

David Guttman

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

185
papers

11,989
citations

63
h-index

106
g-index

204
ext. papers

15,285
ext. citations

8.1
avg. IF

6.5
L-index

#	Paper	IF	Citations
185	RecPD: A Recombination-aware measure of phylogenetic diversity.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009899	5	0
184	The Arabidopsis effector-triggered immunity landscape is conserved in oilseed crops.. <i>Scientific Reports</i> , 2022 , 12, 6534	4.9	0
183	Metaeffector interactions modulate the type III effector-triggered immunity load of <i>Pseudomonas syringae</i> .. <i>PLoS Pathogens</i> , 2022 , 18, e1010541	7.6	0
182	<i>Pseudomonas aeruginosa</i> Strain-sharing in Early Infection Among Children With Cystic Fibrosis. <i>Clinical Infectious Diseases</i> , 2021 , 73, e2521-e2528	11.6	6
181	Characterization and predictive functional profiles on metagenomic 16S rRNA data of liver transplant recipients: A longitudinal study. <i>Clinical Transplantation</i> , 2021 , 36, e14534	3.8	0
180	Micronutrient supplements can promote disruptive protozoan and fungal communities in the developing infant gut. <i>Nature Communications</i> , 2021 , 12, 6729	17.4	3
179	The small molecule Zareactin activates ZAR1-mediated immunity in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	1
178	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	8.7	7
177	Evaluation of digital dispense-assisted broth microdilution antimicrobial susceptibility testing for <i>Pseudomonas aeruginosa</i> isolates. <i>Scientific Reports</i> , 2021 , 11, 9157	4.9	1
176	Ethnicity Associations With Food Sensitization Are Mediated by Gut Microbiota Development in the First Year of Life. <i>Gastroenterology</i> , 2021 , 161, 94-106	13.3	5
175	From Birth to Overweight and Atopic Disease: Multiple and Common Pathways of the Infant Gut Microbiome. <i>Gastroenterology</i> , 2021 , 160, 128-144.e10	13.3	8
174	<i>Bacteroides</i> -dominant gut microbiome of late infancy is associated with enhanced neurodevelopment. <i>Gut Microbes</i> , 2021 , 13, 1-17	8.8	12
173	The Impact of Migration on the Gut Metagenome of South Asian Canadians. <i>Gut Microbes</i> , 2021 , 13, 1-298.8		1
172	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	9.9	6
171	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	8.2	2
170	Diversity and Evolution of Type III Secreted Effectors: A Case Study of Three Families. <i>Current Topics in Microbiology and Immunology</i> , 2020 , 427, 201-230	3.3	5
169	A practical assessment of nano-phosphate on soybean (<i>Glycine max</i>) growth and microbiome establishment. <i>Scientific Reports</i> , 2020 , 10, 9151	4.9	7

168	Natural environments in the urban context and gut microbiota in infants. <i>Environment International</i> , 2020 , 142, 105881	12.9	14
167	Population genomics of Vibrionaceae isolated from an endangered oasis reveals local adaptation after an environmental perturbation. <i>BMC Genomics</i> , 2020 , 21, 418	4.5	5
166	The pan-genome effector-triggered immunity landscape of a host-pathogen interaction. <i>Science</i> , 2020 , 367, 763-768	33.3	70
165	Accumulation of genetic variants associated with immunity in the selective breeding of broilers. <i>BMC Genetics</i> , 2020 , 21, 5	2.6	2
164	Limiting oxidative DNA damage reduces microbe-induced colitis-associated colorectal cancer. <i>Nature Communications</i> , 2020 , 11, 1802	17.4	24
163	Ecological Succession of Polymicrobial Communities in the Cystic Fibrosis Airways. <i>MSystems</i> , 2020 , 5,	7.6	12
162	A High-Throughput, Seedling Screen for Plant Immunity. <i>Molecular Plant-Microbe Interactions</i> , 2020 , 33, 394-401	3.6	3
161	Assessment of Inter-Laboratory Variation in the Characterization and Analysis of the Mucosal Microbiota in Crohn's Disease and Ulcerative Colitis. <i>Frontiers in Microbiology</i> , 2020 , 11, 2028	5.7	3
160	Immunodiversity of the ZAR1 NLR Is Conveyed by Receptor-Like Cytoplasmic Kinase Sensors. <i>Frontiers in Plant Science</i> , 2020 , 11, 1290	6.2	15
159	Associations of NOD2 polymorphisms with Erysipelotrichaceae in stool of in healthy first degree relatives of Crohn's disease subjects. <i>BMC Medical Genetics</i> , 2020 , 21, 204	2.1	3
158	The Arabidopsis ZED1-Related Kinase Genomic Cluster Is Specifically Required for Effector-Triggered Immunity. <i>Plant Physiology</i> , 2020 , 184, 1635-1639	6.6	0
157	Increased Intestinal Permeability Is Associated With Later Development of Crohn's Disease. <i>Gastroenterology</i> , 2020 , 159, 2092-2100.e5	13.3	53
156	Vitamin D supplementation in pregnancy and early infancy in relation to gut microbiota composition and colonization: implications for viral respiratory infections. <i>Gut Microbes</i> , 2020 , 12, 1799-1814	8.8	6
155	Evolutionary and structural analyses of SARS-CoV-2 D614G spike protein mutation now documented worldwide. <i>Scientific Reports</i> , 2020 , 10, 14031	4.9	120
154	Continuing towards optimization of bladder cancer care in Canada: Summary of the third Bladder Cancer Canada-Canadian Urological Association-Canadian Urologic Oncology Group (BCC-CUA-CUOG) bladder cancer quality of care consensus meeting. <i>Canadian Urological Association Journal</i> , 2020 , 14, E115-E125	1.2	1
153	Penicillin-binding protein 3 is a common adaptive target among Pseudomonas aeruginosa isolates from adult cystic fibrosis patients treated with beta-lactams. <i>International Journal of Antimicrobial Agents</i> , 2019 , 53, 620-628	14.3	13
152	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	8.2	35
151	Clostridioides Difficile Colonization Is Differentially Associated with Gut Microbiota Composition in Breastfed versus Formula Fed Infants (OR01-02-19). <i>Current Developments in Nutrition</i> , 2019 , 3,	0.4	78

150	Comparison of Co-housing and Littermate Methods for Microbiota Standardization in Mouse Models. <i>Cell Reports</i> , 2019 , 27, 1910-1919.e2	10.6	80
149	Molecular Evolution of Type III Secreted Effector Proteins. <i>Frontiers in Plant Science</i> , 2019 , 10, 418	6.2	44
148	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	5.7	22
147	Gut-associated IgA immune cells regulate obesity-related insulin resistance. <i>Nature Communications</i> , 2019 , 10, 3650	17.4	70
146	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	4.5	10
145	Perturbations of the ZED1 pseudokinase activate plant immunity. <i>PLoS Pathogens</i> , 2019 , 15, e1007900	7.6	23
144	Map of physical interactions between extracellular domains of Arabidopsis leucine-rich repeat receptor kinases. <i>Scientific Data</i> , 2019 , 6, 190025	8.2	2
143	Colonization Is Differentially Associated With Gut Microbiome Profiles by Infant Feeding Modality at 3-4 Months of Age. <i>Frontiers in Immunology</i> , 2019 , 10, 2866	8.4	9
142	Identifying Type III Secreted Effector Function via a Yeast Genomic Screen. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 535-547	3.2	8
141	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	18.3	45
140	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, 368-377	8.3	144
139	Diversification of <i>Pseudomonas aeruginosa</i> within the cystic fibrosis lung and its effects on antibiotic resistance. <i>FEMS Microbiology Letters</i> , 2018 , 365,	2.9	13
138	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	11.5	401
137	An extracellular network of Arabidopsis leucine-rich repeat receptor kinases. <i>Nature</i> , 2018 , 553, 342-346	50.4	137
136	FUT2 genotype and secretory status are not associated with fecal microbial composition and inferred function in healthy subjects. <i>Gut Microbes</i> , 2018 , 9, 357-368	8.8	27
135	Chloroplast sequence variation and the efficacy of peptide nucleic acids for blocking host amplification in plant microbiome studies. <i>Microbiome</i> , 2018 , 6, 144	16.6	34
134	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	8.3	121
133	Structural and biochemical approaches uncover multiple evolutionary trajectories of plant quinate dehydrogenases. <i>Plant Journal</i> , 2018 , 95, 812	6.9	7

132	A High-Sensitivity, Microtiter-Based Plate Assay for Plant Pattern-Triggered Immunity. <i>Molecular Plant-Microbe Interactions</i> , 2018 , 31, 499-504	3.6	13
131	Design and application of a novel two-amplicon approach for defining eukaryotic microbiota. <i>Microbiome</i> , 2018 , 6, 228	16.6	8
130	A genome-wide association analysis reveals a potential role for recombination in the evolution of antimicrobial resistance in Burkholderia multivorans. <i>PLoS Pathogens</i> , 2018 , 14, e1007453	7.6	11
129	Constructing and Analyzing Microbiome Networks in R. <i>Methods in Molecular Biology</i> , 2018 , 1849, 243-266	6.4	15
128	Postnatal exposure to household disinfectants, infant gut microbiota and subsequent risk of overweight in children. <i>Cmaj</i> , 2018 , 190, E1097-E1107	3.5	29
127	Epidemiology of Clonal Pseudomonas aeruginosa Infection in a Canadian Cystic Fibrosis Population. <i>Annals of the American Thoracic Society</i> , 2018 , 15, 827-836	4.7	8
126	Population genomics of bacterial host adaptation. <i>Nature Reviews Genetics</i> , 2018 , 19, 549-565	30.1	105
125	The HopF family of Pseudomonas syringae type III secreted effectors. <i>Molecular Plant Pathology</i> , 2017 , 18, 457-468	5.7	14
124	Navigating social and ethical challenges of biobanking for human microbiome research. <i>BMC Medical Ethics</i> , 2017 , 18, 1	2.9	53
123	Disentangling Interactions in the Microbiome: A Network Perspective. <i>Trends in Microbiology</i> , 2017 , 25, 217-228	12.4	327
122	Exposure to household furry pets influences the gut microbiota of infant at 3-4 months following various birth scenarios. <i>Microbiome</i> , 2017 , 5, 40	16.6	126
121	Expanded type III effector recognition by the ZAR1 NLR protein using ZED1-related kinases. <i>Nature Plants</i> , 2017 , 3, 17027	11.5	62
120	interaction with biofilm enhances tobramycin resistance. <i>Npj Biofilms and Microbiomes</i> , 2017 , 3, 25	8.2	67
119	Draft Genome Sequences of 10 Environmental Strains Isolated from Soils, Sediments, and Waters. <i>Genome Announcements</i> , 2017 , 5,		4
118	A Practical Guide to Quantitative Interactor Screening with Next-Generation Sequencing (QIS-Seq). <i>Methods in Molecular Biology</i> , 2017 , 1613, 1-20	1.4	1
117	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	4.9	32
116	The study of pattern-triggered immunity in Arabidopsis. <i>Canadian Journal of Plant Pathology</i> , 2017 , 39, 275-281	1.6	1
115	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	4.9	17

114	Evolution, genomics and epidemiology of <i>Pseudomonas syringae</i> : Challenges in Bacterial Molecular Plant Pathology. <i>Molecular Plant Pathology</i> , 2017 , 18, 152-168	5.7	71
113	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	11.6	110
112	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	3.4	50
111	Sex-specific impact of asthma during pregnancy on infant gut microbiota. <i>European Respiratory Journal</i> , 2017 , 50,	13.6	15
110	Topo-phylogeny: Visualizing evolutionary relationships on a topographic landscape. <i>PLoS ONE</i> , 2017 , 12, e0175895	3.7	4
109	Gene Slider: sequence logo interactive data-visualization for education and research. <i>Bioinformatics</i> , 2016 , 32, 3670-3672	7.2	3
108	Phytopathogen Genome Announcement: Draft Genome Sequences of 62 <i>Pseudomonas syringae</i> Type and Pathotype Strains. <i>Molecular Plant-Microbe Interactions</i> , 2016 , 29, 243-6	3.6	27
107	NIN-like protein 8 is a master regulator of nitrate-promoted seed germination in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2016 , 7, 13179	17.4	95
106	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	5.3	62
105	A De-Novo Genome Analysis Pipeline (DeNoGAP) for large-scale comparative prokaryotic genomics studies. <i>BMC Bioinformatics</i> , 2016 , 17, 260	3.6	14
104	86 Association of Environmental Exposures With the Composition and Diversity of the Human Gut Microbiome in Healthy First Degree Relatives (FDR) of Crohn's Patients. <i>Gastroenterology</i> , 2016 , 150, S21-S22	13.3	2
103	Genomic screens identify a new phyto-bacterial microbe-associated molecular pattern and the cognate <i>Arabidopsis</i> receptor-like kinase that mediates its immune elicitation. <i>Genome Biology</i> , 2016 , 17, 98	18.3	48
102	Prophages mediate defense against phage infection through diverse mechanisms. <i>ISME Journal</i> , 2016 , 10, 2854-2866	11.9	176
101	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, 983-93	3.7	328
100	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	5.3	25
99	Metabolic Reprogramming by Hexosamine Biosynthetic and Golgi N-Glycan Branching Pathways. <i>Scientific Reports</i> , 2016 , 6, 23043	4.9	52
98	Image-Based Quantification of Plant Immunity and Disease. <i>Molecular Plant-Microbe Interactions</i> , 2016 , 29, 919-924	3.6	30
97	High fecal IgA is associated with reduced <i>Clostridium difficile</i> colonization in infants. <i>Microbes and Infection</i> , 2016 , 18, 543-9	9.3	18

96	Association of host genome with intestinal microbial composition in a large healthy cohort. <i>Nature Genetics</i> , 2016 , 48, 1413-1417	36.3	257
95	Regulation of obesity-related insulin resistance with gut anti-inflammatory agents. <i>Cell Metabolism</i> , 2015 , 21, 527-42	24.6	197
94	The human microbiome. <i>Cmaj</i> , 2015 , 187, 825	3.5	3
93	Selective Sweeps and Parallel Pathoadaptation Drive <i>Pseudomonas aeruginosa</i> Evolution in the Cystic Fibrosis Lung. <i>MBio</i> , 2015 , 6, e00981-15	7.8	83
92	Phenotypic diversity within a <i>Pseudomonas aeruginosa</i> population infecting an adult with cystic fibrosis. <i>Scientific Reports</i> , 2015 , 5, 10932	4.9	60
91	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	5.7	25
90	Elevated Temperature Differentially Influences Effector-Triggered Immunity Outputs in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2015 , 6, 995	6.2	25
89	Lung microbiota across age and disease stage in cystic fibrosis. <i>Scientific Reports</i> , 2015 , 5, 10241	4.9	226
88	Seasonal community succession of the phyllosphere microbiome. <i>Molecular Plant-Microbe Interactions</i> , 2015 , 28, 274-85	3.6	166
87	Infant gut microbiota and food sensitization: associations in the first year of life. <i>Clinical and Experimental Allergy</i> , 2015 , 45, 632-43	4.1	237
86	Genomic and Gene-Expression Comparisons among Phage-Resistant Type-IV Pilus Mutants of <i>Pseudomonas syringae</i> pathovar phaseolicola. <i>PLoS ONE</i> , 2015 , 10, e0144514	3.7	8
85	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	7.6	54
84	Next-generation mapping of genetic mutations using bulk population sequencing. <i>Methods in Molecular Biology</i> , 2014 , 1062, 301-15	1.4	8
83	Opinion: Conservation and stewardship of the human microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 14312-3	11.5	16
82	Microbial genome-enabled insights into plant-microorganism interactions. <i>Nature Reviews Genetics</i> , 2014 , 15, 797-813	30.1	135
81	Gut microbial metabolism drives transformation of MSH2-deficient colon epithelial cells. <i>Cell</i> , 2014 , 158, 288-299	56.2	283
80	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, 611-23	3.6	38
79	Genomic Analysis of Plant Pathogenic Bacteria 2014 , 392-418		1

78	The rise of the undead: pseudokinases as mediators of effector-triggered immunity. <i>Plant Signaling and Behavior</i> , 2014 , 9, e27563	2.5	13
77	Peptides and small molecules of the plant-pathogen apoplastic arena. <i>Frontiers in Plant Science</i> , 2014 , 5, 677	6.2	31
76	Proteomics of effector-triggered immunity (ETI) in plants. <i>Virulence</i> , 2014 , 5, 752-60	4.7	12
75	Associations between bacterial communities of house dust and infant gut. <i>Environmental Research</i> , 2014 , 131, 25-30	7.9	38
74	The <i>Pseudomonas syringae</i> type III effector HopF2 suppresses <i>Arabidopsis</i> stomatal immunity. <i>PLoS ONE</i> , 2014 , 9, e114921	3.7	44
73	Immunomodulation by the <i>Pseudomonas syringae</i> HopZ type III effector family in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2014 , 9, e116152	3.7	27
72	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	3.2	172
71	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, 18722-7	11.5	121
70	Gut microbiota diversity and atopic disease: does breast-feeding play a role?. <i>Journal of Allergy and Clinical Immunology</i> , 2013 , 131, 247-8	11.5	20
69	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	7.6	165
68	Neutral genomic microevolution of a recently emerged pathogen, <i>Salmonella enterica</i> serovar Agona. <i>PLoS Genetics</i> , 2013 , 9, e1003471	6	75
67	Phytopathogen type III effectors as probes of biological systems. <i>Microbial Biotechnology</i> , 2013 , 6, 230-40	3	18
66	Gut microbiota of healthy Canadian infants: profiles by mode of delivery and infant diet at 4 months. <i>Cmaj</i> , 2013 , 185, 385-94	3.5	604
65	Characterization of the gut-associated microbiome in inflammatory pouch complications following ileal pouch-anal anastomosis. <i>PLoS ONE</i> , 2013 , 8, e66934	3.7	63
64	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	4.5	56
63	E622, a miniature, virulence-associated mobile element. <i>Journal of Bacteriology</i> , 2012 , 194, 509-17	3.5	11
62	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, 3341-50	5.3	42
61	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	4.5	41

60	Forward chemical genetic screens in Arabidopsis identify genes that influence sensitivity to the phytotoxic compound sulfamethoxazole. <i>BMC Plant Biology</i> , 2012 , 12, 226	5.3	12
59	<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	3.7	102
58	HopAS1 recognition significantly contributes to Arabidopsis nonhost resistance to <i>Pseudomonas syringae</i> pathogens. <i>New Phytologist</i> , 2012 , 193, 58-66	9.8	28
57	A bacterial acetyltransferase destroys plant microtubule networks and blocks secretion. <i>PLoS Pathogens</i> , 2012 , 8, e1002523	7.6	116
56	Disruption of the murine Glp2r impairs Paneth cell function and increases susceptibility to small bowel enteritis. <i>Endocrinology</i> , 2012 , 153, 1141-51	4.8	59
55	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, 4215-20	11.5	73
54	Pulmonary bacterial communities in surgically resected noncystic fibrosis bronchiectasis lungs are similar to those in cystic fibrosis. <i>Pulmonary Medicine</i> , 2012 , 2012, 746358	5.3	15
53	Analysis of the cystic fibrosis lung microbiota via serial Illumina sequencing of bacterial 16S rRNA hypervariable regions. <i>PLoS ONE</i> , 2012 , 7, e45791	3.7	40
52	Next-generation genomics of <i>Pseudomonas syringae</i> . <i>Current Opinion in Microbiology</i> , 2011 , 14, 24-30	7.9	30
51	Evolution of plant pathogenesis in <i>Pseudomonas syringae</i> : a genomics perspective. <i>Annual Review of Phytopathology</i> , 2011 , 49, 269-89	10.8	76
50	Next-generation mapping of Arabidopsis genes. <i>Plant Journal</i> , 2011 , 67, 715-25	6.9	228
49	The YopJ superfamily in plant-associated bacteria. <i>Molecular Plant Pathology</i> , 2011 , 12, 928-37	5.7	59
48	Transcriptomic responses of the softwood-degrading white-rot fungus <i>Phanerochaete carnos</i> a during growth on coniferous and deciduous wood. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 3211-8	4.8	92
47	Tri6 is a global transcription regulator in the phytopathogen <i>Fusarium graminearum</i> . <i>PLoS Pathogens</i> , 2011 , 7, e1002266	7.6	85
46	Use of low-coverage, large-insert, short-read data for rapid and accurate generation of enhanced-quality draft <i>Pseudomonas</i> genome sequences. <i>PLoS ONE</i> , 2011 , 6, e27199	3.7	3
45	Population Genomics of Bacteria 2010 , 121-151		3
44	PAMDB, a multilocus sequence typing and analysis database and website for plant-associated microbes. <i>Phytopathology</i> , 2010 , 100, 208-15	3.8	134
43	Allele-specific virulence attenuation of the <i>Pseudomonas syringae</i> HopZ1a type III effector via the Arabidopsis ZAR1 resistance protein. <i>PLoS Genetics</i> , 2010 , 6, e1000894	6	103

42	Pseudomonas syringae strains naturally lacking the classical P. syringae 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	3.6	74
41	Determinants of divergent adaptation and Dobzhansky-Muller interaction in experimental yeast populations. <i>Current Biology</i> , 2010 , 20, 1383-8	6.3	58
40	Using a commercial DiversiLab semiautomated repetitive sequence-based PCR typing technique for identification of Escherichia coli clone ST131 producing CTX-M-15. <i>Journal of Clinical Microbiology</i> , 2009 , 47, 1212-5	9.7	53
39	Bacterial evolution: dynamic genomes and the power of transformation. <i>Current Biology</i> , 2009 , 19, R857-63	9.3	1
38	The targeting of plant cellular systems by injected type III effector proteins. <i>Seminars in Cell and Developmental Biology</i> , 2009 , 20, 1055-63	7.5	52
37	Allelic variants of the Pseudomonas syringae type III effector HopZ1 are differentially recognized by plant resistance systems. <i>Molecular Plant-Microbe Interactions</i> , 2009 , 22, 176-89	3.6	40
36	Evolution of the type III secretion system and its effectors in plant-microbe interactions. <i>New Phytologist</i> , 2008 , 177, 33-47	9.8	92
35	Evolution of prokaryotic and eukaryotic virulence effectors. <i>Current Opinion in Plant Biology</i> , 2008 , 11, 412-9	9.9	63
34	Evolution of the Core Genome of Pseudomonas syringae , a Highly Clonal, Endemic Plant Pathogen. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 1961-1961	4.8	1
33	New and sensitive assay for determining Pseudomonas aeruginosa metallo-beta-lactamase resistance to imipenem. <i>Journal of Clinical Microbiology</i> , 2008 , 46, 1870-2	9.7	9
32	A phylogenomic analysis of the shikimate dehydrogenases reveals broadscale functional diversification and identifies one functionally distinct subclass. <i>Molecular Biology and Evolution</i> , 2008 , 25, 2221-32	8.3	18
31	The HopZ family of Pseudomonas syringae type III effectors require myristoylation for virulence and avirulence functions in Arabidopsis thaliana. <i>Journal of Bacteriology</i> , 2008 , 190, 2880-91	3.5	76
30	Host-pathogen interplay and the evolution of bacterial effectors. <i>Cellular Microbiology</i> , 2008 , 10, 285-92	3.9	79
29	Convergent evolution of phytopathogenic pseudomonads onto hazelnut. <i>Microbiology (United Kingdom)</i> , 2007 , 153, 2067-2073	2.9	23
28	Terminal reassortment drives the quantum evolution of type III effectors in bacterial pathogens. <i>PLoS Pathogens</i> , 2006 , 2, e104	7.6	94
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	6	152
26	Diversifying selection drives the evolution of the type III secretion system pilus of Pseudomonas syringae. <i>Molecular Biology and Evolution</i> , 2006 , 23, 2342-54	8.3	63
25	Comparative genomics of host-specific virulence in Pseudomonas syringae. <i>Genetics</i> , 2006 , 174, 1041-564		117

24	Bioinformatics-enabled identification of the HrpL regulon and type III secretion system effector proteins of <i>Pseudomonas syringae</i> pv. phaseolicola 1448A. <i>Molecular Plant-Microbe Interactions</i> , 2006 , 19, 1193-206	3.6	77
23	Phylogenetic characterization of virulence and resistance phenotypes of <i>Pseudomonas syringae</i> . <i>Applied and Environmental Microbiology</i> , 2005 , 71, 5182-91	4.8	208
22	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, 275-82	3.6	119
21	Complete sequence and evolutionary genomic analysis of the <i>Pseudomonas aeruginosa</i> transposable bacteriophage D3112. <i>Journal of Bacteriology</i> , 2004 , 186, 400-10	3.5	69
20	Nucleotide sequence and evolution of the five-plasmid complement of the phytopathogen <i>Pseudomonas syringae</i> pv. maculicola ES4326. <i>Journal of Bacteriology</i> , 2004 , 186, 5101-15	3.5	42
19	Mosaic evolution of the severe acute respiratory syndrome coronavirus. <i>Journal of Virology</i> , 2004 , 78, 76-82	6.6	122
18	Diverse evolutionary mechanisms shape the type III effector virulence factor repertoire in the plant pathogen <i>Pseudomonas syringae</i> . <i>Genetics</i> , 2004 , 167, 1341-60	4	90
17	The PCR amplification and characterization of entire <i>Pseudomonas syringae</i> hrp/hrc clusters. <i>Molecular Plant Pathology</i> , 2004 , 5, 137-40	5.7	6
16	Plants as models for the study of human pathogenesis. <i>Biotechnology Advances</i> , 2004 , 22, 363-82	17.8	20
15	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	4.8	336
14	A functional screen for the type III (Hrp) secretome of the plant pathogen <i>Pseudomonas syringae</i> . <i>Science</i> , 2002 , 295, 1722-6	33.3	326
13	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, 145-55	3.6	126
12	The gain-of-function <i>Arabidopsis</i> acd6 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, 1695-708	11.6	294
11	An X-linked gene with a degenerate Y-linked homologue in a dioecious plant. <i>Nature</i> , 1998 , 393, 263-6	50.4	120
10	Recombination and clonality in natural populations of <i>Escherichia coli</i> . <i>Trends in Ecology and Evolution</i> , 1997 , 12, 16-22	10.9	41
9	Seeing selection in S allele sequences. <i>Current Biology</i> , 1997 , 7, R34-7	6.3	5
8	Reductions in genetic variation in <i>Drosophila</i> and <i>E. coli</i> caused by selection at linked sites. <i>Journal of Genetics</i> , 1996 , 75, 49-61	1.2	11
7	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, 652-6	9.7	70

6	Clonal divergence in <i>Escherichia coli</i> as a result of recombination, not mutation. <i>Science</i> , 1994 , 266, 1380-1383	3.3	345
5	Detecting selective sweeps in naturally occurring <i>Escherichia coli</i> . <i>Genetics</i> , 1994 , 138, 993-1003	4	93
4	Observations on the Breeding Immigration of Wood Frogs <i>Rana sylvatica</i> Reintroduced in East-central Missouri. <i>American Midland Naturalist</i> , 1991 , 125, 269	0.7	8
3	Population genomics of <i>Vibrionaceae</i> isolated from an endangered oasis reveals local adaptation after an environmental perturbation		1
2	Evolutionary and structural analyses of SARS-CoV-2 D614G spike protein mutation now documented worldwide		5
1	Recombination of ecologically and evolutionarily significant loci maintains genetic cohesion in the <i>Pseudomonas syringae</i> species complex		7