resolves its phylogeny and reveals strong host association. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000099	4.4	30
52	Dietary Shifts May Trigger Dysbiosis and Mucous Stools in Giant Pandas ( <i>Ailuropoda melanoleuca</i> ). <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 661	5.7	21
51	Ruminal Bacterial Community Composition in Dairy Cows Is Dynamic over the Course of Two Lactations and Correlates with Feed Efficiency. <i>Applied and Environmental Microbiology</i> , <b>2015</b> , 81, 4697-710	7.8	149
50	Phylogenetic and amino acid conservation analyses of bacterial L-aspartate-β-decarboxylase and of its zymogen-maturation protein reveal a putative interaction domain. <i>BMC Research Notes</i> , <b>2015</b> , 8, 354	2.3	6

49	Differences in major bacterial populations in the intestines of mature broilers after feeding virginiamycin or bacitracin methylene disalicylate. <i>Journal of Applied Microbiology</i> , <b>2015</b> , 119, 1515-26	4.7	31
48	Evaluating Models of Cellulose Degradation by <i>Fibrobacter succinogenes</i> S85. <i>PLoS ONE</i> , <b>2015</b> , 10, e0143809	3.9	27
47	An analysis of the ruminal bacterial microbiota in West African Dwarf sheep fed grass- and tree-based diets. <i>Journal of Applied Microbiology</i> , <b>2014</b> , 116, 1094-105	4.7	21
46	Unique aspects of fiber degradation by the ruminal ethanologen <i>Ruminococcus albus</i> 7 revealed by physiological and transcriptomic analysis. <i>BMC Genomics</i> , <b>2014</b> , 15, 1066	4.5	47
45	Convergent bacterial microbiotas in the fungal agricultural systems of insects. <i>MBio</i> , <b>2014</b> , 5, e02077	7.8	68
44	Bacterial communities in the rumen of Holstein heifers differ when fed orchardgrass as pasture vs. hay. <i>Frontiers in Microbiology</i> , <b>2014</b> , 5, 689	5.7	26
43	Hibernation alters the diversity and composition of mucosa-associated bacteria while enhancing antimicrobial defence in the gut of 13-lined ground squirrels. <i>Molecular Ecology</i> , <b>2014</b> , 23, 4658-69	5.7	43
42	Nature's bioreactor: the rumen as a model for biofuel production. <i>Biofuels</i> , <b>2013</b> , 4, 511-521	2	8
41	Characterizing the microbiota across the gastrointestinal tract of a Brazilian Nelore steer. <i>Veterinary Microbiology</i> , <b>2013</b> , 164, 307-14	3.3	103
40	<i>Leucoagaricus gongylophorus</i> produces diverse enzymes for the degradation of recalcitrant plant polymers in leaf-cutter ant fungus gardens. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 3770-8	4.8	75
39	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. <i>Genome Research</i> , <b>2013</b> , 23, 1235-47	9.7	166
38	A phylogenetic analysis of the phylum Fibrobacteres. <i>Systematic and Applied Microbiology</i> , <b>2013</b> , 36, 376-82	4.2	18
37	Comparison of 26 sphingomonad genomes reveals diverse environmental adaptations and biodegradative capabilities. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 3724-33	4.8	115
36	Mountain pine beetles colonizing historical and naive host trees are associated with a bacterial community highly enriched in genes contributing to terpene metabolism. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 3468-75	4.8	166
35	The genome sequences of <i>Cellulomonas fimi</i> and " <i>Cellvibrio gilvus</i> " reveal the cellulolytic strategies of two facultative anaerobes, transfer of " <i>Cellvibrio gilvus</i> " to the genus <i>Cellulomonas</i> , and proposal of <i>Cellulomonas gilvus</i> sp. nov. <i>PLoS ONE</i> , <b>2013</b> , 8, e53954	3.7	44
34	The genomic impact of 100 million years of social evolution in seven ant species. <i>Trends in Genetics</i> , <b>2012</b> , 28, 14-21	8.5	92
33	The genomic basis for the evolution of a novel form of cellular reproduction in the bacterium <i>Epulopiscium</i> . <i>BMC Genomics</i> , <b>2012</b> , 13, 265	4.5	17
32	Metagenomic and metaproteomic insights into bacterial communities in leaf-cutter ant fungus gardens. <i>ISME Journal</i> , <b>2012</b> , 6, 1688-701	11.9	100

31	The Evolutionary Innovation of Nutritional Symbioses in Leaf-Cutter Ants. <i>Insects</i> , <b>2012</b> , 3, 41-61	2.8	41
30	The Microbiome of Leaf-Cutter Ant Fungus Gardens <b>2011</b> , 367-379		5
29	The entomopathogenic bacterial endosymbionts <i>Xenorhabdus</i> and <i>Photorhabdus</i> : convergent lifestyles from divergent genomes. <i>PLoS ONE</i> , <b>2011</b> , 6, e27909	3.7	130
28	Cellulose-degrading bacteria associated with the invasive woodwasp <i>Sirex noctilio</i> . <i>ISME Journal</i> , <b>2011</b> , 5, 1323-31	11.9	107
27	Complete genome of the cellulolytic ruminal bacterium <i>Ruminococcus albus</i> 7. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 5574-5	3.5	61
26	Genome sequence of <i>Streptomyces griseus</i> strain XylebKG-1, an ambrosia beetle-associated actinomycete. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2890-1	3.5	24
25	Complete genome sequence of the cellulose-degrading bacterium <i>Cellulosilyticum lentocellum</i> . <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2357-8	3.5	23
24	Draft genome of the globally widespread and invasive Argentine ant ( <i>Linepithema humile</i> ). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 5673-8	11.5	214
23	Draft genome of the red harvester ant <i>Pogonomyrmex barbatus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 5667-72	11.5	200
22	A cascade of coregulating enhancer binding proteins initiates and propagates a multicellular developmental program. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, E431-9	11.5	31
21	The genome sequence of the leaf-cutter ant <i>Atta cephalotes</i> reveals insights into its obligate symbiotic lifestyle. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002007	6	191
20	The complete genome sequence of <i>Fibrobacter succinogenes</i> S85 reveals a cellulolytic and metabolic specialist. <i>PLoS ONE</i> , <b>2011</b> , 6, e18814	3.7	152
19	An insect herbivore microbiome with high plant biomass-degrading capacity. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001129	11.29	172
18	Microbial community structure of leaf-cutter ant fungus gardens and refuse dumps. <i>PLoS ONE</i> , <b>2010</b> , 5, e9922	3.7	66
17	SREB, a GATA transcription factor that directs disparate fates in <i>Blastomyces dermatitidis</i> including morphogenesis and siderophore biosynthesis. <i>PLoS Pathogens</i> , <b>2010</b> , 6, e1000846	7.6	52
16	Symbiosis research, technology, and education: Proceedings of the 6th International Symbiosis Society Congress held in Madison Wisconsin, USA, August 2009. <i>Symbiosis</i> , <b>2010</b> , 51, 1-12	3	1
15	Units of plasticity in bacterial genomes: new insight from the comparative genomics of two bacteria interacting with invertebrates, <i>Photorhabdus</i> and <i>Xenorhabdus</i> . <i>BMC Genomics</i> , <b>2010</b> , 11, 568	4.5	39
14	Insect symbioses: a case study of past, present, and future fungus-growing ant research. <i>Environmental Entomology</i> , <b>2009</b> , 38, 78-92	2.1	59



13	Genome sequences of three agrobacterium biovars help elucidate the evolution of multichromosome genomes in bacteria. <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 2501-11	3.5	184
12	Isolation and characterization of <i>Xenorhabdus nematophila</i> transposon insertion mutants defective in lipase activity against Tween. <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 5325-31	3.5	8
11	Symbiotic nitrogen fixation in the fungus gardens of leaf-cutter ants. <i>Science</i> , <b>2009</b> , 326, 1120-3	33.3	223
10	Practical applications of bacterial functional genomics. <i>Biotechnology and Genetic Engineering Reviews</i> , <b>2007</b> , 24, 213-42	4.1	5
9	Complete genome sequence of the myxobacterium <i>Sorangium cellulosum</i> . <i>Nature Biotechnology</i> , <b>2007</b> , 25, 1281-9	44.5	307
8	Xanthusbase: adapting wikipedia principles to a model organism database. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D422-6	20.1	10
7	Predicting prokaryotic ecological niches using genome sequence analysis. <i>PLoS ONE</i> , <b>2007</b> , 2, e743	3.7	23
6	Bacterial postgenomics: the promise and peril of systems biology. <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 7999-8004	3.5	3
5	Functional genome annotation through phylogenomic mapping. <i>Nature Biotechnology</i> , <b>2005</b> , 23, 691-8	44.5	24
4	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation		3
3	Biogeography and Microscale Diversity Shape the Biosynthetic Potential of Fungus-growing Ant-associated <i>Pseudonocardia</i>		8
2	From Genetics to Genomics 255-266		
1	A Postgenomic Overview of the Myxobacteria 299-311		