

Joseph F Petrosino

List of Publications by Year in descending order

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Version: 2024-02-01

208
papers

32,936
citations

10984

71
h-index

4431

172
g-index

215
all docs

215
docs citations

215
times ranked

42418
citing authors

#	ARTICLE	IF	CITATIONS
1	Gut microbiome modulates response to anti-PD-1 immunotherapy in melanoma patients. <i>Science</i> , 2018, 359, 97-103.	12.6	3,126
2	Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. <i>Genome Research</i> , 2011, 21, 494-504.	5.5	3,015
3	Microbiota Modulate Behavioral and Physiological Abnormalities Associated with Neurodevelopmental Disorders. <i>Cell</i> , 2013, 155, 1451-1463.	28.9	2,596
4	The Placenta Harbors a Unique Microbiome. <i>Science Translational Medicine</i> , 2014, 6, 237ra65.	12.4	1,717
5	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	27.8	1,638
6	Temporal development of the gut microbiome in early childhood from the TEDDY study. <i>Nature</i> , 2018, 562, 583-588.	27.8	1,220
7	Microbial Reconstitution Reverses Maternal Diet-Induced Social and Synaptic Deficits in Offspring. <i>Cell</i> , 2016, 165, 1762-1775.	28.9	840
8	Tumor Microbiome Diversity and Composition Influence Pancreatic Cancer Outcomes. <i>Cell</i> , 2019, 178, 795-806.e12.	28.9	830
9	The human gut microbiome in early-onset type 1 diabetes from the TEDDY study. <i>Nature</i> , 2018, 562, 589-594.	27.8	623
10	A Catalog of Reference Genomes from the Human Microbiome. <i>Science</i> , 2010, 328, 994-999.	12.6	621
11	The gut mycobiome of the Human Microbiome Project healthy cohort. <i>Microbiome</i> , 2017, 5, 153.	11.1	609
12	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	17.5	608
13	The Gut Microbiome Modulates Colon Tumorigenesis. <i>MBio</i> , 2013, 4, e00692-13.	4.1	582
14	A Metagenomic Approach to Characterization of the Vaginal Microbiome Signature in Pregnancy. <i>PLoS ONE</i> , 2012, 7, e36466.	2.5	572
15	Decade-long bacterial community dynamics in cystic fibrosis airways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5809-5814.	7.1	543
16	Metagenomic Pyrosequencing and Microbial Identification. <i>Clinical Chemistry</i> , 2009, 55, 856-866.	3.2	459
17	Metagenomic Analyses of Alcohol Induced Pathogenic Alterations in the Intestinal Microbiome and the Effect of <i>Lactobacillus rhamnosus</i> GG Treatment. <i>PLoS ONE</i> , 2013, 8, e53028.	2.5	439
18	A microbiota signature associated with experimental food allergy promotes allergic sensitization and anaphylaxis. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 131, 201-212.	2.9	381

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19	Microbial community assembly and metabolic function during mammalian corpse decomposition. <i>Science</i> , 2016, 351, 158-162.	12.6	381
20	Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response. <i>Science</i> , 2021, 374, 1632-1640.	12.6	369
21	The Complete Genome Sequence of <i>Escherichia coli</i> DH10B: Insights into the Biology of a Laboratory Workhorse. <i>Journal of Bacteriology</i> , 2008, 190, 2597-2606.	2.2	331
22	The Human Microbiome Project strategy for comprehensive sampling of the human microbiome and why it matters. <i>FASEB Journal</i> , 2013, 27, 1012-1022.	0.5	328
23	Alterations in the gut microbiota can elicit hypertension in rats. <i>Physiological Genomics</i> , 2017, 49, 96-104.	2.3	293
24	Structure and function of the healthy pre-adolescent pediatric gut microbiome. <i>Microbiome</i> , 2015, 3, 36.	11.1	283
25	Altered Mucosal Microbiome Diversity and Disease Severity in Sjögren Syndrome. <i>Scientific Reports</i> , 2016, 6, 23561.	3.3	268
26	Gut Microbiome Associates With Lifetime Cardiovascular Disease Risk Profile Among Bogalusa Heart Study Participants. <i>Circulation Research</i> , 2016, 119, 956-964.	4.5	264
27	Gut Microbiota-Derived Short-Chain Fatty Acids Promote Poststroke Recovery in Aged Mice. <i>Circulation Research</i> , 2020, 127, 453-465.	4.5	263
28	Role of the Gut Microbiome in Obstructive Sleep Apnea-Induced Hypertension. <i>Hypertension</i> , 2016, 67, 469-474.	2.7	252
29	IgA-coated <i>E. coli</i> enriched in Crohn's disease spondyloarthritis promote T _H 17-dependent inflammation. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	246
30	Gut microbiota signatures are associated with toxicity to combined CTLA-4 and PD-1 blockade. <i>Nature Medicine</i> , 2021, 27, 1432-1441.	30.7	216
31	Longitudinal development of the gut microbiome and metabolome in preterm neonates with late onset sepsis and healthy controls. <i>Microbiome</i> , 2017, 5, 75.	11.1	206
32	The Living Dead: Bacterial Community Structure of a Cadaver at the Onset and End of the Bloat Stage of Decomposition. <i>PLoS ONE</i> , 2013, 8, e77733.	2.5	205
33	Fecal microbiota imbalance in Mexican children with type 1 diabetes. <i>Scientific Reports</i> , 2014, 4, 3814.	3.3	193
34	Mathematical modeling of primary succession of murine intestinal microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 439-444.	7.1	183
35	The Genome of Th17 Cell-Inducing Segmented Filamentous Bacteria Reveals Extensive Auxotrophy and Adaptations to the Intestinal Environment. <i>Cell Host and Microbe</i> , 2011, 10, 260-272.	11.0	175
36	Investigating Colonization of the Healthy Adult Gastrointestinal Tract by Fungi. <i>MSphere</i> , 2018, 3, .	2.9	173

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37	Amino Acid Sequence Determinants of β -Lactamase Structure and Activity. <i>Journal of Molecular Biology</i> , 1996, 258, 688-703.	4.2	171
38	Metagenomic Analysis of Nitrate-Reducing Bacteria in the Oral Cavity: Implications for Nitric Oxide Homeostasis. <i>PLoS ONE</i> , 2014, 9, e88645.	2.5	170
39	Measurement of SOS expression in individual <i>Escherichia coli</i> K-12 cells using fluorescence microscopy. <i>Molecular Microbiology</i> , 2004, 53, 1343-1357.	2.5	164
40	Prospective virome analyses in young children at increased genetic risk for type 1 diabetes. <i>Nature Medicine</i> , 2019, 25, 1865-1872.	30.7	161
41	Randomised clinical trial: faecal microbiota transplantation for recurrent <i>Clostridium difficile</i> infection – fresh, or frozen, or lyophilised microbiota from a small pool of healthy donors delivered by colonoscopy. <i>Alimentary Pharmacology and Therapeutics</i> , 2017, 45, 899-908.	3.7	148
42	Association of nasopharyngeal microbiota profiles with bronchiolitis severity in infants hospitalised for bronchiolitis. <i>European Respiratory Journal</i> , 2016, 48, 1329-1339.	6.7	144
43	Transmission event of SARS-CoV-2 delta variant reveals multiple vaccine breakthrough infections. <i>BMC Medicine</i> , 2021, 19, 255.	5.5	137
44	Antibiotics in neonatal life increase murine susceptibility to experimental psoriasis. <i>Nature Communications</i> , 2015, 6, 8424.	12.8	135
45	Temporal bacterial and metabolic development of the preterm gut reveals specific signatures in health and disease. <i>Microbiome</i> , 2016, 4, 67.	11.1	135
46	MHC variation sculpts individualized microbial communities that control susceptibility to enteric infection. <i>Nature Communications</i> , 2015, 6, 8642.	12.8	132
47	Initial insights into bacterial succession during human decomposition. <i>International Journal of Legal Medicine</i> , 2015, 129, 661-671.	2.2	130
48	Human milk oligosaccharides, milk microbiome and infant gut microbiome modulate neonatal rotavirus infection. <i>Nature Communications</i> , 2018, 9, 5010.	12.8	130
49	Stabilization of the murine gut microbiome following weaning. <i>Gut Microbes</i> , 2012, 3, 383-393.	9.8	126
50	The role of the gastrointestinal microbiome in infectious complications during induction chemotherapy for acute myeloid leukemia. <i>Cancer</i> , 2016, 122, 2186-2196.	4.1	121
51	Prebiotics, Probiotics, and Acetate Supplementation Prevent Hypertension in a Model of Obstructive Sleep Apnea. <i>Hypertension</i> , 2018, 72, 1141-1150.	2.7	120
52	Paradoxical DNA Repair and Peroxide Resistance Gene Conservation in <i>Bacillus pumilus</i> SAFR-032. <i>PLoS ONE</i> , 2007, 2, e928.	2.5	118
53	<i>Fusobacterium nucleatum</i> Subspecies <i>Animalis</i> Influences Proinflammatory Cytokine Expression and Monocyte Activation in Human Colorectal Tumors. <i>Cancer Prevention Research</i> , 2017, 10, 398-409.	1.5	116
54	The Gut Microbiome of the Vector <i>Lutzomyia longipalpis</i> Is Essential for Survival of <i>Leishmania infantum</i> . <i>MBio</i> , 2017, 8, .	4.1	115

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55	Associations of Nasopharyngeal Metabolome and Microbiome with Severity among Infants with Bronchiolitis. A Multiomic Analysis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 196, 882-891.	5.6	113
56	Characterization of the human gut microbiome during travelers' diarrhea. <i>Gut Microbes</i> , 2015, 6, 110-119.	9.8	111
57	Human milk oligosaccharide DSLNT and gut microbiome in preterm infants predicts necrotising enterocolitis. <i>Gut</i> , 2021, 70, 2273-2282.	12.1	110
58	Probiotics stimulate enterocyte migration and microbial diversity in the neonatal mouse intestine. <i>FASEB Journal</i> , 2012, 26, 1960-1969.	0.5	96
59	Chromosome Rearrangement and Diversification of <i>Francisella tularensis</i> Revealed by the Type B (OSU18) Genome Sequence. <i>Journal of Bacteriology</i> , 2006, 188, 6977-6985.	2.2	91
60	Single Delivery of High-Diversity Fecal Microbiota Preparation by Colonoscopy Is Safe and Effective in Increasing Microbial Diversity in Active Ulcerative Colitis. <i>Inflammatory Bowel Diseases</i> , 2017, 23, 903-911.	1.9	91
61	β -Lactamases: protein evolution in real time. <i>Trends in Microbiology</i> , 1998, 6, 323-327.	7.7	89
62	Systematic mutagenesis of the active site omega loop of TEM-1 beta-lactamase. <i>Journal of Bacteriology</i> , 1996, 178, 1821-1828.	2.2	88
63	Stress-Induced β -Lactam Antibiotic Resistance Mutation and Sequences of Stationary-Phase Mutations in the <i>Escherichia coli</i> Chromosome. <i>Journal of Bacteriology</i> , 2009, 191, 5881-5889.	2.2	85
64	Effects of tobacco smoke and electronic cigarette vapor exposure on the oral and gut microbiota in humans: a pilot study. <i>PeerJ</i> , 2018, 6, e4693.	2.0	84
65	Respiratory syncytial virus and rhinovirus severe bronchiolitis are associated with distinct nasopharyngeal microbiota. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 1909-1913.e4.	2.9	82
66	Metagenomics of the faecal virome indicate a cumulative effect of enterovirus and gluten amount on the risk of coeliac disease autoimmunity in genetically at risk children: the TEDDY study. <i>Gut</i> , 2020, 69, 1416-1422.	12.1	82
67	Sequence type 1 group B <i>Streptococcus</i> , an emerging cause of invasive disease in adults, evolves by small genetic changes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6431-6436.	7.1	81
68	Microbiome disruption and recovery in the fish <i>Gambusia affinis</i> following exposure to broad-spectrum antibiotic. <i>Infection and Drug Resistance</i> , 2017, Volume 10, 143-154.	2.7	81
69	The microbiome in precision medicine: the way forward. <i>Genome Medicine</i> , 2018, 10, 12.	8.2	81
70	Saturated and Unsaturated Dietary Fats Differentially Modulate Ethanol-Induced Changes in Gut Microbiome and Metabolome in a Mouse Model of Alcoholic Liver Disease. <i>American Journal of Pathology</i> , 2016, 186, 765-776.	3.8	80
71	Characterization of oral and gut microbiome temporal variability in hospitalized cancer patients. <i>Genome Medicine</i> , 2017, 9, 21.	8.2	80
72	Dietary quality and the colonic mucosa-associated gut microbiome in humans. <i>American Journal of Clinical Nutrition</i> , 2019, 110, 701-712.	4.7	78

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73	Transmissible microbial and metabolomic remodeling by soluble dietary fiber improves metabolic homeostasis. <i>Scientific Reports</i> , 2015, 5, 10604.	3.3	77
74	Safety and preliminary efficacy of orally administered lyophilized fecal microbiota product compared with frozen product given by enema for recurrent <i>Clostridium difficile</i> infection: A randomized clinical trial. <i>PLoS ONE</i> , 2018, 13, e0205064.	2.5	77
75	Characterization of the rat oral microbiome and the effects of dietary nitrate. <i>Free Radical Biology and Medicine</i> , 2014, 77, 249-257.	2.9	75
76	Composition and function of the undernourished neonatal mouse intestinal microbiome. <i>Journal of Nutritional Biochemistry</i> , 2015, 26, 1050-1057.	4.2	75
77	Adaptive Amplification and Point Mutation Are Independent Mechanisms: Evidence for Various Stress-Inducible Mutation Mechanisms. <i>PLoS Biology</i> , 2004, 2, e399.	5.6	74
78	Frequency of Tongue Cleaning Impacts the Human Tongue Microbiome Composition and Enterosalivary Circulation of Nitrate. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 39.	3.9	72
79	Young versus aged microbiota transplants to germ-free mice: increased short-chain fatty acids and improved cognitive performance. <i>Gut Microbes</i> , 2020, 12, 1814107.	9.8	72
80	Contributions of Aspartate 49 and Phenylalanine 142 Residues of a Tight Binding Inhibitory Protein of β -Lactamases. <i>Journal of Biological Chemistry</i> , 1999, 274, 2394-2400.	3.4	67
81	Decreased microbiota diversity associated with urinary tract infection in a trial of bacterial interference. <i>Journal of Infection</i> , 2015, 71, 358-367.	3.3	65
82	Isolation and concentration of bacteria from blood using microfluidic membraneless dialysis and dielectrophoresis. <i>Lab on A Chip</i> , 2017, 17, 1340-1348.	6.0	63
83	Host Response to Probiotics Determined by Nutritional Status of Rotavirus-Infected Neonatal Mice. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2012, 55, 299-307.	1.8	62
84	Water management impacts rice methylmercury and the soil microbiome. <i>Science of the Total Environment</i> , 2016, 572, 608-617.	8.0	62
85	Gut microbiome diversity is an independent predictor of survival in cervical cancer patients receiving chemoradiation. <i>Communications Biology</i> , 2021, 4, 237.	4.4	62
86	Dietary inflammatory potential in relation to the gut microbiome: results from a cross-sectional study. <i>British Journal of Nutrition</i> , 2020, 124, 931-942.	2.3	61
87	<i>Bacteroides ovatus</i> ATCC 8483 monotherapy is superior to traditional fecal transplant and multi-strain bacteriotherapy in a murine colitis model. <i>Gut Microbes</i> , 2019, 10, 504-520.	9.8	59
88	Leveraging Human Microbiome Features to Diagnose and Stratify Children with Irritable Bowel Syndrome. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 449-461.	2.8	59
89	Nasal Airway Microbiota Profile and Severe Bronchiolitis in Infants. <i>Pediatric Infectious Disease Journal</i> , 2017, 36, 1044-1051.	2.0	58
90	Impact of Enhanced Staphylococcus DNA Extraction on Microbial Community Measures in Cystic Fibrosis Sputum. <i>PLoS ONE</i> , 2012, 7, e33127.	2.5	57

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91	The role of gut microbiota in fetal methylmercury exposure: Insights from a pilot study. <i>Toxicology Letters</i> , 2016, 242, 60-67.	0.8	56
92	The association between anterior nares and nasopharyngeal microbiota in infants hospitalized for bronchiolitis. <i>Microbiome</i> , 2018, 6, 2.	11.1	56
93	Genome Sequence of <i>Fusobacterium nucleatum</i> Subspecies <i>Polymorphum</i> – a Genetically Tractable <i>Fusobacterium</i> . <i>PLoS ONE</i> , 2007, 2, e659.	2.5	56
94	Conjunctival Microbiome Changes Associated With Soft Contact Lens and Orthokeratology Lens Wearing. , 2017, 58, 128.		55
95	MicroRNA-146a constrains multiple parameters of intestinal immunity and increases susceptibility to DSS colitis. <i>Oncotarget</i> , 2015, 6, 28556-28572.	1.8	53
96	Intermittent fasting from dawn to sunset for 30 consecutive days is associated with anticancer proteomic signature and upregulates key regulatory proteins of glucose and lipid metabolism, circadian clock, DNA repair, cytoskeleton remodeling, immune system and cognitive function in healthy subjects. <i>Journal of Proteomics</i> , 2020, 217, 103645.	2.4	51
97	Bioactivity and Bioavailability of Ginsenosides are Dependent on the Glycosidase Activities of the A/J Mouse Intestinal Microbiome Defined by Pyrosequencing. <i>Pharmaceutical Research</i> , 2013, 30, 836-846.	3.5	50
98	Microbiome – Epigenome Interactions and the Environmental Origins of Inflammatory Bowel Diseases. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2016, 62, 208-219.	1.8	50
99	Increased <i>Moraxella</i> and <i>Streptococcus</i> species abundance after severe bronchiolitis is associated with recurrent wheezing. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 518-527.e8.	2.9	50
100	The gut microbiota is associated with psychiatric symptom severity and treatment outcome among individuals with serious mental illness. <i>Journal of Affective Disorders</i> , 2020, 264, 98-106.	4.1	50
101	<i>Francisella Tularensis</i> Genomics and Proteomics. <i>Annals of the New York Academy of Sciences</i> , 2007, 1105, 98-121.	3.8	49
102	Gut microbiota as a source of a surrogate antigen that triggers autoimmunity in an immune privileged site. <i>Gut Microbes</i> , 2017, 8, 59-66.	9.8	48
103	Implementation of a Pan-Genomic Approach to Investigate Holobiont-Infesting Microbe Interaction: A Case Report of a Leukemic Patient with Invasive <i>Mucormycosis</i> . <i>PLoS ONE</i> , 2015, 10, e0139851.	2.5	47
104	Development of the cutaneous microbiome in the preterm infant: A prospective longitudinal study. <i>PLoS ONE</i> , 2017, 12, e0176669.	2.5	47
105	16S gut community of the Cameron County Hispanic Cohort. <i>Microbiome</i> , 2015, 3, 7.	11.1	46
106	Cesarean or Vaginal Birth Does Not Impact the Longitudinal Development of the Gut Microbiome in a Cohort of Exclusively Preterm Infants. <i>Frontiers in Microbiology</i> , 2017, 8, 1008.	3.5	46
107	Influence of fecal collection conditions and 16S rRNA gene sequencing at two centers on human gut microbiota analysis. <i>Scientific Reports</i> , 2018, 8, 4386.	3.3	46
108	Maximal viral information recovery from sequence data using VirMAP. <i>Nature Communications</i> , 2018, 9, 3205.	12.8	46

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109	Restructuring the Gut Microbiota by Intermittent Fasting Lowers Blood Pressure. <i>Circulation Research</i> , 2021, 128, 1240-1254.	4.5	45
110	Morphine Promotes Colonization of Anastomotic Tissues with Collagenase - Producing <i>Enterococcus faecalis</i> and Causes Leak. <i>Journal of Gastrointestinal Surgery</i> , 2016, 20, 1744-1751.	1.7	43
111	Early nasal microbiota and acute respiratory infections during the first years of life. <i>Thorax</i> , 2019, 74, 592-599.	5.6	43
112	Rotavirus infection induces glycan availability to promote ileum-specific changes in the microbiome aiding rotavirus virulence. <i>Gut Microbes</i> , 2020, 11, 1324-1347.	9.8	43
113	A type VII secretion system of <i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> contributes to gut colonization and the development of colon tumors. <i>PLoS Pathogens</i> , 2021, 17, e1009182.	4.7	41
114	Nasopharyngeal Proteobacteria are associated with viral etiology and acute wheezing in children with severe bronchiolitis. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 133, 1220-1222.e3.	2.9	40
115	Complete Genome Sequence of <i>Turicibacter</i> sp. Strain H121, Isolated from the Feces of a Contaminated Germ-Free Mouse. <i>Genome Announcements</i> , 2016, 4, .	0.8	39
116	Successful collection of stool samples for microbiome analyses from a large community-based population of elderly men. <i>Contemporary Clinical Trials Communications</i> , 2017, 7, 158-162.	1.1	38
117	Antibiotic-mediated bacteriome depletion in <i>Apc^{Min/+}</i> mice is associated with reduction in mucus-producing goblet cells and increased colorectal cancer progression. <i>Cancer Medicine</i> , 2018, 7, 2003-2012.	2.8	36
118	The host effects of <i>Gambusia affinis</i> with an antibiotic-disrupted microbiome. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2015, 178, 163-168.	2.6	35
119	Insular resting state functional connectivity is associated with gut microbiota diversity. <i>European Journal of Neuroscience</i> , 2019, 50, 2446-2452.	2.6	35
120	A Lachnospiraceae-dominated bacterial signature in the fecal microbiota of HIV-infected individuals from Colombia, South America. <i>Scientific Reports</i> , 2018, 8, 4479.	3.3	34
121	Decrease in acetyl-CoA pathway utilizing butyrate-producing bacteria is a key pathogenic feature of alcohol-induced functional gut microbial dysbiosis and development of liver disease in mice. <i>Gut Microbes</i> , 2021, 13, 1946367.	9.8	34
122	Household siblings and nasal and fecal microbiota in infants. <i>Pediatrics International</i> , 2017, 59, 473-481.	0.5	32
123	Oral insulin immunotherapy in children at risk for type 1 diabetes in a randomised controlled trial. <i>Diabetologia</i> , 2021, 64, 1079-1092.	6.3	31
124	Impact of environmental microbiota on human microbiota of workers in academic mouse research facilities: An observational study. <i>PLoS ONE</i> , 2017, 12, e0180969.	2.5	31
125	Longitudinal Changes in Early Nasal Microbiota and the Risk of Childhood Asthma. <i>Pediatrics</i> , 2020, 146, .	2.1	29
126	Oligofructose protects against arsenic-induced liver injury in a model of environment/obesity interaction. <i>Toxicology and Applied Pharmacology</i> , 2015, 284, 304-314.	2.8	28

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127	Serum LL-37 Levels Associated With Severity of Bronchiolitis and Viral Etiology. <i>Clinical Infectious Diseases</i> , 2017, 65, 967-975.	5.8	28
128	Impact of Age-Related Mitochondrial Dysfunction and Exercise on Intestinal Microbiota Composition. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2018, 73, 571-578.	3.6	28
129	Metabolomic signatures distinguish the impact of formula carbohydrates on disease outcome in a preterm piglet model of NEC. <i>Microbiome</i> , 2018, 6, 111.	11.1	28
130	Maternal micronutrients can modify colonic mucosal microbiota maturation in murine offspring. <i>Gut Microbes</i> , 2012, 3, 426-433.	9.8	27
131	Effect of Sample Storage Conditions on Culture-Independent Bacterial Community Measures in Cystic Fibrosis Sputum Specimens. <i>Journal of Clinical Microbiology</i> , 2011, 49, 3717-3718.	3.9	26
132	Houston hurricane Harvey health (Houston-3H) study: assessment of allergic symptoms and stress after hurricane Harvey flooding. <i>Environmental Health</i> , 2021, 20, 9.	4.0	26
133	Serum cathelicidin, nasopharyngeal microbiota, and disease severity among infants hospitalized with bronchiolitis. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 1383-1386.e6.	2.9	25
134	Middle ear microbiome differences in indigenous Filipinos with chronic otitis media due to a duplication in the A2ML1 gene. <i>Infectious Diseases of Poverty</i> , 2016, 5, 97.	3.7	24
135	The relationship between nasopharyngeal <scp>CCL</scp>5 and microbiota on disease severity among infants with bronchiolitis. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2017, 72, 1796-1800.	5.7	24
136	Serum Metabolome Is Associated With the Nasopharyngeal Microbiota and Disease Severity Among Infants With Bronchiolitis. <i>Journal of Infectious Diseases</i> , 2019, 219, 2005-2014.	4.0	24
137	Using formalin fixed paraffin embedded tissue to characterize the preterm gut microbiota in necrotising enterocolitis and spontaneous isolated perforation using marginal and diseased tissue. <i>BMC Microbiology</i> , 2019, 19, 52.	3.3	24
138	Enteroggregative E. coli Adherence to Human Heparan Sulfate Proteoglycans Drives Segment and Host Specific Responses to Infection. <i>PLoS Pathogens</i> , 2020, 16, e1008851.	4.7	24
139	The gut microbiome contributes to blood-brain barrier disruption in spontaneously hypertensive stroke prone rats. <i>FASEB Journal</i> , 2021, 35, e21201.	0.5	24
140	Murine Model of Chemotherapy-Induced Extraintestinal Pathogenic Escherichia coli Translocation. <i>Infection and Immunity</i> , 2015, 83, 3243-3256.	2.2	23
141	Comparison of Methods To Collect Fecal Samples for Microbiome Studies Using Whole-Genome Shotgun Metagenomic Sequencing. <i>MSphere</i> , 2020, 5, .	2.9	23
142	Development and Accuracy of Quantitative Real-Time Polymerase Chain Reaction Assays for Detection and Quantification of Enterotoxigenic Escherichia coli (ETEC) Heat Labile and Heat Stable Toxin Genes in Travelers' Diarrhea Samples. <i>American Journal of Tropical Medicine and Hygiene</i> , 2014, 90, 124-132.	1.4	22
143	Sphingolipid metabolism potential in fecal microbiome and bronchiolitis in infants: a case-control study. <i>BMC Research Notes</i> , 2017, 10, 325.	1.4	22
144	Chromosomal System for Studying AmpC-Mediated β -Lactam Resistance Mutation in Escherichia coli. <i>Antimicrobial Agents and Chemotherapy</i> , 2002, 46, 1535-1539.	3.2	21

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145	Oral microbiota reveals signs of acculturation in Mexican American women. <i>PLoS ONE</i> , 2018, 13, e0194100.	2.5	21
146	Display of Functional β -Lactamase Inhibitory Protein on the Surface of M13 Bacteriophage. <i>Antimicrobial Agents and Chemotherapy</i> , 1998, 42, 2893-2897.	3.2	20
147	Oligonucleotide capture sequencing of the SARS-CoV-2 genome and subgenomic fragments from COVID-19 individuals. <i>PLoS ONE</i> , 2021, 16, e0244468.	2.5	20
148	Microbial-Derived Metabolites Reflect an Altered Intestinal Microbiota during Catch-Up Growth in Undernourished Neonatal Mice. <i>Journal of Nutrition</i> , 2016, 146, 940-948.	2.9	19
149	Genetic and Environmental Determinants of Otitis Media in an Indigenous Filipino Population. <i>Otolaryngology - Head and Neck Surgery</i> , 2016, 155, 856-862.	1.9	19
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