

George M Weinstock

List of Publications by Year in descending order

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403
papers

152,173
citations

906

116
h-index

69

373
g-index

422
all docs

422
docs citations

422
times ranked

144317
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	27.8	21,074
2	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.	27.8	9,614
3	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073.	27.8	7,209
4	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65.	27.8	7,199
5	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. <i>Nature</i> , 2008, 455, 1061-1068.	27.8	6,879
6	Integrated genomic analyses of ovarian carcinoma. <i>Nature</i> , 2011, 474, 609-615.	27.8	6,541
7	The International HapMap Project. <i>Nature</i> , 2003, 426, 789-796.	27.8	5,735
8	The Genome Sequence of <i>Drosophila melanogaster</i> . <i>Science</i> , 2000, 287, 2185-2195.	12.6	5,566
9	A haplotype map of the human genome. <i>Nature</i> , 2005, 437, 1299-1320.	27.8	5,440
10	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
11	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007, 449, 851-861.	27.8	4,137
12	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. <i>Genome Research</i> , 2005, 15, 1034-1050.	5.5	3,517
13	Somatic mutations affect key pathways in lung adenocarcinoma. <i>Nature</i> , 2008, 455, 1069-1075.	27.8	2,694
14	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	27.8	2,249
15	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	27.8	1,943
16	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007, 449, 913-918.	27.8	1,788
17	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006, 443, 931-949.	27.8	1,648
18	The complete genome of an individual by massively parallel DNA sequencing. <i>Nature</i> , 2008, 452, 872-876.	27.8	1,635

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19	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	17.5	1,512
20	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	12.6	1,283
21	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008, 452, 949-955.	27.8	1,255
22	VarScan: variant detection in massively parallel sequencing of individual and pooled samples. <i>Bioinformatics</i> , 2009, 25, 2283-2285.	4.1	1,193
23	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2005, 435, 43-57.	27.8	1,179
24	Genome remodelling in a basal-like breast cancer metastasis and xenograft. <i>Nature</i> , 2010, 464, 999-1005.	27.8	1,077
25	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
26	Characterizing the cancer genome in lung adenocarcinoma. <i>Nature</i> , 2007, 450, 893-898.	27.8	1,020
27	The Genome of the Sea Urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006, 314, 941-952.	12.6	1,018
28	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	27.8	1,016
29	Enteric defensins are essential regulators of intestinal microbial ecology. <i>Nature Immunology</i> , 2010, 11, 76-82.	14.5	1,013
30	Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. <i>Nature Communications</i> , 2019, 10, 5029.	12.8	1,007
31	The DNA sequence of the human X chromosome. <i>Nature</i> , 2005, 434, 325-337.	27.8	985
32	Complete Genome Sequence of <i>Treponema pallidum</i> , the Syphilis Spirochete. <i>Science</i> , 1998, 281, 375-388.	12.6	969
33	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013, 493, 45-50.	27.8	783
34	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	12.6	746
35	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	13.3	717
36	Comparison of the Respiratory Microbiome in Healthy Nonsmokers and Smokers. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013, 187, 1067-1075.	5.6	655

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37	A Catalog of Reference Genomes from the Human Microbiome. <i>Science</i> , 2010, 328, 994-999.	12.6	621
38	Direct selection of human genomic loci by microarray hybridization. <i>Nature Methods</i> , 2007, 4, 903-905.	19.0	617
39	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
40	Propionibacterium acnes Strain Populations in the Human Skin Microbiome Associated with Acne. <i>Journal of Investigative Dermatology</i> , 2013, 133, 2152-2160.	0.7	557
41	Comparison of genomic DNAs of different enterococcal isolates using restriction endonucleases with infrequent recognition sites. <i>Journal of Clinical Microbiology</i> , 1990, 28, 2059-2063.	3.9	555
42	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	27.8	541
43	Biogeography of the ecosystems of the healthy human body. <i>Genome Biology</i> , 2013, 14, R1.	9.6	540
44	Pervasive genetic hitchhiking and clonal interference in forty evolving yeast populations. <i>Nature</i> , 2013, 500, 571-574.	27.8	523
45	Modernizing Reference Genome Assemblies. <i>PLoS Biology</i> , 2011, 9, e1001091.	5.6	458
46	Comparative genome sequencing of <i>Drosophila pseudoobscura</i> : Chromosomal, gene, and cis-element evolution. <i>Genome Research</i> , 2005, 15, 1-18.	5.5	453
47	Patterned progression of bacterial populations in the premature infant gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12522-12527.	7.1	449
48	The Genome Architecture of the Collaborative Cross Mouse Genetic Reference Population. <i>Genetics</i> , 2012, 190, 389-401.	2.9	435
49	Genomic approaches to studying the human microbiota. <i>Nature</i> , 2012, 489, 250-256.	27.8	429
50	Validation of Metagenomic Next-Generation Sequencing Tests for Universal Pathogen Detection. <i>Archives of Pathology and Laboratory Medicine</i> , 2017, 141, 776-786.	2.5	404
51	Longitudinal multi-omics of host-microbe dynamics in prediabetes. <i>Nature</i> , 2019, 569, 663-671.	27.8	391
52	Genome Project Standards in a New Era of Sequencing. <i>Science</i> , 2009, 326, 236-237.	12.6	382
53	Initiation of general recombination catalyzed in vitro by the recA protein of <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1979, 76, 2615-2619.	7.1	365
54	Intermittent Fasting Confers Protection in CNS Autoimmunity by Altering the Gut Microbiota. <i>Cell Metabolism</i> , 2018, 27, 1222-1235.e6.	16.2	352

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55	Gut bacteria dysbiosis and necrotising enterocolitis in very low birthweight infants: a prospective case-control study. <i>Lancet</i> , The, 2016, 387, 1928-1936.	13.7	345
56	Short, interspersed repetitive DNA sequences in prokaryotic genomes. <i>Journal of Bacteriology</i> , 1992, 174, 4525-4529.	2.2	333
57	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
58	ATP-dependent renaturation of DNA catalyzed by the recA protein of <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1979, 76, 126-130.	7.1	330
59	A longitudinal big data approach for precision health. <i>Nature Medicine</i> , 2019, 25, 792-804.	30.7	329
60	Genetic Basis for In Vivo Daptomycin Resistance in Enterococci. <i>New England Journal of Medicine</i> , 2011, 365, 892-900.	27.0	324
61	Effects of <i>Enterococcus faecalis</i> <i>fsr</i> Genes on Production of Gelatinase and a Serine Protease and Virulence. <i>Infection and Immunity</i> , 2000, 68, 2579-2586.	2.2	317
62	Metabolic and metagenomic outcomes from early-life pulsed antibiotic treatment. <i>Nature Communications</i> , 2015, 6, 7486.	12.8	317
63	Finishing a whole-genome shotgun: release 3 of the <i>Drosophila melanogaster</i> euchromatic genome sequence. <i>Genome Biology</i> , 2002, 3, research0079.1.	9.6	313
64	Creating a honey bee consensus gene set. <i>Genome Biology</i> , 2007, 8, R13.	9.6	300
65	Hypothesis Testing and Power Calculations for Taxonomic-Based Human Microbiome Data. <i>PLoS ONE</i> , 2012, 7, e52078.	2.5	289
66	Making the Leap from Research Laboratory to Clinic: Challenges and Opportunities for Next-Generation Sequencing in Infectious Disease Diagnostics. <i>MBio</i> , 2015, 6, e01888-15.	4.1	270
67	The real cost of sequencing: scaling computation to keep pace with data generation. <i>Genome Biology</i> , 2016, 17, 53.	8.8	264
68	Large scale variation in <i>Enterococcus faecalis</i> illustrated by the genome analysis of strain OG1RF. <i>Genome Biology</i> , 2008, 9, R110.	9.6	253
69	recA protein-catalyzed strand assimilation: stimulation by <i>Escherichia coli</i> single-stranded DNA-binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1980, 77, 857-861.	7.1	251
70	Comparison of the genome of the oral pathogen <i>Treponema denticola</i> with other spirochete genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5646-5651.	7.1	251
71	Prepublication data sharing. <i>Nature</i> , 2009, 461, 168-170.	27.8	243
72	Evaluation of 16S rDNA-Based Community Profiling for Human Microbiome Research. <i>PLoS ONE</i> , 2012, 7, e39315.	2.5	240

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73	An <i>Enterococcus faecalis</i> ABC Homologue (Lsa) Is Required for the Resistance of This Species to Clindamycin and Quinupristin-Dalfopristin. <i>Antimicrobial Agents and Chemotherapy</i> , 2002, 46, 1845-1850.	3.2	239
74	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007, 17, 1797-1808.	5.5	237
75	Characteristic Male Urine Microbiomes Associate with Asymptomatic Sexually Transmitted Infection. <i>PLoS ONE</i> , 2010, 5, e14116.	2.5	234
76	Phylogenomic analysis reveals bees and wasps (Hymenoptera) at the base of the radiation of Holometabolous insects. <i>Genome Research</i> , 2006, 16, 1334-1338.	5.5	233
77	The Genome Sequence of the Leaf-Cutter Ant <i>Atta cephalotes</i> Reveals Insights into Its Obligate Symbiotic Lifestyle. <i>PLoS Genetics</i> , 2011, 7, e1002007.	3.5	231
78	Subtle genetic changes enhance virulence of methicillin resistant and sensitive <i>Staphylococcus aureus</i> . <i>BMC Microbiology</i> , 2007, 7, 99.	3.3	227
79	The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , 2014, 46, 850-857.	21.4	225
80	Complete Genome Sequence of <i>Rickettsia typhi</i> and Comparison with Sequences of Other <i>Rickettsiae</i> . <i>Journal of Bacteriology</i> , 2004, 186, 5842-5855.	2.2	223
81	Evidence for Clonal Spread of a Single Strain of β -Lactamase-Producing <i>Enterococcus</i> (<i>Streptococcus</i>) <i>faecalis</i> to Six Hospitals in Five States. <i>Journal of Infectious Diseases</i> , 1991, 163, 780-785.	4.0	222
82	Characterization of <i>fsr</i> , a Regulator Controlling Expression of Gelatinase and Serine Protease in <i>Enterococcus faecalis</i> OG1RF. <i>Journal of Bacteriology</i> , 2001, 183, 3372-3382.	2.2	222
83	Community characteristics of the gut microbiomes of competitive cyclists. <i>Microbiome</i> , 2017, 5, 98.	11.1	219
84	Inflammatory Bowel Diseases Phenotype, <i>C. difficile</i> and NOD2 Genotype Are Associated with Shifts in Human Ileum Associated Microbial Composition. <i>PLoS ONE</i> , 2012, 7, e26284.	2.5	207
85	Generation of restriction map of <i>Enterococcus faecalis</i> OG1 and investigation of growth requirements and regions encoding biosynthetic function. <i>Journal of Bacteriology</i> , 1993, 175, 5216-5223.	2.2	202
86	<i>Enterococcus faecalis</i> Adhesin, Ace, Mediates Attachment to Extracellular Matrix Proteins Collagen Type IV and Laminin as well as Collagen Type I. <i>Infection and Immunity</i> , 2000, 68, 5218-5224.	2.2	193
87	Ace Is a Collagen-binding MSCRAMM from <i>Enterococcus faecalis</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 26939-26945.	3.4	191
88	Bacterial Communities of the Coronal Sulcus and Distal Urethra of Adolescent Males. <i>PLoS ONE</i> , 2012, 7, e36298.	2.5	191
89	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	5.6	190
90	Genomic Analysis of the Nuclear Receptor Family: New Insights Into Structure, Regulation, and Evolution From the Rat Genome. <i>Genome Research</i> , 2004, 14, 580-590.	5.5	187

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91	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007, 17, 760-774.	5.5	184
92	Microbiome Signatures Associated With Steatohepatitis and Moderate to Severe Fibrosis in Children With Nonalcoholic Fatty Liver Disease. <i>Gastroenterology</i> , 2019, 157, 1109-1122.	1.3	184
93	Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. <i>Cell Systems</i> , 2018, 6, 157-170.e8.	6.2	183
94	Metagenomic analysis of double-stranded DNA viruses in healthy adults. <i>BMC Biology</i> , 2014, 12, 71.	3.8	181
95	Widespread Colonization of the Lung by <i>Tropheryma whippelii</i> in HIV Infection. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013, 187, 1110-1117.	5.6	175
96	Genome Sequencing Reveals Widespread Virulence Gene Exchange among Human <i>Neisseria</i> Species. <i>PLoS ONE</i> , 2010, 5, e11835.	2.5	170
97	A SNP discovery method to assess variant allele probability from next-generation resequencing data. <i>Genome Research</i> , 2010, 20, 273-280.	5.5	168
98	Genome sequence of an Australian kangaroo, <i>Macropus eugenii</i> , provides insight into the evolution of mammalian reproduction and development. <i>Genome Biology</i> , 2011, 12, R81.	9.6	167
99	A prospective microbiome-wide association study of food sensitization and food allergy in early childhood. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2018, 73, 145-152.	5.7	163
100	Sepsis From the Gut: The Enteric Habitat of Bacteria That Cause Late-Onset Neonatal Bloodstream Infections. <i>Clinical Infectious Diseases</i> , 2014, 58, 1211-1218.	5.8	160
101	Sequence Analysis of the Human Virome in Febrile and Afebrile Children. <i>PLoS ONE</i> , 2012, 7, e27735.	2.5	159
102	Pan-Genome and Comparative Genome Analyses of <i>Propionibacterium acnes</i> Reveal Its Genomic Diversity in the Healthy and Diseased Human Skin Microbiome. <i>MBio</i> , 2013, 4, e00003-13.	4.1	159
103	Daptomycin-Resistant <i>Enterococcus faecalis</i> Diverts the Antibiotic Molecule from the Division Septum and Remodels Cell Membrane Phospholipids. <i>MBio</i> , 2013, 4, .	4.1	152
104	Identification of Functional Variants for Cleft Lip with or without Cleft Palate in or near PAX7, FGFR2, and NOG by Targeted Sequencing of GWAS Loci. <i>American Journal of Human Genetics</i> , 2015, 96, 397-411.	6.2	150
105	Clinical isolates of <i>Enterococcus faecium</i> exhibit strain-specific collagen binding mediated by Acm, a new member of the MSCRAMM family. <i>Molecular Microbiology</i> , 2003, 47, 1733-1747.	2.5	149
106	Phylogenomics and the Dynamic Genome Evolution of the Genus <i>Streptococcus</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 741-753.	2.5	149
107	Longitudinal Analysis of the Premature Infant Intestinal Microbiome Prior to Necrotizing Enterocolitis: A Case-Control Study. <i>PLoS ONE</i> , 2015, 10, e0118632.	2.5	146
108	In vivo testing of an <i>Enterococcus faecalis</i> efaA mutant and use of efaA homologs for species identification. <i>FEMS Immunology and Medical Microbiology</i> , 1998, 21, 323-331.	2.7	145

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109	The conjunctival microbiome in health and trachomatous disease: a case control study. <i>Genome Medicine</i> , 2014, 6, 99.	8.2	144
110	The Atlas Genome Assembly System. <i>Genome Research</i> , 2004, 14, 721-732.	5.5	139
111	Dynamic Changes in the Subgingival Microbiome and Their Potential for Diagnosis and Prognosis of Periodontitis. <i>MBio</i> , 2015, 6, e01926-14.	4.1	139
112	Deciphering functional redundancy in the human microbiome. <i>Nature Communications</i> , 2020, 11, 6217.	12.8	139
113	<i>Bos taurus</i> genome assembly. <i>BMC Genomics</i> , 2009, 10, 180.	2.8	137
114	High-throughput whole-genome sequencing to dissect the epidemiology of <i>Acinetobacter baumannii</i> isolates from a hospital outbreak. <i>Journal of Hospital Infection</i> , 2010, 75, 37-41.	2.9	136
115	Transferable Vancomycin Resistance in a Community-Associated MRSA Lineage. <i>New England Journal of Medicine</i> , 2014, 370, 1524-1531.	27.0	136
116	A dominant mutation in RPE65 identified by whole-exome sequencing causes retinitis pigmentosa with choroidal involvement. <i>European Journal of Human Genetics</i> , 2011, 19, 1074-1081.	2.8	135
117	<i>Bifidobacterium bifidum</i> strains synergize with immune checkpoint inhibitors to reduce tumour burden in mice. <i>Nature Microbiology</i> , 2021, 6, 277-288.	13.3	130
118	Bacterial classifications derived from recA protein sequence comparisons. <i>Journal of Bacteriology</i> , 1995, 177, 6881-6893.	2.2	128
119	Complete genome sequence of <i>Enterococcus faecium</i> strain TX16 and comparative genomic analysis of <i>Enterococcus faecium</i> genomes. <i>BMC Microbiology</i> , 2012, 12, 135.	3.3	126
120	Factors influencing the infant gut microbiome at age 3-6 months: Findings from the ethnically diverse Vitamin D Antenatal Asthma Reduction Trial (VDAART). <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 482-491.e14.	2.9	125
121	Symbiotic organs shaped by distinct modes of genome evolution in cephalopods. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3030-3035.	7.1	123
122	Emerging view of the human virome. <i>Translational Research</i> , 2012, 160, 283-290.	5.0	122
123	Transposable lambda placMu bacteriophages for creating lacZ operon fusions and kanamycin resistance insertions in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1985, 162, 1092-1099.	2.2	122
124	Resistance to Ceftazidime-Avibactam Is Due to Transposition of KPC in a Porin-Deficient Strain of <i>Klebsiella pneumoniae</i> with Increased Efflux Activity. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	121
125	Systems Biology of the Vervet Monkey. <i>ILAR Journal</i> , 2013, 54, 122-143.	1.8	120
126	Multicenter Comparison of Lung and Oral Microbiomes of HIV-infected and HIV-uninfected Individuals. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 192, 1335-1344.	5.6	120

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127	Open reading frame expression vectors: a general method for antigen production in <i>Escherichia coli</i> using protein fusions to beta-galactosidase.. Proceedings of the National Academy of Sciences of the United States of America, 1983, 80, 4432-4436.	7.1	119
128	Whole-Genome Analyses of <i>Enterococcus faecium</i> Isolates with Diverse Daptomycin MICs. Antimicrobial Agents and Chemotherapy, 2014, 58, 4527-4534.	3.2	119
129	Paradoxical DNA Repair and Peroxide Resistance Gene Conservation in <i>Bacillus pumilus</i> SAFR-032. PLoS ONE, 2007, 2, e928.	2.5	118
130	The genome of the vervet (<i>Chlorocebus aethiops sabaeus</i>). Genome Research, 2015, 25, 1921-1933.	5.5	114
131	Characterization of <i>emeA</i> , a <i>norA</i> Homolog and Multidrug Resistance Efflux Pump, in <i>Enterococcus faecalis</i> . Antimicrobial Agents and Chemotherapy, 2001, 45, 3574-3579.	3.2	113
132	Exploration of bacterial community classes in major human habitats. Genome Biology, 2014, 15, R66.	9.6	109
133	A Novel <i>Treponema pallidum</i> Antigen, TP0136, Is an Outer Membrane Protein That Binds Human Fibronectin. Infection and Immunity, 2008, 76, 1848-1857.	2.2	108
134	DNA Sequence of the <i>Pasteurella haemolytica</i> Leukotoxin Gene Cluster. DNA and Cell Biology, 1989, 8, 15-28.	5.2	107
135	Parallel Epidemics of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 Infection in North and South America. Journal of Infectious Diseases, 2015, 212, 1874-1882.	4.0	107
136	Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. Nature Genetics, 2017, 49, 1705-1713.	21.4	107
137	Whole Genome Sequences of Three <i>Treponema pallidum</i> ssp. <i>pertenue</i> Strains: Yaws and Syphilis Treponemes Differ in Less than 0.2% of the Genome Sequence. PLoS Neglected Tropical Diseases, 2012, 6, e1471.	3.0	106
138	Evolutionary Genomics of <i>Salmonella enterica</i> Subspecies. MBio, 2013, 4, .	4.1	106
139	Lambda <i>placMu</i> : a transposable derivative of bacteriophage lambda for creating <i>lacZ</i> protein fusions in a single step. Journal of Bacteriology, 1984, 158, 1084-1093.	2.2	106
140	Plant-Associated Symbiotic <i>Burkholderia</i> Species Lack Hallmark Strategies Required in Mammalian Pathogenesis. PLoS ONE, 2014, 9, e83779.	2.5	106
141	Diversity of <i>ace</i> , a Gene Encoding a Microbial Surface Component Recognizing Adhesive Matrix Molecules, from Different Strains of <i>Enterococcus faecalis</i> and Evidence for Production of <i>Ace</i> during Human Infections. Infection and Immunity, 2000, 68, 5210-5217.	2.2	105
142	Macrolide treatment failure in a case of secondary syphilis: a novel A2059G mutation in the 23S rRNA gene of <i>Treponema pallidum</i> subsp. <i>pallidum</i> . Journal of Medical Microbiology, 2009, 58, 832-836.	1.8	104
143	Whole-Genome Analysis of a Daptomycin-Susceptible <i>Enterococcus faecium</i> Strain and Its Daptomycin-Resistant Variant Arising during Therapy. Antimicrobial Agents and Chemotherapy, 2013, 57, 261-268.	3.2	101
144	The upper-airway microbiota and loss of asthma control among asthmatic children. Nature Communications, 2019, 10, 5714.	12.8	100

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145	Leucoagaricus gongylophorus Produces Diverse Enzymes for the Degradation of Recalcitrant Plant Polymers in Leaf-Cutter Ant Fungus Gardens. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3770-3778.	3.1	98
146	Metagenomic Approach for Identification of the Pathogens Associated with Diarrhea in Stool Specimens. <i>Journal of Clinical Microbiology</i> , 2016, 54, 368-375.	3.9	98
147	NIH working group report using genomic information to guide weight management: From universal to precision treatment. <i>Obesity</i> , 2016, 24, 14-22.	3.0	96
148	A Prospective Cohort Multicenter Study of Molecular Epidemiology and Phylogenomics of <i>Staphylococcus aureus</i> Bacteremia in Nine Latin American Countries. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	95
149	The Genome Sequence of <i>Mannheimia haemolytica</i> A1: Insights into Virulence, Natural Competence, and Pasteurellaceae Phylogeny. <i>Journal of Bacteriology</i> , 2006, 188, 7257-7266.	2.2	94
150	Genome sequences of the honey bee pathogens <i>Paenibacillus larvae</i> and <i>Ascosphaera apis</i> . <i>Insect Molecular Biology</i> , 2006, 15, 715-718.	2.0	92
151	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
152	Genetic diversity in <i>Treponema pallidum</i> : Implications for pathogenesis, evolution and molecular diagnostics of syphilis and yaws. <i>Infection, Genetics and Evolution</i> , 2012, 12, 191-202.	2.3	90
153	Quantitation and Composition of Cutaneous Microbiota in Diabetic and Nondiabetic Men. <i>Journal of Infectious Diseases</i> , 2013, 207, 1105-1114.	4.0	90
154	Analysis of a Gene Cluster of <i>Enterococcus faecalis</i> Involved in Polysaccharide Biosynthesis. <i>Infection and Immunity</i> , 2000, 68, 815-823.	2.2	89
155	Identification and phenotypic characterization of a second collagen adhesin, Scm, and genome-based identification and analysis of 13 other predicted MSCRAMMs, including four distinct pilus loci, in <i>Enterococcus faecium</i> . <i>Microbiology (United Kingdom)</i> , 2008, 154, 3199-3211.	1.8	89
156	Molecular Characterization of a Widespread, Pathogenic, and Antibiotic Resistance-Receptive <i>Enterococcus faecalis</i> Lineage and Dissemination of Its Putative Pathogenicity Island. <i>Journal of Bacteriology</i> , 2005, 187, 5709-5718.	2.2	88
157	Detection of Viruses in Young Children With Fever Without an Apparent Source. <i>Pediatrics</i> , 2012, 130, e1455-e1462.	2.1	87
158	Genomic Epidemiology of <i>Salmonella enterica</i> Serotype Enteritidis based on Population Structure of Prevalent Lineages. <i>Emerging Infectious Diseases</i> , 2014, 20, 1481-1489.	4.3	87
159	A Cluster of Genes Involved in Polysaccharide Biosynthesis from <i>Enterococcus faecalis</i> OG1RF. <i>Infection and Immunity</i> , 1998, 66, 4313-4323.	2.2	86
160	Novel Bacterial Taxa in the Human Microbiome. <i>PLoS ONE</i> , 2012, 7, e35294.	2.5	86
161	Measurement of in vivo expression of the <i>recA</i> gene of <i>Escherichia coli</i> by using <i>lacZ</i> gene fusions. <i>Journal of Bacteriology</i> , 1984, 160, 112-121.	2.2	85
162	Repetitive Sequence-Based PCR versus Pulsed-Field Gel Electrophoresis for Typing of <i>Enterococcus faecalis</i> at the Subspecies Level. <i>Journal of Clinical Microbiology</i> , 1998, 36, 211-215.	3.9	84

#	ARTICLE	IF	CITATIONS
163	Effect of Advanced HIV Infection on the Respiratory Microbiome. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 226-235.	5.6	83
164	TIGRA: A targeted iterative graph routing assembler for breakpoint assembly. <i>Genome Research</i> , 2014, 24, 310-317.	5.5	81
165	Evidence that the Enterococcal Polysaccharide Antigen Gene (<i>epa</i>) Cluster Is Widespread in <i>Enterococcus faecalis</i> and Influences Resistance to Phagocytic Killing of <i>E. faecalis</i> . <i>Infection and Immunity</i> , 2002, 70, 2010-2015.	2.2	80
166	Identification of Disease-Causing Mutations in Autosomal Dominant Retinitis Pigmentosa (adRP) Using Next-Generation DNA Sequencing. , 2011, 52, 494.		80
167	Identification and transcriptional analysis of a <i>Treponema pallidum</i> operon encoding a putative ABC transport system, an iron-activated repressor protein homolog, and a glycolytic pathway enzyme homolog. <i>Gene</i> , 1997, 197, 47-64.	2.2	78
168	Impact of Age, Caloric Restriction, and Influenza Infection on Mouse Gut Microbiome: An Exploratory Study of the Role of Age-Related Microbiome Changes on Influenza Responses. <i>Frontiers in Immunology</i> , 2017, 8, 1164.	4.8	77
169	A Collagen-Binding Adhesin, <i>Acb</i> , and Ten Other Putative MSCRAMM and Pilus Family Proteins of <i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> (<i>Streptococcus bovis</i> Group.) <i>Tj ETQq1 1 0.784214 rgBT 76</i> <i>overlock</i>		76
170	A Multi-Megabase Copy Number Gain Causes Maternal Transmission Ratio Distortion on Mouse Chromosome 2. <i>PLoS Genetics</i> , 2015, 11, e1004850.	3.5	76
171	Association of the Infant Gut Microbiome With Early Childhood Neurodevelopmental Outcomes. <i>JAMA Network Open</i> , 2019, 2, e190905.	5.9	75
172	Characterization of the bacterial and fungal microbiome in indoor dust and outdoor air samples: a pilot study. <i>Environmental Sciences: Processes and Impacts</i> , 2016, 18, 713-724.	3.5	74
173	Whole Genome Sequence of <i>Treponema pallidum</i> ssp. <i>pallidum</i> , Strain Mexico A, Suggests Recombination between Yaws and Syphilis Strains. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1832.	3.0	73
174	Segment-directed mutagenesis: construction in vitro of point mutations limited to a small predetermined region of a circular DNA molecule.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1980, 77, 5375-5379.	7.1	71
175	An <i>Enterococcus faecium</i> Secreted Antigen, <i>SagA</i> , Exhibits Broad-Spectrum Binding to Extracellular Matrix Proteins and Appears Essential for <i>E. faecium</i> Growth. <i>Infection and Immunity</i> , 2003, 71, 5033-5041.	2.2	71
176	<i>NotI</i> genomic cleavage map of <i>Escherichia coli</i> K-12 strain MG1655. <i>Journal of Bacteriology</i> , 1992, 174, 558-567.	2.2	70
177	Involvement of PhoP-PhoS Homologs in <i>Enterococcus faecalis</i> Virulence. <i>Infection and Immunity</i> , 2002, 70, 1991-1996.	2.2	70
178	Transcriptome of <i>Treponema pallidum</i> : Gene Expression Profile during Experimental Rabbit Infection. <i>Journal of Bacteriology</i> , 2005, 187, 1866-1874.	2.2	70
179	Phosphate transporters in marine phytoplankton and their viruses: cross-domain commonalities in viral-host gene exchanges. <i>Environmental Microbiology</i> , 2012, 14, 162-176.	3.8	70
180	An Analysis of the Epidemic of <i>Klebsiella pneumoniae</i> Carbapenemase-Producing <i>K. pneumoniae</i> : Convergence of Two Evolutionary Mechanisms Creates the "Perfect Storm". <i>Journal of Infectious Diseases</i> , 2018, 217, 82-92.	4.0	70

#	ARTICLE	IF	CITATIONS
181	Secretion and expression of the <i>Pasteurella haemolytica</i> Leukotoxin. <i>Journal of Bacteriology</i> , 1990, 172, 2343-2350.	2.2	69
182	<i>Enterococcus faecalis</i> antigens in human infections. <i>Infection and Immunity</i> , 1997, 65, 4207-4215.	2.2	68
183	Complete genome sequence of <i>Treponema pallidum</i> ssp. <i>pallidum</i> strain SS14 determined with oligonucleotide arrays. <i>BMC Microbiology</i> , 2008, 8, 76.	3.3	66
184	Resequencing of <i>Treponema pallidum</i> ssp. <i>pallidum</i> Strains Nichols and SS14: Correction of Sequencing Errors Resulted in Increased Separation of Syphilis <i>Treponema</i> Subclusters. <i>PLoS ONE</i> , 2013, 8, e74319.	2.5	66
185	Diet during Pregnancy and Infancy and the Infant Intestinal Microbiome. <i>Journal of Pediatrics</i> , 2018, 203, 47-54.e4.	1.8	66
186	Complete Genome Sequence of <i>Treponema paraluis-cuniculi</i> , Strain Cuniculi A: The Loss of Infectivity to Humans Is Associated with Genome Decay. <i>PLoS ONE</i> , 2011, 6, e20415.	2.5	66
187	Reactivity of Antibodies from Syphilis Patients to a Protein Array Representing the <i>Treponema pallidum</i> Proteome. <i>Journal of Clinical Microbiology</i> , 2006, 44, 888-891.	3.9	65
188	Enterococci: New Aspects of an Old Organism. <i>Proceedings of the Association of American Physicians</i> , 1999, 111, 328-334.	2.0	64
189	The genome of <i>Treponema pallidum</i> : new light on the agent of syphilis. <i>FEMS Microbiology Reviews</i> , 1998, 22, 323-332.	8.6	63
190	Conservation of Ebp-Type Pilus Genes among Enterococci and Demonstration of Their Role in Adherence of <i>Enterococcus faecalis</i> to Human Platelets. <i>Infection and Immunity</i> , 2011, 79, 2911-2920.	2.2	63
191	The transcriptional profile of coronary arteritis in Kawasaki disease. <i>BMC Genomics</i> , 2015, 16, 1076.	2.8	63
192	Symbiotic <i>Burkholderia</i> Species Show Diverse Arrangements of <i>nif</i> / <i>fix</i> and <i>nod</i> Genes and Lack Typical High-Affinity Cytochrome <i>cbb3</i> Oxidase Genes. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 609-619.	2.6	62
193	Generation of auxotrophic mutants of <i>Enterococcus faecalis</i> . <i>Journal of Bacteriology</i> , 1995, 177, 6866-6873.	2.2	61
194	Genome Scale Identification of <i>Treponema pallidum</i> Antigens. <i>Infection and Immunity</i> , 2005, 73, 4445-4450.	2.2	61
195	Increased Prevalence of Anellovirus in Pediatric Patients with Fever. <i>PLoS ONE</i> , 2012, 7, e50937.	2.5	61
196	XbaI and BlnI Genomic Cleavage Maps of <i>Escherichia coli</i> K-12 Strain MG1655 and Comparative Analysis of Other Strains. <i>Journal of Molecular Biology</i> , 1993, 232, 419-445.	4.2	60
197	Genome Analysis of <i>Treponema pallidum</i> subsp. <i>pallidum</i> and subsp. <i>pertenue</i> Strains: Most of the Genetic Differences Are Localized in Six Regions. <i>PLoS ONE</i> , 2010, 5, e15713.	2.5	59
198	REGIONAL SPECIFICITY OF ILLEGITIMATE RECOMBINATION BY THE TRANSLOCATABLE AMPICILLIN-RESISTANCE ELEMENT Tn1 IN THE GENOME OF PHAGE P22. <i>Genetics</i> , 1979, 92, 685-710.	2.9	59

#	ARTICLE	IF	CITATIONS
199	Characterization of Dihydrofolate Reductase Genes from Trimethoprim-Susceptible and Trimethoprim-Resistant Strains of <i>Enterococcus faecalis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 1999, 43, 141-147.	3.2	58
200	Detection of a murine coronavirus nonstructural protein encoded in a downstream open reading frame. <i>Virology</i> , 1988, 164, 156-164.	2.4	57
201	Anaerobic control of colicin E1 production. <i>Journal of Bacteriology</i> , 1992, 174, 5101-5109.	2.2	57
202	Astrovirus MLB2 Viremia in Febrile Child. <i>Emerging Infectious Diseases</i> , 2011, 17, 2050-2.	4.3	57
203	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. <i>Nature Genetics</i> , 2017, 49, 1714-1721.	21.4	57
204	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
205	Longitudinal Prediction of the Infant Gut Microbiome with Dynamic Bayesian Networks. <i>Scientific Reports</i> , 2016, 6, 20359.	3.3	55
206	<i>R2d2</i> Drives Selfish Sweeps in the House Mouse. <i>Molecular Biology and Evolution</i> , 2016, 33, 1381-1395.	8.9	55
207	Effect of Disruption of a Gene Encoding an Autolysin of <i>Enterococcus faecalis</i> OG1RF. <i>Antimicrobial Agents and Chemotherapy</i> , 1998, 42, 2883-2888.	3.2	54
208	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , 2006, 440, 1194-1198.	27.8	53
209	Whole Genome Sequence of the <i>Treponema</i> Fribourg-Blanc: Unspecified Simian Isolate Is Highly Similar to the Yaws Subspecies. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2172.	3.0	53
210	Circadian rhythms and the gut microbiome synchronize the host's metabolic response to diet. <i>Cell Metabolism</i> , 2021, 33, 873-887.	16.2	53
211	The finished DNA sequence of human chromosome 12. <i>Nature</i> , 2006, 440, 346-351.	27.8	51
212	A non-human primate system for large-scale genetic studies of complex traits. <i>Human Molecular Genetics</i> , 2012, 21, 3307-3316.	2.9	51
213	Graph concordance of next-generation sequence assemblies. <i>Bioinformatics</i> , 2012, 28, 13-16.	4.1	51
214	Whole Genome Sequence of the <i>Treponema pallidum</i> subsp. <i>endemicum</i> Strain Bosnia A: The Genome Is Related to Yaws Treponemes but Contains Few Loci Similar to Syphilis Treponemes. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3261.	3.0	51
215	Temporal control of colicin E1 induction. <i>Journal of Bacteriology</i> , 1987, 169, 5028-5034.	2.2	50
216	Human Glutamate Pyruvate Transaminase (GPT): Localization to 8q24.3, cDNA and Genomic Sequences, and Polymorphic Sites. <i>Genomics</i> , 1997, 40, 247-252.	2.9	50

#	ARTICLE	IF	CITATIONS
217	Nodulation and effective nitrogen fixation of <i>Macroptilium atropurpureum</i> (siratro) by <i>Burkholderia tuberum</i> , a nodulating and plant growth promoting beta-proteobacterium, are influenced by environmental factors. <i>Plant and Soil</i> , 2013, 369, 543-562.	3.7	50
218	Effects of Walnut Consumption on Colon Carcinogenesis and Microbial Community Structure. <i>Cancer Prevention Research</i> , 2016, 9, 692-703.	1.5	50
219	Biology of <i>Treponema pallidum</i> : correlation of functional activities with genome sequence data. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2001, 3, 37-62.	1.0	50
220	Multiple chromosomes in bacteria: structure and function of chromosome II of <i>Rhodobacter sphaeroides</i> 2.4.1T. <i>Journal of Bacteriology</i> , 1994, 176, 7694-7702.	2.2	49
221	Household air pollution and the lung microbiome of healthy adults in Malawi: a cross-sectional study. <i>BMC Microbiology</i> , 2016, 16, 182.	3.3	49
222	Rapid replacement by non-vaccine pneumococcal serotypes may mitigate the impact of the pneumococcal conjugate vaccine on nasopharyngeal bacterial ecology. <i>Scientific Reports</i> , 2017, 7, 8127.	3.3	49
223	The Genome of C57BL/6J "Eve", the Mother of the Laboratory Mouse Genome Reference Strain. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1795-1805.	1.8	49
224	Optimizing Read Mapping to Reference Genomes to Determine Composition and Species Prevalence in Microbial Communities. <i>PLoS ONE</i> , 2012, 7, e36427.	2.5	48
225	Characterization of mutations in the <i>PAS</i> domain of the <i>EvgS</i> sensor kinase selected by laboratory evolution for acid resistance in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2014, 93, 911-927.	2.5	48
226	Meta-analysis of the lung microbiota in pulmonary tuberculosis. <i>Tuberculosis</i> , 2018, 109, 102-108.	1.9	48
227	Analysis of transcriptome data in the red flour beetle, <i>Tribolium castaneum</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 380-386.	2.7	46
228	High-Resolution Genetic Mapping in the Diversity Outbred Mouse Population Identifies <i>Apobec1</i> as a Candidate Gene for Atherosclerosis. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2353-2363.	1.8	46
229	tif-1 mutation alters polynucleotide recognition by the <i>recA</i> protein of <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1981, 78, 6061-6065.	7.1	45
230	The relationships between environmental bacterial exposure, airway bacterial colonization, and asthma. <i>Current Opinion in Allergy and Clinical Immunology</i> , 2014, 14, 137-142.	2.3	45
231	Sequencing strategies and characterization of 721 vervet monkey genomes for future genetic analyses of medically relevant traits. <i>BMC Biology</i> , 2015, 13, 41.	3.8	45
232	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	12.6	45
233	Systematic Cloning of <i>Treponema pallidum</i> Open Reading Frames for Protein Expression and Antigen Discovery. <i>Genome Research</i> , 2003, 13, 1665-1674.	5.5	43
234	Translocation of <i>Enterococcus faecalis</i> Strains across a Monolayer of Polarized Human Enterocyte-Like T84 Cells. <i>Journal of Clinical Microbiology</i> , 2004, 42, 1149-1154.	3.9	43

#	ARTICLE	IF	CITATIONS
235	What everybody should know about the rat genome and its online resources. <i>Nature Genetics</i> , 2008, 40, 523-527.	21.4	43
236	A Dominant Mutation in Hexokinase 1 (<i>HK1</i>) Causes Retinitis Pigmentosa. , 2014, 55, 7147.		43
237	Antigenic and virulence properties of <i>Pasteurella haemolytica</i> leukotoxin mutants. <i>Infection and Immunity</i> , 1995, 63, 1033-1039.	2.2	43
238	Community annotation: Procedures, protocols, and supporting tools. <i>Genome Research</i> , 2006, 16, 1329-1333.	5.5	42
239	Genome Differences between <i>Treponema pallidum</i> subsp. <i>pallidum</i> Strain Nichols and <i>T. paraluisuniculi</i> Strain Cuniculi A. <i>Infection and Immunity</i> , 2007, 75, 5859-5866.	2.2	42
240	Conditional adherence of <i>Enterococcus faecalis</i> to extracellular matrix proteins. <i>FEMS Immunology and Medical Microbiology</i> , 1998, 21, 287-295.	2.7	41
241	Small Bowel Resection Induces Long-Term Changes in the Enteric Microbiota of Mice. <i>Journal of Gastrointestinal Surgery</i> , 2015, 19, 56-64.	1.7	41
242	Identification of Candidate Adherent-Invasive <i>E. coli</i> Signature Transcripts by Genomic/Transcriptomic Analysis. <i>PLoS ONE</i> , 2015, 10, e0130902.	2.5	40
243	Conjugal Transfer of Plasmid DNA from <i>Escherichia coli</i> to <i>Enterococci</i> : A Method to Make Insertion Mutations. <i>Plasmid</i> , 1998, 39, 182-186.	1.4	39
244	Virome genomics: a tool for defining the human virome. <i>Current Opinion in Microbiology</i> , 2013, 16, 479-484.	5.1	38
245	Evolutionary Genomics of <i>Salmonella enterica</i> Subspecies. <i>MBio</i> , 2013, 4, .	4.1	38
246	Methicillin-Susceptible, Vancomycin-Resistant <i>Staphylococcus aureus</i> , Brazil. <i>Emerging Infectious Diseases</i> , 2015, 21, 1844-1848.	4.3	38
247	Genetic Organization of Plasmid ColJ, Encoding Colicin J _s Activity, Immunity, and Release Genes. <i>Journal of Bacteriology</i> , 2001, 183, 3949-3957.	2.2	37
248	The Iron- and Temperature-Regulated <i>cjrBC</i> Genes of <i>Shigella</i> and Enteroinvasive <i>Escherichia coli</i> Strains Code for Colicin J _s Uptake. <i>Journal of Bacteriology</i> , 2001, 183, 3958-3966.	2.2	37
249	Comparative analysis of the bovine MHC class IIb sequence1 identifies inversion breakpoints and three unexpected genes. <i>Animal Genetics</i> , 2006, 37, 121-129.	1.7	37
250	ENCODE: More genomic empowerment. <i>Genome Research</i> , 2007, 17, 667-668.	5.5	37
251	Complete genome sequence of <i>Treponema pallidum</i> strain DAL-1. <i>Standards in Genomic Sciences</i> , 2012, 7, 12-21.	1.5	37
252	Exome-Based Mapping and Variant Prioritization for Inherited Mendelian Disorders. <i>American Journal of Human Genetics</i> , 2014, 94, 373-384.	6.2	37

#	ARTICLE	IF	CITATIONS
253	Application of Next-Generation Sequencing to Identify Genes and Mutations Causing Autosomal Dominant Retinitis Pigmentosa (adRP). <i>Advances in Experimental Medicine and Biology</i> , 2014, 801, 123-129.	1.6	37
254	Candidate Genes That May Be Responsible for the Unusual Resistances Exhibited by <i>Bacillus pumilus</i> SAFR-032 Spores. <i>PLoS ONE</i> , 2013, 8, e66012.	2.5	37
255	Mapping protein-ligand interactions using whole genome phage display libraries. <i>Gene</i> , 1998, 221, 79-83.	2.2	36
256	Revised Sequence and Annotation of the <i>Rhodobacter sphaeroides</i> 2.4.1 Genome. <i>Journal of Bacteriology</i> , 2012, 194, 7016-7017.	2.2	36
257	A Novel Intronic Single Nucleotide Polymorphism in the <i>Myosin heavy polypeptide 4</i> Gene Is Responsible for the Mini-Muscle Phenotype Characterized by Major Reduction in Hind-Limb Muscle Mass in Mice. <i>Genetics</i> , 2013, 195, 1385-1395.	2.9	36
258	Physical map of the genome of <i>Treponema pallidum</i> subsp. <i>pallidum</i> (Nichols). <i>Journal of Bacteriology</i> , 1995, 177, 1797-1804.	2.2	35
259	Interaction of the RecA Protein of <i>Escherichia coli</i> with Single-stranded Oligodeoxyribonucleotides. <i>Nucleic Acids Research</i> , 1996, 24, 4933-4939.	14.5	35
260	From microbial genome sequence to applications. <i>Research in Microbiology</i> , 2000, 151, 151-158.	2.1	35
261	Use of bronchoalveolar lavage to assess the respiratory microbiome: signal in the noise. <i>Lancet Respiratory Medicine</i> , 2013, 1, 354-356.	10.7	35
262	Precise Dissection of an <i>Escherichia coli</i> O157:H7 Outbreak by Single Nucleotide Polymorphism Analysis. <i>Journal of Clinical Microbiology</i> , 2013, 51, 3950-3954.	3.9	35
263	Phenotypic and Genotypic Analysis of <i>Clostridium difficile</i> Isolates: a Single-Center Study. <i>Journal of Clinical Microbiology</i> , 2014, 52, 4260-4266.	3.9	35
264	The importance of the microbiome in epidemiologic research. <i>Annals of Epidemiology</i> , 2016, 26, 301-305.	1.9	35
265	Effects of diet on the childhood gut microbiome and its implications for atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 1636-1637.e5.	2.9	35
266	Host genetic control of gut microbiome composition. <i>Mammalian Genome</i> , 2021, 32, 263-281.	2.2	35
267	Targeted High-Throughput DNA Sequencing for Gene Discovery in Retinitis Pigmentosa. <i>Advances in Experimental Medicine and Biology</i> , 2010, 664, 325-331.	1.6	35
268	Expression of the <i>Pasteurella haemolytica</i> leukotoxin is inhibited by a locus that encodes an ATP-binding cassette homolog. <i>Infection and Immunity</i> , 1993, 61, 3942-3951.	2.2	35
269	Genomics and Bacterial Pathogenesis. <i>Emerging Infectious Diseases</i> , 2000, 6, 496-504.	4.3	35
270	Rapid growth is a dominant predictor of hepcidin suppression and declining ferritin in Gambian infants. <i>Haematologica</i> , 2019, 104, 1542-1553.	3.5	34

#	ARTICLE	IF	CITATIONS
271	Increased production of colicin E1 in stationary phase. <i>Journal of Bacteriology</i> , 1996, 178, 1928-1935.	2.2	33
272	Epidemiology of <i>Staphylococcus aureus</i> during space flight. <i>FEMS Immunology and Medical Microbiology</i> , 1996, 16, 273-281.	2.7	33
273	Rapid Evolution by Positive Darwinian Selection in T-Cell Antigen CD4 in Primates. <i>Journal of Molecular Evolution</i> , 2008, 66, 446-456.	1.8	33
274	Coverage theories for metagenomic DNA sequencing based on a generalization of Stevens's theorem. <i>Journal of Mathematical Biology</i> , 2013, 67, 1141-1161.	1.9	33
275	Genetics of bacteriophage P22 III. The late operon. <i>Virology</i> , 1980, 106, 82-91.	2.4	32
276	A vertebrate case study of the quality of assemblies derived from next-generation sequences. <i>Genome Biology</i> , 2011, 12, R31.	9.6	32
277	Structure of <i>rrn</i> operons in pathogenic non-cultivable treponemes: sequence but not genomic position of intergenic spacers correlates with classification of <i>Treponema pallidum</i> and <i>Treponema paraluis-cuniculi</i> strains. <i>Journal of Medical Microbiology</i> , 2013, 62, 196-207.	1.8	32
278	DNA and Nucleoside Triphosphate Binding Properties of <i>recA</i> Protein from <i>Escherichia coli</i> . <i>Progress in Molecular Biology and Translational Science</i> , 1981, 26, 265-279.	1.9	31
279	DNA repair mutants of <i>Rhodobacter sphaeroides</i> . <i>Journal of Bacteriology</i> , 1995, 177, 3027-3035.	2.2	31
280	HCoDES Reveals Chromosomal DNA End Structures with Single-Nucleotide Resolution. <i>Molecular Cell</i> , 2014, 56, 808-818.	9.7	31
281	Transmission of <i>Staphylococcus aureus</i> from Humans to Green Monkeys in The Gambia as Revealed by Whole-Genome Sequencing. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5910-5917.	3.1	30
282	Host Genes Related to Paneth Cells and Xenobiotic Metabolism Are Associated with Shifts in Human Ileum-Associated Microbial Composition. <i>PLoS ONE</i> , 2012, 7, e30044.	2.5	28
283	Characterization of the cytoplasmic filament protein gene (<i>cfpA</i>) of <i>Treponema pallidum</i> subsp. <i>pallidum</i> . <i>Journal of Bacteriology</i> , 1996, 178, 3177-3187.	2.2	27
284	<i>CcpA</i> Is Important for Growth and Virulence of <i>Enterococcus faecium</i> . <i>Infection and Immunity</i> , 2014, 82, 3580-3587.	2.2	27
285	Discriminatory Indices of Typing Methods for Epidemiologic Analysis of Contemporary <i>Staphylococcus aureus</i> Strains. <i>Medicine (United States)</i> , 2015, 94, e1534.	1.0	27
286	BAC Library of <i>T. pallidum</i> DNA in <i>E. coli</i> . <i>Genome Research</i> , 2002, 12, 515-522.	5.5	26
287	Shedding genomic light on Aristotle's lantern. <i>Developmental Biology</i> , 2006, 300, 2-8.	2.0	26
288	Oral Microbiome in HIV-Infected Women: Shifts in the Abundance of Pathogenic and Beneficial Bacteria Are Associated with Aging, HIV Load, CD4 Count, and Antiretroviral Therapy. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 276-286.	1.1	26

#	ARTICLE	IF	CITATIONS
289	Transposition of λ placMu is mediated by the A protein altered at its carboxy-terminal end. <i>Gene</i> , 1988, 71, 177-186.	2.2	25
290	Extreme Sensory Complexity Encoded in the 10-Megabase Draft Genome Sequence of the Chromatically Acclimating Cyanobacterium <i>Tolypothrix</i> sp. PCC 7601. <i>Genome Announcements</i> , 2015, 3, .	0.8	25
291	Lung microbiome in human immunodeficiency virus infection. <i>Translational Research</i> , 2017, 179, 97-107.	5.0	25
292	Analysis of Nuclear Receptor Pseudogenes in Vertebrates: How the Silent Tell Their Stories. <i>Molecular Biology and Evolution</i> , 2007, 25, 131-143.	8.9	24
293	Ceftaroline-Resistant, Daptomycin-Tolerant, and Heterogeneous Vancomycin-Intermediate Methicillin-Resistant <i>Staphylococcus aureus</i> Causing Infective Endocarditis. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	24
294	Direct selection of mutations reducing transcription or translation of the <i>recA</i> gene of <i>Escherichia coli</i> with a <i>recA-lacZ</i> protein fusion. <i>Journal of Bacteriology</i> , 1985, 163, 748-755.	2.2	24
295	Interaction of the CRP-cAMP complex with the <i>cea</i> regulatory region. <i>Molecular Genetics and Genomics</i> , 1989, 215, 537-542.	2.4	23
296	Tandem duplications of the <i>lac</i> region of the <i>Escherichia coli</i> chromosome. <i>Biochimie</i> , 1991, 73, 343-352.	2.6	23
297	Sweetness and light: illuminating the honey bee genome. <i>Insect Molecular Biology</i> , 2006, 15, 535-539.	2.0	23
298	A Cluster of Genes Involved in Polysaccharide Biosynthesis from <i>Enterococcus faecalis</i> OG1RF. <i>Infection and Immunity</i> , 1998, 66, 4313-4323.	2.2	23
299	Mutations at the Cysteine Codons of the <i>recA</i> Gene of <i>Escherichia coli</i> . <i>DNA and Cell Biology</i> , 1988, 7, 389-398.	5.2	22
300	Genome sequence of an Australian kangaroo, <i>Macropus eugenii</i> , provides insight into the evolution of mammalian reproduction and development. <i>Genome Biology</i> , 2011, 12, 414.	9.6	22
301	SfiI genomic cleavage map of <i>Escherichia coli</i> K-12 strain MG1655. <i>Nucleic Acids Research</i> , 1992, 20, 1129-1137.	14.5	21
302	Comparing Vertebrate Whole-Genome Shotgun Reads to the Human Genome. <i>Genome Research</i> , 2001, 11, 1807-1816.	5.5	21
303	A high-throughput percentage-of-binding strategy to measure binding energies in DNA-protein interactions: application to genome-scale site discovery. <i>Nucleic Acids Research</i> , 2008, 36, 4863-4871.	14.5	21
304	A Microbe Associated with Sleep Revealed by a Novel Systems Genetic Analysis of the Microbiome in Collaborative Cross Mice. <i>Genetics</i> , 2020, 214, 719-733.	2.9	20
305	The Gut Microbiome and Substance Use Disorder. <i>Frontiers in Neuroscience</i> , 2021, 15, 725500.	2.8	20
306	Hormonal Regulation of Cytochrome Oxidase Subunit Messenger RNAs in Rat Sertoli Cells. <i>Molecular Endocrinology</i> , 1991, 5, 1669-1676.	3.7	19

#	ARTICLE	IF	CITATIONS
307	Cyanobacterial signature genes. <i>Photosynthesis Research</i> , 2003, 75, 211-221.	2.9	19
308	A Retrospective Study on Genetic Heterogeneity within <i>Treponema</i> Strains: Subpopulations Are Genetically Distinct in a Limited Number of Positions. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004110.	3.0	19
309	The promoter of the <i>recA</i> gene of <i>Escherichia coli</i> . <i>Biochimie</i> , 1991, 73, 457-470.	2.6	18
310	Complete nucleotide sequence of a P2 family lysogenic bacteriophage, <i>ϕ</i> MhaA1-PHL101, from <i>Mannheimia haemolytica</i> serotype A1. <i>Virology</i> , 2006, 350, 79-89.	2.4	18
311	Rats in the genomic era. <i>Physiological Genomics</i> , 2008, 32, 273-282.	2.3	18
312	Genome Sequence of the Emerging Pathogen <i>Helicobacter canadensis</i> . <i>Journal of Bacteriology</i> , 2009, 191, 5566-5567.	2.2	18
313	Characterization of Mucosal Dysbiosis of Early Colonic Neoplasia. <i>Npj Precision Oncology</i> , 2019, 3, 29.	5.4	18
314	Colicins produced by the <i>Escherichia fergusonii</i> strains closely resemble colicins encoded by <i>Escherichia coli</i> . <i>FEMS Microbiology Letters</i> , 2002, 208, 259-262.	1.8	17
315	Genome Analysis of a Highly Virulent Serotype 1 Strain of <i>Streptococcus pneumoniae</i> from West Africa. <i>PLoS ONE</i> , 2012, 7, e26742.	2.5	17
316	Static DNA Bending and Protein Interactions Within the <i>Pasteurella haemolytica</i> Leukotoxin Promoter Region: Development of an Activation Model for Leukotoxin Transcriptional Control. <i>DNA and Cell Biology</i> , 1994, 13, 171-181.	1.9	16
317	Sensitization of bacteria to danofloxacin by temperate prophages. <i>Antimicrobial Agents and Chemotherapy</i> , 1996, 40, 1561-1563.	3.2	16
318	Dynamic Building of a BAC Clone Tiling Path for the Rat Genome Sequencing Project. <i>Genome Research</i> , 2004, 14, 679-684.	5.5	16
319	Isolation of <i>Pasteurella haemolytica</i> leukotoxin mutants. <i>Infection and Immunity</i> , 1995, 63, 1027-1032.	2.2	16
320	mBLAST: Keeping up with the Sequencing Explosion for (Meta) Genome Analysis. <i>Journal of Data Mining in Genomics & Proteomics</i> , 2013, 04, .	0.5	16
321	22 The <i>recA</i> Enzyme of <i>Escherichia coli</i> and Recombination Assays. <i>The Enzymes</i> , 1981, 14, 445-470.	1.7	15
322	The genome of <i>Apis mellifera</i> : dialog between linkage mapping and sequence assembly. <i>Genome Biology</i> , 2007, 8, 403.	9.6	15
323	Statistical Object Data Analysis of Taxonomic Trees from Human Microbiome Data. <i>PLoS ONE</i> , 2012, 7, e48996.	2.5	15
324	Genetic Basis of Aerobically Supported Voluntary Exercise: Results from a Selection Experiment with House Mice. <i>Genetics</i> , 2020, 216, 781-804.	2.9	15

#	ARTICLE	IF	CITATIONS
325	Generation and Validation of a <i>Shewanella oneidensis</i> MR-1 Clone Set for Protein Expression and Phage Display. <i>PLoS ONE</i> , 2008, 3, e2983.	2.5	15
326	High-Resolution Quantification of Hepatitis C Virus Genome-Wide Mutation Load and Its Correlation with the Outcome of Peginterferon-Alpha2a and Ribavirin Combination Therapy. <i>PLoS ONE</i> , 2014, 9, e100131.	2.5	15
327	The genome sequence of <i>Treponema pallidum</i> , the syphilis spirochete: will clinicians benefit?. <i>Current Opinion in Infectious Diseases</i> , 2000, 13, 29-36.	3.1	14
328	Pooled genomic indexing of rhesus macaque. <i>Genome Research</i> , 2005, 15, 292-301.	5.5	14
329	High mobility group (HMG-box) genes in the honeybee fungal pathogen <i>Ascosphaera apis</i> . <i>Mycologia</i> , 2007, 99, 553-561.	1.9	14
330	Simple sequence repeats in <i>Helicobacter canadensis</i> and their role in phase variable expression and C-terminal sequence switching. <i>BMC Genomics</i> , 2010, 11, 67.	2.8	14
331	Enzymatic activities of the RecA protein of <i>Escherichia coli</i> . <i>Biochimie</i> , 1982, 64, 611-616.	2.6	13
332	Mutation of the promoter and LexA binding sites of <i>cea</i> , the gene encoding colicin E1. <i>Molecular Genetics and Genomics</i> , 1989, 215, 483-489.	2.4	13
333	Selection of models for the analysis of risk-factor trees: leveraging biological knowledge to mine large sets of risk factors with application to microbiome data. <i>Bioinformatics</i> , 2015, 31, 1607-1613.	4.1	12
334	Differences in Gut Microbiome in Hospitalized Immunocompetent vs. Immunocompromised Children, Including Those With Sickle Cell Disease. <i>Frontiers in Pediatrics</i> , 2020, 8, 583446.	1.9	12
335	A general method for the induction and screening of antisera for cDNA-encoded polypeptides: antibodies specific for a coronavirus putative polymerase-encoding gene. <i>Gene</i> , 1989, 85, 413-420.	2.2	10
336	Inactivation of SAM-Methyltransferase is the Mechanism of Attenuation of a Historic Louse Borne Typhus Vaccine Strain. <i>PLoS ONE</i> , 2014, 9, e113285.	2.5	10
337	Longitudinal Analysis of Serum Cytokine Levels and Gut Microbial Abundance Links IL-17/IL-22 With <i>Clostridia</i> and Insulin Sensitivity in Humans. <i>Diabetes</i> , 2020, 69, 1833-1842.	0.6	10
338	Genome Sequences of 15 <i>Gardnerella vaginalis</i> Strains Isolated from the Vaginas of Women with and without Bacterial Vaginosis. <i>Genome Announcements</i> , 2016, 4, .	0.8	9
339	Use of transcription and translation signals from the colicin E1 gene to express DNA sequences in <i>Escherichia coli</i> . <i>Gene Analysis Techniques</i> , 1985, 2, 9-16.	1.0	8
340	The volatile microbiome. <i>Genome Biology</i> , 2011, 12, 114.	9.6	8
341	Hypothesis Testing of Metagenomic Data. , 2015, , 81-96.		8
342	Identification of a Novel Gene on 10q22.1 Causing Autosomal Dominant Retinitis Pigmentosa (adRP). <i>Advances in Experimental Medicine and Biology</i> , 2016, 854, 193-200.	1.6	8

#	ARTICLE	IF	CITATIONS
343	Characterization of RecA1332in vivoandin vitro. A role for helix E as a liaison between the subunit-subunit interface and the DNA and ATP binding domains of RecA protein. <i>Genes To Cells</i> , 1998, 3, 79-97.	1.2	7
344	Recognition of pore-forming colicin Y by its cognate immunity protein. <i>FEMS Microbiology Letters</i> , 2006, 258, 108-113.	1.8	7
345	[9] Use of open reading frame expression vectors. <i>Methods in Enzymology</i> , 1987, 154, 156-163.	1.0	6
346	Illuminating the agent of syphilis: The <i>Treponema pallidum</i> genome project (minireview). <i>Electrophoresis</i> , 1998, 19, 551-553.	2.4	6
347	Sixty years of genome biology. <i>Genome Biology</i> , 2013, 14, 113.	9.6	6
348	Emergence of Rotavirus G12P[8] in St. Louis During the 2012-2013 Rotavirus Season. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2015, 4, e84-e89.	1.3	6
349	Genome Sequence of <i>Acetomicrobium hydrogeniformans</i> OS1. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
350	MSC: a metagenomic sequence classification algorithm. <i>Bioinformatics</i> , 2019, 35, 2932-2940.	4.1	6
351	Targeted mutagenesis of enterococcal genes. <i>Cytotechnology</i> , 1998, 20, 21-33.	0.7	5
352	Transduction in Gram-Negative Bacteria. , 0, , 561-579.		5
353	The <i>Escherichia fergusonii</i> iucABCD iutA genes are located within a larger chromosomal region similar to pathogenicity islands. <i>Folia Microbiologica</i> , 2003, 48, 139-147.	2.3	5
354	Expression capable library for studies of <i>Neisseria gonorrhoeae</i> , version 1.0. <i>BMC Microbiology</i> , 2005, 5, 50.	3.3	5
355	Comparison of Whole and Acellular Bronchoalveolar Lavage to Oral Wash Microbiomes. Should Acellular Bronchoalveolar Lavage Be the Standard?. <i>Annals of the American Thoracic Society</i> , 2014, 11, S72-S73.	3.2	5
356	Similar Bacterial Signatures in Intestinal Tissues, Milk, and Dendritic Cells of Lactating Mice Suggest a Possible Entero-Mammary Pathway. <i>Gastroenterology</i> , 2017, 152, S172.	1.3	5
357	Consent insufficient for data release-Response. <i>Science</i> , 2019, 364, 446-446.	12.6	5
358	New statistical method identifies cytokines that distinguish stool microbiomes. <i>Scientific Reports</i> , 2019, 9, 20082.	3.3	5
359	Approaches for integrating heterogeneous RNA-seq data reveal cross-talk between microbes and genes in asthmatic patients. <i>Genome Biology</i> , 2020, 21, 150.	8.8	5
360	Alterations in subgingival microbiota during full-fixed appliance orthodontic treatment-A prospective study. <i>Orthodontics and Craniofacial Research</i> , 2022, 25, 260-268.	2.8	5

#	ARTICLE	IF	CITATIONS
361	Evolving Methods for the Assembly of Large Genomes. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 189-194.	1.1	5
362	Genetics of bacteriophage P22 IV. Correlation of genetic and physical map using translocatable drug-resistance elements. Virology, 1980, 106, 92-99.	2.4	4
363	A Glimpse of Microbial Power in Preventive Medicine. JAMA Pediatrics, 2016, 170, 11.	6.2	4
364	Proteomics and metabolomics for analysis of the dynamics of microbiota. Expert Review of Proteomics, 2018, 15, 101-104.	3.0	4
365	Supraglottic Lung Microbiome Taxa Are Associated with Pulmonary Abnormalities in an HIV Longitudinal Cohort. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 1727-1731.	5.6	4
366	Defining the microbiome of the head and neck: A contemporary review. American Journal of Otolaryngology - Head and Neck Medicine and Surgery, 2022, 43, 103224.	1.3	4
367	Microbial sequencing to improve individual and population health. Genome Medicine, 2014, 6, 103.	8.2	3
368	Isolation of Methicillin-resistant Staphylococcus aureus and Multidrug-resistant Elizabethkingia meningoseptica From Neonates Within Minutes of Birth. Pediatric Infectious Disease Journal, 2017, 36, 123-124.	2.0	3
369	Colon Cancer Prevention with Walnuts: A Longitudinal Study in Mice from the Perspective of a Gut Enterotype-like Cluster. Cancer Prevention Research, 2020, 13, 15-24.	1.5	3
370	Association of gut microbiota and environment in children with AD, comparison of three cohorts of children. Clinical and Experimental Allergy, 2022, 52, 447-450.	2.9	3
371	Shotgun sequencing, clone pooling, and comparative strategies for mapping and sequencing. Targets, 2003, 2, 245-252.	0.3	2
372	A new era in the genomics of bacteria. Current Opinion in Microbiology, 2010, 13, 616-618.	5.1	2
373	The Impact of Next-Generation Sequencing Technologies on Metagenomics. , 2011, , 143-147.		2
374	Next-generation pathogen genomics. Genome Biology, 2014, 15, 528.	8.8	2
375	Improving Characterization of Understudied Human Microbiomes Using Targeted Phylogenetics. MSystems, 2020, 5, .	3.8	2
376	Introduction to mammalian genome special issue: the microbiome in human health and disease. Mammalian Genome, 2021, 32, 205-205.	2.2	2
377	Bacterial Virulence Factors as Targets for Chemotherapy. , 1992, , 323-346.		2
378	The genome of Treponema pallidum: new light on the agent of syphilis. FEMS Microbiology Reviews, 1998, 22, 323-332.	8.6	2

#	ARTICLE	IF	CITATIONS
379	Epidemiology of Staphylococcus aureus during space flight. FEMS Immunology and Medical Microbiology, 1996, 16, 273-281.	2.7	2
380	UTP Is a Cofactor for the DNA Strand Exchange Reaction Performed by the RecA Protein of Escherichia coli. Biochemistry, 1998, 37, 7313-7320.	2.5	1
381	Construction of Small Genome BAC Library for Functional and Genomic Applications. , 2004, 255, 047-056.		1
382	Genetic testing, biotechnology, and GMOs: A snapshot of public opinion, 2003 through 2004. Genetics in Medicine, 2005, 7, 454-455.	2.4	1
383	Host genes related to Paneth cells and xenobiotic metabolism are associated with shifts in human ileum-associated microbial composition. Inflammatory Bowel Diseases, 2011, 17, S80.	1.9	1
384	Cluster analysis of genome-wide expression differences in disease-unaffected ileal mucosa in inflammatory bowel diseases. , 2011, , .		1
385	Identification of novel and cross-species seroreactive proteins from Bacillus anthracis using a ligation-independent cloning-based, SOS-inducible expression system. Microbial Pathogenesis, 2012, 53, 250-258.	2.9	1
386	Abstract 4746: Microbes in the tumor microenvironment: Bacterial influences on host immunity in colorectal cancer. , 2018, , .		1
387	Targeted mutagenesis of enterococcal genes. , 1998, , 21-33.		1
388	Murine Model for Measuring Effects of Humanized-Dosing of Antibiotics on the Gut Microbiome. Frontiers in Microbiology, 2022, 13, 813849.	3.5	1
389	Isolation of enterococcal antigen-encoding genes from genomic libraries. Cytotechnology, 1998, 20, 95-106.	0.7	0
390	Preparation of BAC Libraries From Bacterial Genomes by In Vitro Packaging. , 2004, 255, 057-068.		0
391	Spirochete genomes. , 2005, , .		0
392	Microbial sequence assembly. , 2005, , .		0
393	The Human Virome in Children and its Relationship to Febrile Illness. Nature Precedings, 2010, , .	0.1	0
394	The Human Microbiome Project. , 2011, , 307-312.		0
395	NOD2 Genotype is Associated With Shifts in Human Ileal Mucosa-Associated Microbial Composition. Gastroenterology, 2011, 140, S-27.	1.3	0
396	1097 The Intestinal Microbiome in Children With Nonalcoholic Fatty Liver Disease—A Case-Control Study. Gastroenterology, 2016, 150, S219.	1.3	0

#	ARTICLE	IF	CITATIONS
397	“ROLE OF THE BETA-ADRENERGIC RECEPTORS IN THE CARDIAC RESPONSE TO BETA-BLOCKER THERAPY”, FASEB Journal, 2008, 22, 1046-4.	0.5	0
398	Resources for the Escherichia coli Genome Project. , 1998, , 489-497.		0
399	Comparative Pathogenomics of Spirochetes. , 0, , 141-159.		0
400	Abstract 2252: Microbial profiling of the head and neck tumor microenvironment as a biomarker of clinical response to chemoradiation. , 2017, , .		0
401	Indoor Dust Bacterial and Fungal Microbiome in Homes of Asthmatic Children from 5 US Cities. Journal of Allergy and Clinical Immunology, 2022, 149, AB83.	2.9	0
402	Abstract O.20: Deep RNA Sequencing Reveals a Transcriptional Profile of Cytotoxic T Lymphocyte Activation, Antigen Presentation, Immunoglobulin Production, and Type I Interferon Response in Kawasaki Disease Arteritis. Circulation, 2015, 131, .	1.6	0
403	Colicins produced by the Escherichia fergusonii strains closely resemble colicins encoded by Escherichia coli. FEMS Microbiology Letters, 2002, 208, 259-262.	1.8	0