

David Guttman

List of Publications by Year in descending order

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Version: 2024-02-01

186
papers

17,272
citations

11608

70
h-index

17055

122
g-index

204
all docs

204
docs citations

204
times ranked

21312
citing authors

#	ARTICLE	IF	CITATIONS
1	Gut microbiota of healthy Canadian infants: profiles by mode of delivery and infant diet at 4 months. <i>Cmaj</i> , 2013, 185, 385-394.	0.9	741
2	Assembly and ecological function of the root microbiome across angiosperm plant species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1157-E1165.	3.3	739
3	Disentangling Interactions in the Microbiome: A Network Perspective. <i>Trends in Microbiology</i> , 2017, 25, 217-228.	3.5	559
4	Impact of maternal intrapartum antibiotics, method of birth and breastfeeding on gut microbiota during the first year of life: a prospective cohort study. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2016, 123, 983-993.	1.1	453
5	Evolution of the Core Genome of <i>Pseudomonas syringae</i> , a Highly Clonal, Endemic Plant Pathogen. <i>Applied and Environmental Microbiology</i> , 2004, 70, 1999-2012.	1.4	414
6	Association of host genome with intestinal microbial composition in a large healthy cohort. <i>Nature Genetics</i> , 2016, 48, 1413-1417.	9.4	388
7	Clonal divergence in <i>Escherichia coli</i> as a result of recombination, not mutation. <i>Science</i> , 1994, 266, 1380-1383.	6.0	386
8	Gut Microbial Metabolism Drives Transformation of Msh2-Deficient Colon Epithelial Cells. <i>Cell</i> , 2014, 158, 288-299.	13.5	375
9	Prophages mediate defense against phage infection through diverse mechanisms. <i>ISME Journal</i> , 2016, 10, 2854-2866.	4.4	363
10	A Functional Screen for the Type III (Hrp) Secretome of the Plant Pathogen <i>Pseudomonas syringae</i> . <i>Science</i> , 2002, 295, 1722-1726.	6.0	353
11	The Gain-of-Function <i>Arabidopsis acd6</i> Mutant Reveals Novel Regulation and Function of the Salicylic Acid Signaling Pathway in Controlling Cell Death, Defenses, and Cell Growth. <i>Plant Cell</i> , 1999, 11, 1695-1708.	3.1	337
12	Infant gut microbiota and food sensitization: associations in the first year of life. <i>Clinical and Experimental Allergy</i> , 2015, 45, 632-643.	1.4	333
13	Lung microbiota across age and disease stage in cystic fibrosis. <i>Scientific Reports</i> , 2015, 5, 10241.	1.6	316
14	Next-generation mapping of <i>Arabidopsis</i> genes. <i>Plant Journal</i> , 2011, 67, 715-725.	2.8	284
15	Regulation of Obesity-Related Insulin Resistance with Gut Anti-inflammatory Agents. <i>Cell Metabolism</i> , 2015, 21, 527-542.	7.2	283
16	Seasonal Community Succession of the Phyllosphere Microbiome. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 274-285.	1.4	275
17	Phylogenetic Characterization of Virulence and Resistance Phenotypes of <i>Pseudomonas syringae</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 5182-5191.	1.4	260
18	Genomic Analysis of the Kiwifruit Pathogen <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> Provides Insight into the Origins of an Emergent Plant Disease. <i>PLoS Pathogens</i> , 2013, 9, e1003503.	2.1	247

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19	An extracellular network of Arabidopsis leucine-rich repeat receptor kinases. <i>Nature</i> , 2018, 553, 342-346.	13.7	241
20	Roles of Birth Mode and Infant Gut Microbiota in Intergenerational Transmission of Overweight and Obesity From Mother to Offspring. <i>JAMA Pediatrics</i> , 2018, 172, 368.	3.3	235
21	Infant gut microbiota and the hygiene hypothesis of allergic disease: impact of household pets and siblings on microbiota composition and diversity. <i>Allergy, Asthma and Clinical Immunology</i> , 2013, 9, 15.	0.9	219
22	Association of Exposure to Formula in the Hospital and Subsequent Infant Feeding Practices With Gut Microbiota and Risk of Overweight in the First Year of Life. <i>JAMA Pediatrics</i> , 2018, 172, e181161.	3.3	218
23	Exposure to household furry pets influences the gut microbiota of infants at 3-4 months following various birth scenarios. <i>Microbiome</i> , 2017, 5, 40.	4.9	197
24	Microbial genome-enabled insights into plant-microorganism interactions. <i>Nature Reviews Genetics</i> , 2014, 15, 797-813.	7.7	187
25	Population genomics of bacterial host adaptation. <i>Nature Reviews Genetics</i> , 2018, 19, 549-565.	7.7	186
26	The <i>Arabidopsis</i> ZED1 pseudokinase is required for ZAR1-mediated immunity induced by the <i>Pseudomonas syringae</i> type III effector HopZ1a. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18722-18727.	3.3	183
27	Type III Effector Diversification via Both Pathoadaptation and Horizontal Transfer in Response to a Coevolutionary Arms Race. <i>PLoS Genetics</i> , 2006, 2, e209.	1.5	179
28	A Bacterial Acetyltransferase Destroys Plant Microtubule Networks and Blocks Secretion. <i>PLoS Pathogens</i> , 2012, 8, e1002523.	2.1	178
29	Evolutionary and structural analyses of SARS-CoV-2 D614G spike protein mutation now documented worldwide. <i>Scientific Reports</i> , 2020, 10, 14031.	1.6	173
30	PAMDB, A Multilocus Sequence Typing and Analysis Database and Website for Plant-Associated Microbes. <i>Phytopathology</i> , 2010, 100, 208-215.	1.1	166
31	Increased Intestinal Permeability Is Associated With Later Development of Crohn's Disease. <i>Gastroenterology</i> , 2020, 159, 2092-2100.e5.	0.6	156
32	Allele-Specific Virulence Attenuation of the <i>Pseudomonas syringae</i> HopZ1a Type III Effector via the <i>Arabidopsis</i> ZAR1 Resistance Protein. <i>PLoS Genetics</i> , 2010, 6, e1000894.	1.5	151
33	Proposed Guidelines for a Unified Nomenclature and Phylogenetic Analysis of Type III Hop Effector Proteins in the Plant Pathogen <i>Pseudomonas syringae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 275-282.	1.4	148
34	NIN-like protein 8 is a master regulator of nitrate-promoted seed germination in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2016, 7, 13179.	5.8	147
35	The pan-genome effector-triggered immunity landscape of a host-pathogen interaction. <i>Science</i> , 2020, 367, 763-768.	6.0	146
36	Oral Vancomycin Followed by Fecal Transplantation Versus Tapering Oral Vancomycin Treatment for Recurrent <i>Clostridium difficile</i> Infection: An Open-Label, Randomized Controlled Trial. <i>Clinical Infectious Diseases</i> , 2017, 64, 265-271.	2.9	145

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37	Comparative Genomics of Host-Specific Virulence in <i>Pseudomonas syringae</i> . <i>Genetics</i> , 2006, 174, 1041-1056.	1.2	139
38	Functional Analysis of the Type III Effectors AvrRpt2 and AvrRpm1 of <i>Pseudomonas syringae</i> with the Use of a Single-Copy Genomic Integration System. <i>Molecular Plant-Microbe Interactions</i> , 2001, 14, 145-155.	1.4	136
39	Comparison of Co-housing and Littermate Methods for Microbiota Standardization in Mouse Models. <i>Cell Reports</i> , 2019, 27, 1910-1919.e2.	2.9	134
40	Selective Sweeps and Parallel Pathoadaptation Drive <i>Pseudomonas aeruginosa</i> Evolution in the Cystic Fibrosis Lung. <i>MBio</i> , 2015, 6, e00981-15.	1.8	133
41	An X-linked gene with a degenerate Y-linked homologue in a dioecious plant. <i>Nature</i> , 1998, 393, 263-266.	13.7	132
42	Gut-associated IgA+ immune cells regulate obesity-related insulin resistance. <i>Nature Communications</i> , 2019, 10, 3650.	5.8	131
43	Mosaic Evolution of the Severe Acute Respiratory Syndrome Coronavirus. <i>Journal of Virology</i> , 2004, 78, 76-82.	1.5	130
44	Evolution, genomics and epidemiology of <i>Pseudomonas syringae</i> . <i>Molecular Plant Pathology</i> , 2017, 18, 152-168.	2.0	130
45	<i>Pseudomonas syringae</i> pv. <i>actinidiae</i> (PSA) Isolates from Recent Bacterial Canker of Kiwifruit Outbreaks Belong to the Same Genetic Lineage. <i>PLoS ONE</i> , 2012, 7, e36518.	1.1	124
46	Detecting selective sweeps in naturally occurring <i>Escherichia coli</i> . <i>Genetics</i> , 1994, 138, 993-1003.	1.2	124
47	Terminal Reassortment Drives the Quantum Evolution of Type III Effectors in Bacterial Pathogens. <i>PLoS Pathogens</i> , 2006, 2, e104.	2.1	123
48	Evolution of the type III secretion system and its effectors in plant-microbe interactions. <i>New Phytologist</i> , 2008, 177, 33-47.	3.5	121
49	Molecular Evolution of <i>Pseudomonas syringae</i> Type III Secreted Effector Proteins. <i>Frontiers in Plant Science</i> , 2019, 10, 418.	1.7	121
50	Diverse Evolutionary Mechanisms Shape the Type III Effector Virulence Factor Repertoire in the Plant Pathogen <i>Pseudomonas syringae</i> . <i>Genetics</i> , 2004, 167, 1341-1360.	1.2	114
51	Recombination of ecologically and evolutionarily significant loci maintains genetic cohesion in the <i>Pseudomonas syringae</i> species complex. <i>Genome Biology</i> , 2019, 20, 3.	3.8	114
52	Tri6 Is a Global Transcription Regulator in the Phytopathogen <i>Fusarium graminearum</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002266.	2.1	109
53	The HopZ Family of <i>Pseudomonas syringae</i> Type III Effectors Require Myristoylation for Virulence and Avirulence Functions in <i>Arabidopsis thaliana</i> . <i>Journal of Bacteriology</i> , 2008, 190, 2880-2891.	1.0	105
54	Evolution of Plant Pathogenesis in <i>Pseudomonas syringae</i> : A Genomics Perspective. <i>Annual Review of Phytopathology</i> , 2011, 49, 269-289.	3.5	105

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55	Transcriptomic Responses of the Softwood-Degrading White-Rot Fungus <i>Phanerochaete carnos</i> during Growth on Coniferous and Deciduous Wood. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3211-3218.	1.4	105
56	<i>Staphylococcus aureus</i> interaction with <i>Pseudomonas aeruginosa</i> biofilm enhances tobramycin resistance. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 25.	2.9	105
57	<i>Pseudomonas syringae</i> Strains Naturally Lacking the Classical <i>P. syringae</i> hrp/hrc Locus Are Common Leaf Colonizers Equipped with an Atypical Type III Secretion System. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 198-210.	1.4	102
58	Expanded type III effector recognition by the ZAR1 NLR protein using ZED1-related kinases. <i>Nature Plants</i> , 2017, 3, 17027.	4.7	101
59	Host-pathogen interplay and the evolution of bacterial effectors. <i>Cellular Microbiology</i> , 2007, 10, 071127144819001-???	1.1	95
60	Neutral Genomic Microevolution of a Recently Emerged Pathogen, <i>Salmonella enterica</i> Serovar Agona. <i>PLoS Genetics</i> , 2013, 9, e1003471.	1.5	94
61	Navigating social and ethical challenges of biobanking for human microbiome research. <i>BMC Medical Ethics</i> , 2017, 18, 1.	1.0	94
62	Multiple infections of <i>Ixodes scapularis</i> ticks by <i>Borrelia burgdorferi</i> as revealed by single-strand conformation polymorphism analysis. <i>Journal of Clinical Microbiology</i> , 1996, 34, 652-656.	1.8	93
63	NKT Cell-Deficient Mice Harbor an Altered Microbiota That Fuels Intestinal Inflammation during Chemically Induced Colitis. <i>Journal of Immunology</i> , 2016, 197, 4464-4472.	0.4	92
64	Phenotypic diversity within a <i>Pseudomonas aeruginosa</i> population infecting an adult with cystic fibrosis. <i>Scientific Reports</i> , 2015, 5, 10932.	1.6	88
65	Quantitative Interactor Screening with next-generation Sequencing (QIS-Seq) identifies <i>Arabidopsis thaliana</i> MLO2 as a target of the <i>Pseudomonas syringae</i> type III effector HopZ2. <i>BMC Genomics</i> , 2012, 13, 8.	1.2	85
66	Metabolic Reprogramming by Hexosamine Biosynthetic and Golgi N-Glycan Branching Pathways. <i>Scientific Reports</i> , 2016, 6, 23043.	1.6	84
67	Bioinformatics-Enabled Identification of the HrpL Regulon and Type III Secretion System Effector Proteins of <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1193-1206.	1.4	81
68	Identification of innate immunity elicitors using molecular signatures of natural selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4215-4220.	3.3	81
69	Characterization of the Gut-Associated Microbiome in Inflammatory Pouch Complications Following Ileal Pouch-Anal Anastomosis. <i>PLoS ONE</i> , 2013, 8, e66934.	1.1	77
70	Complete Sequence and Evolutionary Genomic Analysis of the <i>Pseudomonas aeruginosa</i> Transposable Bacteriophage D3112. <i>Journal of Bacteriology</i> , 2004, 186, 400-410.	1.0	74
71	Chloroplast sequence variation and the efficacy of peptide nucleic acids for blocking host amplification in plant microbiome studies. <i>Microbiome</i> , 2018, 6, 144.	4.9	74
72	<i>Bacteroides</i> -dominant gut microbiome of late infancy is associated with enhanced neurodevelopment. <i>Gut Microbes</i> , 2021, 13, 1-17.	4.3	74

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73	Global Analysis of the Fungal Microbiome in Cystic Fibrosis Patients Reveals Loss of Function of the Transcriptional Repressor Nrg1 as a Mechanism of Pathogen Adaptation. <i>PLoS Pathogens</i> , 2015, 11, e1005308.	2.1	74
74	The YopJ superfamily in plant-associated bacteria. <i>Molecular Plant Pathology</i> , 2011, 12, 928-937.	2.0	71
75	Evolution of prokaryotic and eukaryotic virulence effectors. <i>Current Opinion in Plant Biology</i> , 2008, 11, 412-419.	3.5	69
76	Cesarean Section, Formula Feeding, and Infant Antibiotic Exposure: Separate and Combined Impacts on Gut Microbial Changes in Later Infancy. <i>Frontiers in Pediatrics</i> , 2017, 5, 200.	0.9	69
77	Diversifying Selection Drives the Evolution of the Type III Secretion System Pilus of <i>Pseudomonas syringae</i> . <i>Molecular Biology and Evolution</i> , 2006, 23, 2342-2354.	3.5	68
78	Determinants of Divergent Adaptation and Dobzhansky-Muller Interaction in Experimental Yeast Populations. <i>Current Biology</i> , 2010, 20, 1383-1388.	1.8	68
79	The targeting of plant cellular systems by injected type III effector proteins. <i>Seminars in Cell and Developmental Biology</i> , 2009, 20, 1055-1063.	2.3	67
80	Extensive remodeling of the <i>Pseudomonas syringae</i> pv. <i>avellanae</i> type III secretome associated with two independent host shifts onto hazelnut. <i>BMC Microbiology</i> , 2012, 12, 141.	1.3	67
81	Disruption of the Murine Glp2r Impairs Paneth Cell Function and Increases Susceptibility to Small Bowel Enteritis. <i>Endocrinology</i> , 2012, 153, 1141-1151.	1.4	65
82	Nucleotide Sequence and Evolution of the Five-Plasmid Complement of the Phytopathogen <i>Pseudomonas syringae</i> pv. <i>maculicola</i> ES4326. <i>Journal of Bacteriology</i> , 2004, 186, 5101-5115.	1.0	64
83	Genomic screens identify a new phyto-bacterial microbe-associated molecular pattern and the cognate Arabidopsis receptor-like kinase that mediates its immune elicitation. <i>Genome Biology</i> , 2016, 17, 98.	3.8	62
84	Microbiome networks and change-point analysis reveal key community changes associated with cystic fibrosis pulmonary exacerbations. <i>Npj Biofilms and Microbiomes</i> , 2019, 5, 4.	2.9	58
85	Limiting oxidative DNA damage reduces microbe-induced colitis-associated colorectal cancer. <i>Nature Communications</i> , 2020, 11, 1802.	5.8	58
86	The <i>Pseudomonas syringae</i> Type III Effector HopF2 Suppresses Arabidopsis Stomatal Immunity. <i>PLoS ONE</i> , 2014, 9, e114921.	1.1	57
87	Recombination and clonality in natural populations of <i>Escherichia coli</i> . <i>Trends in Ecology and Evolution</i> , 1997, 12, 16-22.	4.2	56
88	Allelic Variants of the <i>Pseudomonas syringae</i> Type III Effector HopZ1 Are Differentially Recognized by Plant Resistance Systems. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 176-189.	1.4	56
89	HopZ4 from <i>Pseudomonas syringae</i> , a Member of the HopZ Type III Effector Family from the YopJ Superfamily, Inhibits the Proteasome in Plants. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 611-623.	1.4	56
90	Immunomodulation by the <i>Pseudomonas syringae</i> HopZ Type III Effector Family in Arabidopsis. <i>PLoS ONE</i> , 2014, 9, e116152.	1.1	56

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91	Phytopathogen Genome Announcement: Draft Genome Sequences of 62 <i>Pseudomonas syringae</i> Type and Pathotype Strains. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 243-246.	1.4	55
92	Analysis of the Cystic Fibrosis Lung Microbiota via Serial Illumina Sequencing of Bacterial 16S rRNA Hypervariable Regions. <i>PLoS ONE</i> , 2012, 7, e45791.	1.1	54
93	Image-Based Quantification of Plant Immunity and Disease. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 919-924.	1.4	54
94	Using a Commercial DiversiLab Semiautomated Repetitive Sequence-Based PCR Typing Technique for Identification of <i>Escherichia coli</i> Clone ST131 Producing CTX-M-15. <i>Journal of Clinical Microbiology</i> , 2009, 47, 1212-1215.	1.8	53
95	Comparative genomic analysis of multiple strains of two unusual plant pathogens: <i>Pseudomonas corrugata</i> and <i>Pseudomonas mediterranea</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 811.	1.5	50
96	Associations between bacterial communities of house dust and infant gut. <i>Environmental Research</i> , 2014, 131, 25-30.	3.7	49
97	Impact of Immunosuppression on the Metagenomic Composition of the Intestinal Microbiome: a Systems Biology Approach to Post-Transplant Diabetes. <i>Scientific Reports</i> , 2017, 7, 10277.	1.6	49
98	Comparison of three typing methods for <i>Pseudomonas aeruginosa</i> isolates from patients with cystic fibrosis. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2012, 31, 3341-3350.	1.3	46
99	Postnatal exposure to household disinfectants, infant gut microbiota and subsequent risk of overweight in children. <i>Cmaj</i> , 2018, 190, E1097-E1107.	0.9	46
100	Elevated Temperature Differentially Influences Effector-Triggered Immunity Outputs in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 995.	1.7	44
101	Perturbations of the ZED1 pseudokinase activate plant immunity. <i>PLoS Pathogens</i> , 2019, 15, e1007900.	2.1	43
102	Peptides and small molecules of the plant-pathogen apoplastic arena. <i>Frontiers in Plant Science</i> , 2014, 5, 677.	1.7	37
103	Mediterranean-Like Dietary Pattern Associations With Gut Microbiome Composition and Subclinical Gastrointestinal Inflammation. <i>Gastroenterology</i> , 2022, 163, 685-698.	0.6	37
104	Next-generation genomics of <i>Pseudomonas syringae</i> . <i>Current Opinion in Microbiology</i> , 2011, 14, 24-30.	2.3	35
105	Identification and analysis of seven effector protein families with different adaptive and evolutionary histories in plant-associated members of the Xanthomonadaceae. <i>Scientific Reports</i> , 2017, 7, 16133.	1.6	35
106	Mycobiome Sequencing and Analysis Applied to Fungal Community Profiling of the Lower Respiratory Tract During Fungal Pathogenesis. <i>Frontiers in Microbiology</i> , 2019, 10, 512.	1.5	34
107	Chronic infection phenotypes of <i>Pseudomonas aeruginosa</i> are associated with failure of eradication in children with cystic fibrosis. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2016, 35, 67-74.	1.3	33
108	FUT2 genotype and secretory status are not associated with fecal microbial composition and inferred function in healthy subjects. <i>Gut Microbes</i> , 2018, 9, 1-12.	4.3	33

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109	Immunodiversity of the Arabidopsis ZAR1 NLR Is Conveyed by Receptor-Like Cytoplasmic Kinase Sensors. <i>Frontiers in Plant Science</i> , 2020, 11, 1290.	1.7	33
110	HopAS1 recognition significantly contributes to Arabidopsis nonhost resistance to <i>Pseudomonas syringae</i> pathogens. <i>New Phytologist</i> , 2012, 193, 58-66.	3.5	32
111	Ecological Succession of Polymicrobial Communities in the Cystic Fibrosis Airways. <i>MSystems</i> , 2020, 5, .	1.7	32
112	Constructing and Analyzing Microbiome Networks in R. <i>Methods in Molecular Biology</i> , 2018, 1849, 243-266.	0.4	31
113	From Birth to Overweight and Atopic Disease: Multiple and Common Pathways of the Infant Gut Microbiome. <i>Gastroenterology</i> , 2021, 160, 128-144.e10.	0.6	31
114	Natural environments in the urban context and gut microbiota in infants. <i>Environment International</i> , 2020, 142, 105881.	4.8	30
115	Diversification of <i>Pseudomonas aeruginosa</i> within the cystic fibrosis lung and its effects on antibiotic resistance. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	29
116	Proteomics of effector-triggered immunity (ETI) in plants. <i>Virulence</i> , 2014, 5, 752-760.	1.8	28
117	A genome-wide association analysis reveals a potential role for recombination in the evolution of antimicrobial resistance in <i>Burkholderia multivorans</i> . <i>PLoS Pathogens</i> , 2018, 14, e1007453.	2.1	28
118	Convergent evolution of phytopathogenic pseudomonads onto hazelnut. <i>Microbiology (United Kingdom)</i> , 2019, 159, 1027-1037.	0.7	27
119	High fecal IgA is associated with reduced <i>Clostridium difficile</i> colonization in infants. <i>Microbes and Infection</i> , 2016, 18, 543-549.	1.0	26
120	The HopF family of <i>Pseudomonas syringae</i> type III secreted effectors. <i>Molecular Plant Pathology</i> , 2017, 18, 457-468.	2.0	26
121	The ETS-ETI cycle: evolutionary processes and metapopulation dynamics driving the diversification of pathogen effectors and host immune factors. <i>Current Opinion in Plant Biology</i> , 2021, 62, 102011.	3.5	26
122	Gut microbiota diversity and atopic disease: Does breast-feeding play a role?. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 131, 247-248.	1.5	24
123	A High-Sensitivity, Microtiter-Based Plate Assay for Plant Pattern-Triggered Immunity. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 499-504.	1.4	24
124	Plants as models for the study of human pathogenesis. <i>Biotechnology Advances</i> , 2004, 22, 363-382.	6.0	23
125	<i>Clostridioides difficile</i> Colonization Is Differentially Associated With Gut Microbiome Profiles by Infant Feeding Modality at 4 Months of Age. <i>Frontiers in Immunology</i> , 2019, 10, 2866.	2.2	22
126	Conservation and stewardship of the human microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14312-14313.	3.3	21

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127	Analysis of Genetic Association of Intestinal Permeability in Healthy First-degree Relatives of Patients with Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2019, 25, 1796-1804.	0.9	21
128	Penicillin-binding protein 3 is a common adaptive target among <i>Pseudomonas aeruginosa</i> isolates from adult cystic fibrosis patients treated with β -lactams. <i>International Journal of Antimicrobial Agents</i> , 2019, 53, 620-628.	1.1	21
129	A Phylogenomic Analysis of the Shikimate Dehydrogenases Reveals Broad-scale Functional Diversification and Identifies One Functionally Distinct Subclass. <i>Molecular Biology and Evolution</i> , 2008, 25, 2221-2232.	3.5	20
130	Phytopathogen type III effectors as probes of biological systems. <i>Microbial Biotechnology</i> , 2013, 6, 230-240.	2.0	20
131	Identifying <i>Pseudomonas syringae</i> Type III Secreted Effector Function via a Yeast Genomic Screen. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 535-547.	0.8	20
132	Sex-specific impact of asthma during pregnancy on infant gut microbiota. <i>European Respiratory Journal</i> , 2017, 50, 1700280.	3.1	20
133	Pulmonary Bacterial Communities in Surgically Resected Noncystic Fibrosis Bronchiectasis Lungs Are Similar to Those in Cystic Fibrosis. <i>Pulmonary Medicine</i> , 2012, 2012, 1-9.	0.5	19
134	Transitions in oral and gut microbiome of HPV+ oropharyngeal squamous cell carcinoma following definitive chemoradiotherapy (ROMA LA-OPSCC study). <i>British Journal of Cancer</i> , 2021, 124, 1543-1551.	2.9	19
135	Diversity, Evolution, and Function of <i>Pseudomonas syringae</i> Effectoromes. <i>Annual Review of Phytopathology</i> , 2022, 60, 211-236.	3.5	19
136	Design and application of a novel two-amplicon approach for defining eukaryotic microbiota. <i>Microbiome</i> , 2018, 6, 228.	4.9	18
137	A practical assessment of nano-phosphate on soybean (<i>Glycine max</i>) growth and microbiome establishment. <i>Scientific Reports</i> , 2020, 10, 9151.	1.6	18
138	The role of Psl in the failure to eradicate <i>Pseudomonas aeruginosa</i> biofilms in children with cystic fibrosis. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 63.	2.9	18
139	A De-Novo Genome Analysis Pipeline (DeNoGAP) for large-scale comparative prokaryotic genomics studies. <i>BMC Bioinformatics</i> , 2016, 17, 260.	1.2	17
140	Map of physical interactions between extracellular domains of <i>Arabidopsis</i> leucine-rich repeat receptor kinases. <i>Scientific Data</i> , 2019, 6, 190025.	2.4	17
141	Micronutrient supplements can promote disruptive protozoan and fungal communities in the developing infant gut. <i>Nature Communications</i> , 2021, 12, 6729.	5.8	17
142	The rise of the undead. <i>Plant Signaling and Behavior</i> , 2014, 9, e27563.	1.2	16
143	Vitamin D supplementation in pregnancy and early infancy in relation to gut microbiota composition and <i>C. difficile</i> colonization: implications for viral respiratory infections. <i>Gut Microbes</i> , 2020, 12, 1799734.	4.3	16
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