

Scot E Dowd

List of Publications by Year in descending order

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252
papers

24,100
citations

5261

83
h-index

8852

145
g-index

259
all docs

259
docs citations

259
times ranked

27872
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluation of the bacterial diversity in the feces of cattle using 16S rDNA bacterial tag-encoded FLX amplicon pyrosequencing (bTEFAP). <i>BMC Microbiology</i> , 2008, 8, 125.	1.3	982
2	Exposure to a social stressor alters the structure of the intestinal microbiota: Implications for stressor-induced immunomodulation. <i>Brain, Behavior, and Immunity</i> , 2011, 25, 397-407.	2.0	929
3	Pyrosequencing study of fecal microflora of autistic and control children. <i>Anaerobe</i> , 2010, 16, 444-453.	1.0	811
4	Survey of bacterial diversity in chronic wounds using Pyrosequencing, DGGE, and full ribosome shotgun sequencing. <i>BMC Microbiology</i> , 2008, 8, 43.	1.3	634
5	Soil Bacteria Confer Plant Salt Tolerance by Tissue-Specific Regulation of the Sodium Transporter <i><i>HKT1</i></i> . <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 737-744.	1.4	462
6	Polymicrobial Nature of Chronic Diabetic Foot Ulcer Biofilm Infections Determined Using Bacterial Tag Encoded FLX Amplicon Pyrosequencing (bTEFAP). <i>PLoS ONE</i> , 2008, 3, e3326.	1.1	456
7	Inherent bacterial DNA contamination of extraction and sequencing reagents may affect interpretation of microbiota in low bacterial biomass samples. <i>Cut Pathogens</i> , 2016, 8, 24.	1.6	446
8	Tag-encoded pyrosequencing analysis of bacterial diversity in a single soil type as affected by management and land use. <i>Soil Biology and Biochemistry</i> , 2008, 40, 2762-2770.	4.2	418
9	Diversity of the Human Skin Microbiome Early in Life. <i>Journal of Investigative Dermatology</i> , 2011, 131, 2026-2032.	0.3	402
10	Bacterial Tag-Encoded FLX Amplicon Pyrosequencing (bTEFAP) for Microbiome Studies: Bacterial Diversity in the Ileum of Newly Weaned <i>Salmonella</i> -Infected Pigs. <i>Foodborne Pathogens and Disease</i> , 2008, 5, 459-472.	0.8	373
11	Biofilm maturity studies indicate sharp debridement opens a time-dependent therapeutic window. <i>Journal of Wound Care</i> , 2010, 19, 320-328.	0.5	346
12	The Fecal Microbiome in Dogs with Acute Diarrhea and Idiopathic Inflammatory Bowel Disease. <i>PLoS ONE</i> , 2012, 7, e51907.	1.1	339
13	Biofilms and chronic wound inflammation. <i>Journal of Wound Care</i> , 2008, 17, 333-341.	0.5	336
14	Massive parallel 16S rRNA gene pyrosequencing reveals highly diverse fecal bacterial and fungal communities in healthy dogs and cats. <i>FEMS Microbiology Ecology</i> , 2011, 76, 301-310.	1.3	324
15	A soil bacterium regulates plant acquisition of iron via deficiency-inducible mechanisms. <i>Plant Journal</i> , 2009, 58, 568-577.	2.8	319
16	Stressor Exposure Disrupts Commensal Microbial Populations in the Intestines and Leads to Increased Colonization by <i>Citrobacter rodentium</i> . <i>Infection and Immunity</i> , 2010, 78, 1509-1519.	1.0	317
17	An In Vivo Polymicrobial Biofilm Wound Infection Model to Study Interspecies Interactions. <i>PLoS ONE</i> , 2011, 6, e27317.	1.1	299
18	Rumen Bacterial Diversity Dynamics Associated with Changing from Bermudagrass Hay to Grazed Winter Wheat Diets. <i>Microbial Ecology</i> , 2010, 59, 511-522.	1.4	298

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19	Phylogenetic and gene-centric metagenomics of the canine intestinal microbiome reveals similarities with humans and mice. <i>ISME Journal</i> , 2011, 5, 639-649.	4.4	292
20	Exposure to a social stressor disrupts the community structure of the colonic mucosa-associated microbiota. <i>BMC Microbiology</i> , 2014, 14, 189.	1.3	292
21	Assessment of bacterial diversity in the cattle tick <i>Rhipicephalus (Boophilus) microplus</i> through tag-encoded pyrosequencing. <i>BMC Microbiology</i> , 2011, 11, 6.	1.3	263
22	Pglyrp-Regulated Gut Microflora <i>Prevotella falsenii</i> , <i>Parabacteroides distasonis</i> and <i>Bacteroides eggerthii</i> Enhance and <i>Alistipes finegoldii</i> Attenuates Colitis in Mice. <i>PLoS ONE</i> , 2016, 11, e0146162.	1.1	259
23	The potential use of bacterial community succession in forensics as described by high throughput metagenomic sequencing. <i>International Journal of Legal Medicine</i> , 2014, 128, 193-205.	1.2	254
24	Chronic wounds and the medical biofilm paradigm. <i>Journal of Wound Care</i> , 2010, 19, 45-53.	0.5	251
25	Evaluation of bacterial diversity in the rumen and feces of cattle fed different levels of dried distillers grains plus solubles using bacterial tag-encoded FLX amplicon pyrosequencing ¹ . <i>Journal of Animal Science</i> , 2010, 88, 3977-3983.	0.2	247
26	Direct sampling of cystic fibrosis lungs indicates that DNA-based analyses of upper-airway specimens can misrepresent lung microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13769-13774.	3.3	232
27	Pyrosequencing and mid-infrared spectroscopy reveal distinct aggregate stratification of soil bacterial communities and organic matter composition. <i>Soil Biology and Biochemistry</i> , 2012, 46, 63-72.	4.2	228
28	Delineating the Specific Influence of Virus Isoelectric Point and Size on Virus Adsorption and Transport through Sandy Soils. <i>Applied and Environmental Microbiology</i> , 1998, 64, 405-410.	1.4	226
29	454 Pyrosequencing Reveals a Shift in Fecal Microbiota of Healthy Adult Men Consuming Polydextrose or Soluble Corn Fiber. <i>Journal of Nutrition</i> , 2012, 142, 1259-1265.	1.3	226
30	Confirmation of the Human-Pathogenic Microsporidia <i>Enterocytozoon bienersi</i> , <i>Encephalitozoon intestinalis</i> , and <i>Vittaforma corneae</i> in Water. <i>Applied and Environmental Microbiology</i> , 1998, 64, 3332-3335.	1.4	224
31	Memory and learning behavior in mice is temporally associated with diet-induced alterations in gut bacteria. <i>Physiology and Behavior</i> , 2009, 96, 557-567.	1.0	215
32	Choline and Osmotic-Stress Tolerance Induced in <i>Arabidopsis</i> by the Soil Microbe <i>Bacillus subtilis</i> (GB03). <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 1097-1104.	1.4	208
33	Generalized antifungal activity and 454-screening of <i>Pseudonocardia</i> and <i>Amycolatopsis</i> bacteria in nests of fungus-growing ants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17805-17810.	3.3	199
34	Target Region Selection Is a Critical Determinant of Community Fingerprints Generated by 16S Pyrosequencing. <i>PLoS ONE</i> , 2011, 6, e20956.	1.1	195
35	Microbiome analysis among bats describes influences of host phylogeny, life history, physiology and geography. <i>Molecular Ecology</i> , 2012, 21, 2617-2627.	2.0	195
36	16S rRNA Gene Pyrosequencing Reveals Bacterial Dysbiosis in the Duodenum of Dogs with Idiopathic Inflammatory Bowel Disease. <i>PLoS ONE</i> , 2012, 7, e39333.	1.1	187

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37	Bacterial Diversity in <i>Solenopsis invicta</i> and <i>Solenopsis geminata</i> Ant Colonies Characterized by 16S amplicon 454 Pyrosequencing. <i>Microbial Ecology</i> , 2011, 61, 821-831.	1.4	178
38	Xylooligosaccharide increases bifidobacteria but not lactobacilli in human gut microbiota. <i>Food and Function</i> , 2014, 5, 436.	2.1	177
39	Inflammation Drives Dysbiosis and Bacterial Invasion in Murine Models of Ileal Crohn's Disease. <i>PLoS ONE</i> , 2012, 7, e41594.	1.1	176
40	The Skin Microbiome in Healthy and Allergic Dogs. <i>PLoS ONE</i> , 2014, 9, e83197.	1.1	173
41	Exploring the Diversity of <i>Gardnerella vaginalis</i> in the Genitourinary Tract Microbiota of Monogamous Couples Through Subtle Nucleotide Variation. <i>PLoS ONE</i> , 2011, 6, e26732.	1.1	172
42	Comparison of Culture and Molecular Identification of Bacteria in Chronic Wounds. <i>International Journal of Molecular Sciences</i> , 2012, 13, 2535-2550.	1.8	172
43	Culture Enriched Molecular Profiling of the Cystic Fibrosis Airway Microbiome. <i>PLoS ONE</i> , 2011, 6, e22702.	1.1	171
44	In vitro multispecies Lubbock chronic wound biofilm model. <i>Wound Repair and Regeneration</i> , 2008, 16, 805-813.	1.5	166
45	The effect of the macrolide antibiotic tylosin on microbial diversity in the canine small intestine as demonstrated by massive parallel 16S rRNA gene sequencing. <i>BMC Microbiology</i> , 2009, 9, 210.	1.3	165
46	Black Box Chimera Check (B2C2): a Windows-Based Software for Batch Depletion of Chimeras from Bacterial 16S rRNA Gene Datasets. <i>Open Microbiology Journal</i> , 2010, 4, 47-52.	0.2	165
47	Detection of Protozoan Parasites and Microsporidia in Irrigation Waters Used for Crop Production. <i>Journal of Food Protection</i> , 2002, 65, 378-382.	0.8	163
48	The rehydration transcriptome of the desiccation-tolerant bryophyte <i>Tortula ruralis</i> : transcript classification and analysis. <i>BMC Genomics</i> , 2004, 5, 89.	1.2	162
49	Survey of fungi and yeast in polymicrobial infections in chronic wounds. <i>Journal of Wound Care</i> , 2011, 20, 40-47.	0.5	155
50	Evaluation of the bacterial diversity among and within individual venous leg ulcers using bacterial tag-encoded FLX and Titanium amplicon pyrosequencing and metagenomic approaches. <i>BMC Microbiology</i> , 2009, 9, 226.	1.3	147
51	Prenatal stress affects placental cytokines and neurotrophins, commensal microbes, and anxiety-like behavior in adult female offspring. <i>Brain, Behavior, and Immunity</i> , 2017, 64, 50-58.	2.0	144
52	Pyrosequencing of 16S rRNA genes in fecal samples reveals high diversity of hindgut microflora in horses and potential links to chronic laminitis. <i>BMC Veterinary Research</i> , 2012, 8, 231.	0.7	143
53	Environment or kin: whence do bees obtain acidophilic bacteria?. <i>Molecular Ecology</i> , 2012, 21, 1754-1768.	2.0	136
54	Maternal methyl-donor supplementation induces prolonged murine offspring colitis susceptibility in association with mucosal epigenetic and microbiomic changes. <i>Human Molecular Genetics</i> , 2011, 20, 1687-1696.	1.4	135

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55	The Role of Biofilms: Are We Hitting the Right Target?. Plastic and Reconstructive Surgery, 2011, 127, 28S-35S.	0.7	129
56	Comparative Analysis of Salivary Bacterial Microbiome Diversity in Edentulous Infants and Their Mothers or Primary Care Givers Using Pyrosequencing. PLoS ONE, 2011, 6, e23503.	1.1	128
57	Colonic mucosal DNA methylation, immune response, and microbiome patterns in Tollâ€like receptor 2â€knockout mice. FASEB Journal, 2011, 25, 1449-1460.	0.2	123
58	A Comparison of Bacterial Composition in Diabetic Ulcers and Contralateral Intact Skin. Open Microbiology Journal, 2010, 4, 8-19.	0.2	122
59	Microbial Population Differentials between Mucosal and Submucosal Intestinal Tissues in Advanced Crohn's Disease of the Ileum. PLoS ONE, 2015, 10, e0134382.	1.1	121
60	A study of ticks and tick-borne livestock pathogens in Pakistan. PLoS Neglected Tropical Diseases, 2017, 11, e0005681.	1.3	121
61	Microbial Dysbiosis in Pediatric Patients with Crohn's Disease. Journal of Clinical Microbiology, 2012, 50, 3258-3266.	1.8	118
62	Fecal microbial communities of healthy adult dogs fed raw meat-based diets with or without inulin or yeast cell wall extracts as assessed by 454 pyrosequencing. FEMS Microbiology Ecology, 2013, 84, 532-541.	1.3	118
63	Windows .NET Network Distributed Basic Local Alignment Search Toolkit (W.ND-BLAST). BMC Bioinformatics, 2005, 6, 93.	1.2	117
64	Xylooligosaccharide supplementation alters gut bacteria in both healthy and prediabetic adults: a pilot study. Frontiers in Physiology, 2015, 6, 216.	1.3	117
65	Effect of a multi-species synbiotic formulation on fecal bacterial microbiota of healthy cats and dogs as evaluated by pyrosequencing. FEMS Microbiology Ecology, 2011, 78, 542-554.	1.3	116
66	An Insight Into the Microbiome of the<i>Amblyomma maculatum</i>(Acari: Ixodidae). Journal of Medical Entomology, 2014, 51, 119-129.	0.9	115
67	Frequency-dependent response of the vascular endothelium to pulsatile shear stress. American Journal of Physiology - Heart and Circulatory Physiology, 2007, 293, H645-H653.	1.5	112
68	Distinct Soil Bacterial Communities Revealed under a Diversely Managed Agroecosystem. PLoS ONE, 2012, 7, e40338.	1.1	112
69	Effect of the proton pump inhibitor omeprazole on the gastrointestinal bacterial microbiota of healthy dogs. FEMS Microbiology Ecology, 2012, 80, 624-636.	1.3	111
70	A Survey of Bacterial Diversity From Successive Life Stages of Black Soldier Fly (Diptera:) Tj ETQq0 0 0 rgBT /Overlock, 10 Tf 50,142 Td (S	0.9	111
71	Evaluation of the bacterial diversity of Pressure ulcers using bTEFAP pyrosequencing. BMC Medical Genomics, 2010, 3, 41.	0.7	108
72	Pyrosequencing analysis for characterization of soil bacterial populations as affected by an integrated livestock-cotton production system. Applied Soil Ecology, 2010, 45, 13-25.	2.1	105

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73	Faecal microbiota in lean and obese dogs. <i>FEMS Microbiology Ecology</i> , 2013, 84, 332-343.	1.3	103
74	The gut microbiome of kittens is affected by dietary protein:carbohydrate ratio and associated with blood metabolite and hormone concentrations. <i>British Journal of Nutrition</i> , 2013, 109, 1637-1646.	1.2	103
75	Modulation of the faecal microbiome of healthy adult dogs by inclusion of potato fibre in the diet. <i>British Journal of Nutrition</i> , 2015, 113, 125-133.	1.2	99
76	Gut Microbiome of an 11th Century A.D. Pre-Columbian Andean Mummy. <i>PLoS ONE</i> , 2015, 10, e0138135.	1.1	97
77	Comparative Metagenomic Analysis of Soil Microbial Communities across Three Hexachlorocyclohexane Contamination Levels. <i>PLoS ONE</i> , 2012, 7, e46219.	1.1	97
78	A metagenomic assessment of the bacteria associated with <i>Lucilia sericata</i> and <i>Lucilia cuprina</i> (Diptera: Tj ETQq0 0,0 rgBT /Overlock 10	1.7	95
79	Histamineâ€2 Receptor Blockers Alter the Fecal Microbiota in Premature Infants. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2013, 56, 397-400.	0.9	94
80	Gene-centric metagenomics analysis of feline intestinal microbiome using 454 junior pyrosequencing. <i>Journal of Microbiological Methods</i> , 2012, 88, 369-376.	0.7	93
81	Evaluation of the bacterial diversity in cecal contents of laying hens fed various molting diets by using bacterial tag-encoded FLX amplicon pyrosequencing. <i>Poultry Science</i> , 2009, 88, 298-302.	1.5	92
82	The structures of the colonic mucosa-associated and luminal microbial communities are distinct and differentially affected by a prolonged murine stressor. <i>Gut Microbes</i> , 2014, 5, 748-760.	4.3	91
83	Prospective randomized controlled study on the effects of <i>Saccharomyces boulardii</i> CNCM I-745 and amoxicillin-clavulanate or the combination on the gut microbiota of healthy volunteers. <i>Gut Microbes</i> , 2017, 8, 17-32.	4.3	89
84	Tag-Encoded FLX Amplicon Pyrosequencing for the Elucidation of Microbial and Functional Gene Diversity in Any Environment. <i>Methods in Molecular Biology</i> , 2011, 733, 129-141.	0.4	84
85	Abundance and short-term temporal variability of fecal microbiota in healthy dogs. <i>MicrobiologyOpen</i> , 2012, 1, 340-347.	1.2	84
86	Composition and function of the pediatric colonic mucosal microbiome in untreated patients with ulcerative colitis. <i>Gut Microbes</i> , 2016, 7, 384-396.	4.3	84
87	Bacteria Mediate Oviposition by the Black Soldier Fly, <i>Hermetia illucens</i> (L.), (Diptera: Stratiomyidae). <i>Scientific Reports</i> , 2013, 3, 2563.	1.6	83
88	Bioaerosol Transport Modeling and Risk Assessment in Relation to Biosolid Placement. <i>Journal of Environmental Quality</i> , 2000, 29, 343-348.	1.0	81
89	L-Arginine Destabilizes Oral Multi-Species Biofilm Communities Developed in Human Saliva. <i>PLoS ONE</i> , 2015, 10, e0121835.	1.1	81
90	Effects of Dietary Fiber on the Feline Gastrointestinal Metagenome. <i>Journal of Proteome Research</i> , 2012, 11, 5924-5933.	1.8	79

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91	Endophyte Microbiome Diversity in Micropropagated <i>Atriplex canescens</i> and <i>Atriplex torreyi</i> var <i>griffithsii</i> . PLoS ONE, 2011, 6, e17693.	1.1	77
92	The fungal microbiome in chronic rhinosinusitis: richness, diversity, postoperative changes and patient outcomes. International Forum of Allergy and Rhinology, 2014, 4, 259-265.	1.5	76
93	Small RNA profiling reveals antisense transcription throughout the KSHV genome and novel small RNAs. Rna, 2010, 16, 1540-1558.	1.6	74
94	Intestinal aganglionosis is associated with early and sustained disruption of the colonic microbiome. Neurogastroenterology and Motility, 2012, 24, 874.	1.6	74
95	Gene expression profiling in chicken heterophils with <i>Salmonella enteritidis</i> stimulation using a chicken 44 K Agilent microarray. BMC Genomics, 2008, 9, 526.	1.2	73
96	A high-throughput microfluidic dental plaque biofilm system to visualize and quantify the effect of antimicrobials. Journal of Antimicrobial Chemotherapy, 2013, 68, 2550-2560.	1.3	73
97	Effect of sublethal heat stress on <i>Salmonella Typhimurium</i> virulence. Journal of Applied Microbiology, 2011, 110, 813-822.	1.4	71
98	Characterization of a newly developed chicken 44K Agilent microarray. BMC Genomics, 2008, 9, 60.	1.2	68
99	Photoperiod modulates gut bacteria composition in male Siberian hamsters (<i>Phodopus sungorus</i>). Brain, Behavior, and Immunity, 2010, 24, 577-584.	2.0	68
100	Intestinal dysbiosis and bacterial enteroinvasion in a murine model of Hirschsprung's disease. Journal of Pediatric Surgery, 2014, 49, 1242-1251.	0.8	68
101	Confirmed detection of <i>Cyclospora cayentensis</i> , <i>Encephalitozoon intestinalis</i> and <i>Cryptosporidium parvum</i> in water used for drinking. Journal of Water and Health, 2003, 1, 117-123.	1.1	66
102	Microbial Community Composition as Affected by Dryland Cropping Systems and Tillage in a Semiarid Sandy Soil. Diversity, 2010, 2, 910-931.	0.7	66
103	Transcriptome Analysis of Genes Controlled by <i>luxS</i> /Autoinducer-2 in <i>Salmonella enterica</i> Serovar <i>Typhimurium</i> . Foodborne Pathogens and Disease, 2010, 7, 399-410.	0.8	65
104	Characterization of Bacterial Communities in Venous Insufficiency Wounds by Use of Conventional Culture and Molecular Diagnostic Methods. Journal of Clinical Microbiology, 2011, 49, 3812-3819.	1.8	65
105	Effects of polysaccharopeptide from <i>Trametes Versicolor</i> and amoxicillin on the gut microbiome of healthy volunteers. Gut Microbes, 2014, 5, 458-467.	4.3	64
106	Microbiomes of ant castes implicate new microbial roles in the fungus-growing ant <i>Trachymyrmex septentrionalis</i> . Scientific Reports, 2011, 1, 204.	1.6	63
107	Iron regulated genes of <i>Salmonella enterica</i> serovar <i>Typhimurium</i> in response to norepinephrine and the requirement of <i>fepDGC</i> for norepinephrine-enhanced growth. Microbes and Infection, 2008, 10, 807-816.	1.0	62
108	Immune and production responses of dairy cows to postruminal supplementation with phytonutrients. Journal of Dairy Science, 2013, 96, 7830-7843.	1.4	62

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109	Molecular characterization of the polymicrobial flora in chronic rhinosinusitis. <i>Journal of Otolaryngology - Head and Neck Surgery</i> , 2010, 39, 182-7.	0.9	61
110	Equine Stomachs Harbor an Abundant and Diverse Mucosal Microbiota. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2522-2532.	1.4	60
111	Transcriptome Profiling of the Intoxication Response of <i>Tenebrio molitor</i> Larvae to <i>Bacillus thuringiensis</i> Cry3Aa Protoxin. <i>PLoS ONE</i> , 2012, 7, e34624.	1.1	60
112	Rumen bacterial, archaeal, and fungal diversity of dairy cows in response to ingestion of lauric or myristic acid1. <i>Journal of Animal Science</i> , 2012, 90, 4449-4457.	0.2	59
113	Effects of a synbiotic on fecal quality, short-chain fatty acid concentrations, and the microbiome of healthy sled dogs. <i>BMC Veterinary Research</i> , 2013, 9, 246.	0.7	59
114	Differences in the faecal microbiome of non-diarrhoeic clinically healthy dogs and cats associated with <i>Giardia duodenalis</i> infection: impact of hookworms and coccidia. <i>International Journal for Parasitology</i> , 2015, 45, 585-594.	1.3	59
115	Dogs Leaving the ICU Carry a Very Large Multi-Drug Resistant Enterococcal Population with Capacity for Biofilm Formation and Horizontal Gene Transfer. <i>PLoS ONE</i> , 2011, 6, e22451.	1.1	58
116	Consumption of different soymilk formulations differentially affects the gut microbiomes of overweight and obese men. <i>Gut Microbes</i> , 2012, 3, 490-500.	4.3	58
117	Culture-Independent Characterization of Bacteria and Fungi in a Poultry Bioaerosol Using Pyrosequencing: A New Approach. <i>Journal of Occupational and Environmental Hygiene</i> , 2010, 7, 693-699.	0.4	56
118	Complete Genome Sequence of Adherent Invasive <i>Escherichia coli</i> UM146 Isolated from Ileal Crohn's Disease Biopsy Tissue. <i>Journal of Bacteriology</i> , 2011, 193, 583-583.	1.0	55
119	CattleTickBase: An integrated Internet-based bioinformatics resource for <i>Rhipicephalus (Boophilus) microplus</i> . <i>International Journal for Parasitology</i> , 2012, 42, 161-169.	1.3	55
120	Influence of wet distillers grains diets on beef cattle fecal bacterial community structure. <i>BMC Microbiology</i> , 2012, 12, 25.	1.3	51
121	Characterization of the Fungal Microbiome (Mycobiome) in Fecal Samples from Dogs. <i>Veterinary Medicine International</i> , 2013, 2013, 1-8.	0.6	51
122	A Multi-Platform Draft de novo Genome Assembly and Comparative Analysis for the Scarlet Macaw (<i>Ara macao</i>). <i>PLoS ONE</i> , 2013, 8, e62415.	1.1	51
123	Development of colonic microflora as assessed by pyrosequencing in dairy calves fed waste milk. <i>Journal of Dairy Science</i> , 2012, 95, 4519-4525.	1.4	49
124	Functional divergence in gastrointestinal microbiota in physically-separated genetically identical mice. <i>Scientific Reports</i> , 2014, 4, 5437.	1.6	49
125	Detecting Microbial Dysbiosis Associated with Pediatric Crohn Disease Despite the High Variability of the Gut Microbiota. <i>Cell Reports</i> , 2016, 14, 945-955.	2.9	49
126	<i>Escherichia coli</i> O157:H7 gene expression in the presence of catecholamine norepinephrine. <i>FEMS Microbiology Letters</i> , 2007, 273, 214-223.	0.7	48

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127	Evolution of the Bovine TLR Gene Family and Member Associations with Mycobacterium avium Subspecies Paratuberculosis Infection. PLoS ONE, 2011, 6, e27744.	1.1	48
128	Ovine pedomics: the first study of the ovine foot 16S rRNA-based microbiome. ISME Journal, 2011, 5, 1426-1437.	4.4	46
129	Soil Rhizosphere Microbial Communities and Enzyme Activities under Organic Farming in Alabama. Diversity, 2011, 3, 308-328.	0.7	45
130	Microarray based comparison of two Escherichia coli O157:H7 lineages. BMC Microbiology, 2006, 6, 30.	1.3	44
131	Mining and validating grape (Vitis L.) ESTs to develop EST-SSR markers for genotyping and mapping. Molecular Breeding, 2011, 28, 241-254.	1.0	44
132	Microbiota Separation and C-reactive Protein Elevation in Treatment-naïve Pediatric Granulomatous Crohn Disease. Journal of Pediatric Gastroenterology and Nutrition, 2012, 55, 243-250.	0.9	44
133	Genome-Wide Polymorphism and Comparative Analyses in the White-Tailed Deer (Odocoileus Tj ETQq1 1 0.784314 rgBT /Overlock 10 F	1.1	41
134	Longitudinal shifts in bacterial diversity and fermentation pattern in the rumen of steers grazing wheat pasture. Anaerobe, 2014, 30, 11-17.	1.0	41
135	PCR Amplification and Species Determination of Microsporidia in Formalin-Fixed Feces after Immunomagnetic Separation. Applied and Environmental Microbiology, 1998, 64, 333-336.	1.4	40
136	Culture Independent Survey of the Microbiota of the Glassy-Winged Sharpshooter (<i>Homalodisca</i> Tj ETQq0 0 0 rgBT /Overlock 10 F	0.7	39
137	Characterization of Metabolically Active Bacterial Populations in Subseafloor Nankai Trough Sediments above, within, and below the Sulfate-Methane Transition Zone. Frontiers in Microbiology, 2012, 3, 113.	1.5	39
138	Effect of dark sweet cherry powder consumption on the gut microbiota, short-chain fatty acids, and biomarkers of gut health in obese db/db mice. PeerJ, 2018, 6, e4195.	0.9	39
139	Impact of Short-Term Acidification on Nitrification and Nitrifying Bacterial Community Dynamics in Soilless Cultivation Media. Applied and Environmental Microbiology, 2012, 78, 6576-6582.	1.4	38
140	Diversity of Bacterial Communities of Fitness Center Surfaces in a U.S. Metropolitan Area. International Journal of Environmental Research and Public Health, 2014, 11, 12544-12561.	1.2	38
141	Fungal Microbiota Profile in Newly Diagnosed Treatment-naïve Children with Crohn's Disease. Journal of Crohn's and Colitis, 2017, 11, 586-592.	0.6	38
142	Coaggregation occurs amongst bacteria within and between biofilms in domestic showerheads. Biofouling, 2013, 29, 53-68.	0.8	37
143	Gut transcriptome of replete adult female cattle ticks, Rhipicephalus (Boophilus) microplus, feeding upon a Babesia bovis-infected bovine host. Parasitology Research, 2013, 112, 3075-3090.	0.6	37
144	A rapid viability assay for Cryptosporidium oocysts and Giardia cysts for use in conjunction with indirect fluorescent antibody detection. Canadian Journal of Microbiology, 1997, 43, 658-662.	0.8	36

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145	Pyrosequencing-Based Analysis of the Microbiome Associated with the Horn Fly, <i>Haematobia irritans</i> . PLoS ONE, 2012, 7, e44390.	1.1	35
146	Microbiota profile in new-onset pediatric Crohn's disease: data from a non-Western population. Gut Pathogens, 2018, 10, 49.	1.6	35
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