

Scot E Dowd

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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.

252
papers

18,830
citations

75
h-index

130
g-index

258
ext. papers

21,909
ext. citations

4.2
avg, IF

6.64
L-index

#	Paper	IF	Citations
252	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	4.5	841
251	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	16.6	694
250	Pyrosequencing study of fecal microflora of autistic and control children. <i>Anaerobe</i> , 2010 , 16, 444-53	2.8	617
249	Survey of bacterial diversity in chronic wounds using pyrosequencing, DGGE, and full ribosome shotgun sequencing. <i>BMC Microbiology</i> , 2008 , 8, 43	4.5	532
248	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	3.7	380
247	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	7.5	369
246	Soil bacteria confer plant salt tolerance by tissue-specific regulation of the sodium transporter HKT1. <i>Molecular Plant-Microbe Interactions</i> , 2008 , 21, 737-44	3.6	339
245	Bacterial tag-encoded FLX amplicon pyrosequencing (bTEFAP) for microbiome studies: bacterial diversity in the ileum of newly weaned Salmonella-infected pigs. <i>Foodborne Pathogens and Disease</i> , 2008 , 5, 459-72	3.8	319
244	Diversity of the human skin microbiome early in life. <i>Journal of Investigative Dermatology</i> , 2011 , 131, 2026-32	4.3	302
243	Biofilm maturity studies indicate sharp debridement opens a time- dependent therapeutic window. <i>Journal of Wound Care</i> , 2010 , 19, 320-8	2.2	280
242	Biofilms and chronic wound inflammation. <i>Journal of Wound Care</i> , 2008 , 17, 333-41	2.2	273
241	Inherent bacterial DNA contamination of extraction and sequencing reagents may affect interpretation of microbiota in low bacterial biomass samples. <i>Gut Pathogens</i> , 2016 , 8, 24	5.4	266
240	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, 301-10	4.3	259
239	A soil bacterium regulates plant acquisition of iron via deficiency-inducible mechanisms. <i>Plant Journal</i> , 2009 , 58, 568-77	6.9	254
238	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, 1509-19	3.7	247
237	The fecal microbiome in dogs with acute diarrhea and idiopathic inflammatory bowel disease. <i>PLoS ONE</i> , 2012 , 7, e51907	3.7	237
236	Phylogenetic and gene-centric metagenomics of the canine intestinal microbiome reveals similarities with humans and mice. <i>ISME Journal</i> , 2011 , 5, 639-49	11.9	229

235	An in vivo polymicrobial biofilm wound infection model to study interspecies interactions. <i>PLoS ONE</i> , 2011 , 6, e27317	3.7	217
234	Rumen bacterial diversity dynamics associated with changing from bermudagrass hay to grazed winter wheat diets. <i>Microbial Ecology</i> , 2010 , 59, 511-22	4.4	212
233	Assessment of bacterial diversity in the cattle tick <i>Rhipicephalus (Boophilus) microplus</i> through tag-encoded pyrosequencing. <i>BMC Microbiology</i> , 2011 , 11, 6	4.5	204
232	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. <i>Journal of Animal Science</i> , 2010 , 88, 3977-83	0.7	204
231	Exposure to a social stressor disrupts the community structure of the colonic mucosa-associated microbiota. <i>BMC Microbiology</i> , 2014 , 14, 189	4.5	203
230	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, 3332-5	4.8	201
229	Chronic wounds and the medical biofilm paradigm. <i>Journal of Wound Care</i> , 2010 , 19, 45-6, 48-50, 52-3	2.2	200
228	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, 13769-74	11.5	200
227	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, 405-10	4.8	199
226	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	3.1	190
225	Memory and learning behavior in mice is temporally associated with diet-induced alterations in gut bacteria. <i>Physiology and Behavior</i> , 2009 , 96, 557-67	3.5	180
224	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, 1259-65	4.1	178
223	Target region selection is a critical determinant of community fingerprints generated by 16S pyrosequencing. <i>PLoS ONE</i> , 2011 , 6, e20956	3.7	174
222	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	7.5	168
221	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, 17805-10	11.5	168
220	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, 1097-104	3.6	165
219	Culture enriched molecular profiling of the cystic fibrosis airway microbiome. <i>PLoS ONE</i> , 2011 , 6, e22702	3.7	152
218	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	0.8	150

217	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, 821-31	4.4	149
216	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	3.7	147
215	Detection of protozoan parasites and microsporidia in irrigation waters used for crop production. <i>Journal of Food Protection</i> , 2002 , 65, 378-82	2.5	145
214	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	3.7	141
213	Microbiome analysis among bats describes influences of host phylogeny, life history, physiology and geography. <i>Molecular Ecology</i> , 2012 , 21, 2617-27	5.7	140
212	Inflammation drives dysbiosis and bacterial invasion in murine models of ileal Crohn's disease. <i>PLoS ONE</i> , 2012 , 7, e41594	3.7	140
211	16S rRNA gene pyrosequencing reveals bacterial dysbiosis in the duodenum of dogs with idiopathic inflammatory bowel disease. <i>PLoS ONE</i> , 2012 , 7, e39333	3.7	137
210	Xylooligosaccharide increases bifidobacteria but not lactobacilli in human gut microbiota. <i>Food and Function</i> , 2014 , 5, 436-45	6.1	134
209	Comparison of culture and molecular identification of bacteria in chronic wounds. <i>International Journal of Molecular Sciences</i> , 2012 , 13, 2535-50	6.3	133
208	In vitro multispecies Lubbock chronic wound biofilm model. <i>Wound Repair and Regeneration</i> , 2008 , 16, 805-13	3.6	132
207	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	4.5	130
206	The skin microbiome in healthy and allergic dogs. <i>PLoS ONE</i> , 2014 , 9, e83197	3.7	125
205	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	4.5	124
204	The rehydration transcriptome of the desiccation-tolerant bryophyte <i>Tortula ruralis</i> : transcript classification and analysis. <i>BMC Genomics</i> , 2004 , 5, 89	4.5	124
203	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, 1687-96	5.6	117
202	Survey of fungi and yeast in polymicrobial infections in chronic wounds. <i>Journal of Wound Care</i> , 2011 , 20, 40-7	2.2	111
201	Windows .NET Network Distributed Basic Local Alignment Search Toolkit (W.ND-BLAST). <i>BMC Bioinformatics</i> , 2005 , 6, 93	3.6	108
200	Comparative analysis of salivary bacterial microbiome diversity in edentulous infants and their mothers or primary care givers using pyrosequencing. <i>PLoS ONE</i> , 2011 , 6, e23503	3.7	108

199	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	16.6	106
198	The role of biofilms: are we hitting the right target?. <i>Plastic and Reconstructive Surgery</i> , 2011 , 127 Suppl 1, 28S-35S	2.7	104
197	Colonic mucosal DNA methylation, immune response, and microbiome patterns in Toll-like receptor 2-knockout mice. <i>FASEB Journal</i> , 2011 , 25, 1449-60	0.9	104
196	A comparison of bacterial composition in diabetic ulcers and contralateral intact skin. <i>Open Microbiology Journal</i> , 2010 , 4, 8-19	0.8	102
195	Environment or kin: whence do bees obtain acidophilic bacteria?. <i>Molecular Ecology</i> , 2012 , 21, 1754-68	5.7	99
194	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	2.7	99
193	Frequency-dependent response of the vascular endothelium to pulsatile shear stress. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2007 , 293, H645-53	5.2	95
192	Effect of a multi-species synbiotic formulation on fecal bacterial microbiota of healthy cats and dogs as evaluated by pyrosequencing. <i>FEMS Microbiology Ecology</i> , 2011 , 78, 542-54	4.3	91
191	Distinct soil bacterial communities revealed under a diversely managed agroecosystem. <i>PLoS ONE</i> , 2012 , 7, e40338	3.7	91
190	An insight into the microbiome of the <i>Amblyomma maculatum</i> (Acari: Ixodidae). <i>Journal of Medical Entomology</i> , 2014 , 51, 119-29	2.2	90
189	Pyrosequencing analysis for characterization of soil bacterial populations as affected by an integrated livestock-cotton production system. <i>Applied Soil Ecology</i> , 2010 , 45, 13-25	5	90
188	Microbial dysbiosis in pediatric patients with Crohn's disease. <i>Journal of Clinical Microbiology</i> , 2012 , 50, 3258-66	9.7	89
187	Microbial Population Differentials between Mucosal and Submucosal Intestinal Tissues in Advanced Crohn's Disease of the Ileum. <i>PLoS ONE</i> , 2015 , 10, e0134382	3.7	87
186	Effect of the proton pump inhibitor omeprazole on the gastrointestinal bacterial microbiota of healthy dogs. <i>FEMS Microbiology Ecology</i> , 2012 , 80, 624-36	4.3	86
185	Evaluation of the bacterial diversity of pressure ulcers using bTEFAP pyrosequencing. <i>BMC Medical Genomics</i> , 2010 , 3, 41	3.7	86
184	A survey of bacterial diversity from successive life stages of black soldier fly (Diptera: Stratiomyidae) by using 16S rDNA pyrosequencing. <i>Journal of Medical Entomology</i> , 2013 , 50, 647-58	2.2	82
183	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	3.9	82
182	Histamine-2 receptor blockers alter the fecal microbiota in premature infants. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2013 , 56, 397-400	2.8	80

181	Xylooligosaccharide supplementation alters gut bacteria in both healthy and prediabetic adults: a pilot study. <i>Frontiers in Physiology</i> , 2015 , 6, 216	4.6	79
180	Gut Microbiome of an 11th Century A.D. Pre-Columbian Andean Mummy. <i>PLoS ONE</i> , 2015 , 10, e0138135	3.7	78
179	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, 129-41	1.4	76
178	Comparative metagenomic analysis of soil microbial communities across three hexachlorocyclohexane contamination levels. <i>PLoS ONE</i> , 2012 , 7, e46219	3.7	76
177	Gene-centric metagenomics analysis of feline intestinal microbiome using 454 junior pyrosequencing. <i>Journal of Microbiological Methods</i> , 2012 , 88, 369-76	2.8	75
176	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. <i>FEMS Microbiology Ecology</i> , 2013 , 84, 532-43	4.3	71
175	Faecal microbiota in lean and obese dogs. <i>FEMS Microbiology Ecology</i> , 2013 , 84, 332-43	4.3	71
174	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, 1637-46	3.6	71
173	A metagenomic assessment of the bacteria associated with <i>Lucilia sericata</i> and <i>Lucilia cuprina</i> (Diptera: Calliphoridae). <i>Applied Microbiology and Biotechnology</i> , 2015 , 99, 869-83	5.7	70
172	Bioaerosol Transport Modeling and Risk Assessment in Relation to Biosolid Placement. <i>Journal of Environmental Quality</i> , 2000 , 29, 343-348	3.4	70
171	Small RNA profiling reveals antisense transcription throughout the KSHV genome and novel small RNAs. <i>Rna</i> , 2010 , 16, 1540-58	5.8	69
170	A study of ticks and tick-borne livestock pathogens in Pakistan. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005681	4.8	68
169	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, 748-60	8.8	66
168	Endophyte microbiome diversity in micropropagated <i>Atriplex canescens</i> and <i>Atriplex torreyi</i> var <i>griffithsii</i> . <i>PLoS ONE</i> , 2011 , 6, e17693	3.7	65
167	Composition and function of the pediatric colonic mucosal microbiome in untreated patients with ulcerative colitis. <i>Gut Microbes</i> , 2016 , 7, 384-96	8.8	65
166	Effects of dietary fiber on the feline gastrointestinal metagenome. <i>Journal of Proteome Research</i> , 2012 , 11, 5924-33	5.6	63
165	Abundance and short-term temporal variability of fecal microbiota in healthy dogs. <i>MicrobiologyOpen</i> , 2012 , 1, 340-7	3.4	62
164	Characterization of a newly developed chicken 44K Agilent microarray. <i>BMC Genomics</i> , 2008 , 9, 60	4.5	62

163	Gene expression profiling in chicken heterophils with <i>Salmonella enteritidis</i> stimulation using a chicken 44 K Agilent microarray. <i>BMC Genomics</i> , 2008 , 9, 526	4.5	60
162	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	8.8	59
161	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, 125-33	3.6	58
160	Effect of sublethal heat stress on <i>Salmonella Typhimurium</i> virulence. <i>Journal of Applied Microbiology</i> , 2011 , 110, 813-22	4.7	58
159	A high-throughput microfluidic dental plaque biofilm system to visualize and quantify the effect of antimicrobials. <i>Journal of Antimicrobial Chemotherapy</i> , 2013 , 68, 2550-60	5.1	57
158	L-arginine destabilizes oral multi-species biofilm communities developed in human saliva. <i>PLoS ONE</i> , 2015 , 10, e0121835	3.7	57
157	Bacteria mediate oviposition by the black soldier fly, <i>Hermetia illucens</i> (L.), (Diptera: Stratiomyidae). <i>Scientific Reports</i> , 2013 , 3, 2563	4.9	57
156	Microbial Community Composition as Affected by Dryland Cropping Systems and Tillage in a Semiarid Sandy Soil. <i>Diversity</i> , 2010 , 2, 910-931	2.5	56
155	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. <i>Microbes and Infection</i> , 2008 , 10, 807-16	9.3	56
154	Molecular characterization of the polymicrobial flora in chronic rhinosinusitis. <i>Journal of Otolaryngology - Head and Neck Surgery</i> , 2010 , 39, 182-7	5.4	56
153	Intestinal aganglionosis is associated with early and sustained disruption of the colonic microbiome. <i>Neurogastroenterology and Motility</i> , 2012 , 24, 874-e400	4	55
152	Confirmed detection of <i>Cyclospora cayetanensis</i> , <i>Encephalitozoon intestinalis</i> and <i>Cryptosporidium parvum</i> in water used for drinking. <i>Journal of Water and Health</i> , 2003 , 1, 117-123	2.2	53
151	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	3.7	52
150	CattleTickBase: an integrated Internet-based bioinformatics resource for <i>Rhipicephalus (Boophilus) microplus</i> . <i>International Journal for Parasitology</i> , 2012 , 42, 161-9	4.3	51
149	Transcriptome analysis of genes controlled by <i>luxS</i> /autoinducer-2 in <i>Salmonella enterica</i> serovar <i>Typhimurium</i> . <i>Foodborne Pathogens and Disease</i> , 2010 , 7, 399-410	3.8	51
148	Microbiomes of ant castes implicate new microbial roles in the fungus-growing ant <i>Trachymyrmex septentrionalis</i> . <i>Scientific Reports</i> , 2011 , 1, 204	4.9	51
147	Equine stomachs harbor an abundant and diverse mucosal microbiota. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 2522-32	4.8	51
146	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, 693-9	2.9	50

145	Rumen bacterial, archaeal, and fungal diversity of dairy cows in response to ingestion of lauric or myristic acid. <i>Journal of Animal Science</i> , 2012 , 90, 4449-57	0.7	50
144	Characterization of bacterial communities in venous insufficiency wounds by use of conventional culture and molecular diagnostic methods. <i>Journal of Clinical Microbiology</i> , 2011 , 49, 3812-9	9.7	47
143	Complete genome sequence of adherent invasive Escherichia coli UM146 isolated from ileal Crohn's disease biopsy tissue. <i>Journal of Bacteriology</i> , 2011 , 193, 583	3.5	47
142	Differences in the faecal microbiome of non-diarrhoeic clinically healthy dogs and cats associated with Giardia duodenalis infection: impact of hookworms and coccidia. <i>International Journal for Parasitology</i> , 2015 , 45, 585-94	4.3	46
141	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	2.7	46
140	Immune and production responses of dairy cows to postruminal supplementation with phytonutrients. <i>Journal of Dairy Science</i> , 2013 , 96, 7830-43	4	46
139	Effects of polysaccharopeptide from Trametes versicolor and amoxicillin on the gut microbiome of healthy volunteers: a randomized clinical trial. <i>Gut Microbes</i> , 2014 , 5, 458-67	8.8	46
138	Intestinal dysbiosis and bacterial enteroinvasion in a murine model of Hirschsprung's disease. <i>Journal of Pediatric Surgery</i> , 2014 , 49, 1242-51	2.6	45
137	Photoperiod modulates gut bacteria composition in male Siberian hamsters (Phodopus sungorus). <i>Brain, Behavior, and Immunity</i> , 2010 , 24, 577-84	16.6	45
136	Consumption of different soymilk formulations differentially affects the gut microbiomes of overweight and obese men. <i>Gut Microbes</i> , 2012 , 3, 490-500	8.8	44
135	Escherichia coli O157:H7 gene expression in the presence of catecholamine norepinephrine. <i>FEMS Microbiology Letters</i> , 2007 , 273, 214-23	2.9	44
134	Functional divergence in gastrointestinal microbiota in physically-separated genetically identical mice. <i>Scientific Reports</i> , 2014 , 4, 5437	4.9	41
133	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	3.7	41
132	The fungal microbiome in chronic rhinosinusitis: richness, diversity, postoperative changes and patient outcomes. <i>International Forum of Allergy and Rhinology</i> , 2014 , 4, 259-65	6.3	40
131	Microarray based comparison of two Escherichia coli O157:H7 lineages. <i>BMC Microbiology</i> , 2006 , 6, 30	4.5	40
130	A multi-platform draft de novo genome assembly and comparative analysis for the Scarlet Macaw (Ara macao). <i>PLoS ONE</i> , 2013 , 8, e62415	3.7	39
129	Characterization of the fungal microbiome (mycobiome) in fecal samples from dogs. <i>Veterinary Medicine International</i> , 2013 , 2013, 658373	1.5	38
128	Mining and validating grape (Vitis L.) ESTs to develop EST-SSR markers for genotyping and mapping. <i>Molecular Breeding</i> , 2011 , 28, 241-254	3.4	38

127	Microbiota separation and C-reactive protein elevation in treatment-naïve pediatric granulomatous Crohn disease. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2012 , 55, 243-50	2.8	38
126	Soil Rhizosphere Microbial Communities and Enzyme Activities under Organic Farming in Alabama. <i>Diversity</i> , 2011 , 3, 308-328	2.5	37
125	Evolution of the bovine TLR gene family and member associations with Mycobacterium avium subspecies paratuberculosis infection. <i>PLoS ONE</i> , 2011 , 6, e27744	3.7	37
124	Detecting Microbial Dysbiosis Associated with Pediatric Crohn Disease Despite the High Variability of the Gut Microbiota. <i>Cell Reports</i> , 2016 , 14, 945-955	10.6	36
123	Genome-wide polymorphism and comparative analyses in the white-tailed deer (<i>Odocoileus virginianus</i>): a model for conservation genomics. <i>PLoS ONE</i> , 2011 , 6, e15811	3.7	35
122	Influence of wet distillers grains diets on beef cattle fecal bacterial community structure. <i>BMC Microbiology</i> , 2012 , 12, 25	4.5	34
121	Development of colonic microflora as assessed by pyrosequencing in dairy calves fed waste milk. <i>Journal of Dairy Science</i> , 2012 , 95, 4519-25	4	33
120	Coaggregation occurs amongst bacteria within and between biofilms in domestic showerheads. <i>Biofouling</i> , 2013 , 29, 53-68	3.3	32
119	Ovine pedomics: the first study of the ovine foot 16S rRNA-based microbiome. <i>ISME Journal</i> , 2011 , 5, 1426-37	11.9	32
118	A rapid viability assay for Cryptosporidium oocysts and Giardia cysts for use in conjunction with indirect fluorescent antibody detection. <i>Canadian Journal of Microbiology</i> , 1997 , 43, 658-62	3.2	32
117	Gut transcriptome of replete adult female cattle ticks, Rhipicephalus (Boophilus) microplus, feeding upon a Babesia bovis-infected bovine host. <i>Parasitology Research</i> , 2013 , 112, 3075-90	2.4	31
116	Thermotolerant Clostridia as an Airborne Pathogen Indicator during Land Application of Biosolids. <i>Journal of Environmental Quality</i> , 1997 , 26, 194-199	3.4	31
115	Diversity of bacterial communities of fitness center surfaces in a U.S. metropolitan area. <i>International Journal of Environmental Research and Public Health</i> , 2014 , 11, 12544-61	4.6	30
114	Culture independent survey of the microbiota of the glassy-winged sharpshooter (<i>Homalodisca vitripennis</i>) using 454 pyrosequencing. <i>Environmental Entomology</i> , 2011 , 40, 23-9	2.1	30
113	PCR amplification and species determination of microsporidia in formalin-fixed feces after immunomagnetic separation. <i>Applied and Environmental Microbiology</i> , 1998 , 64, 333-6	4.8	30
112	Inability of polymerase chain reaction, pyrosequencing, and culture of infected and uninfected site skin biopsy specimens to identify the cause of cellulitis. <i>Clinical Infectious Diseases</i> , 2015 , 61, 1679-87	11.6	29
111	Impact of short-term acidification on nitrification and nitrifying bacterial community dynamics in soilless cultivation media. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 6576-82	4.8	29
110	Prospecting environmental mycobacteria: combined molecular approaches reveal unprecedented diversity. <i>PLoS ONE</i> , 2013 , 8, e68648	3.7	29

109	Gene expression profiling within the spleen of <i>Clostridium perfringens</i> -challenged broilers fed antibiotic-medicated and non-medicated diets. <i>BMC Genomics</i> , 2009 , 10, 260	4.5	29
108	A combined subtractive suppression hybridization and expression profiling strategy to identify novel desiccation response transcripts from <i>Tortula ruralis</i> gametophytes. <i>Physiologia Plantarum</i> , 2009 , 136, 437-60	4.6	29
107	Pyrosequencing-based analysis of the microbiome associated with the horn fly, <i>Haematobia irritans</i> . <i>PLoS ONE</i> , 2012 , 7, e44390	3.7	28
106	Characterization of Metabolically Active Bacterial Populations in Subseafloor Nankai Trough Sediments above, within, and below the Sulfate-Methane Transition Zone. <i>Frontiers in Microbiology</i> , 2012 , 3, 113	5.7	28
105	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. <i>PeerJ</i> , 2018 , 6, e4195	3.1	28
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- 1 Analysis of the microbial diversity in the fecal material of the critically endangered African wild dog, *Lycaon pictus*. *Archives of Microbiology*, **2021**, 204, 42 3